

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:34 ; Search time 35.93 Seconds
(without alignments)
44.781 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQGFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 556

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	72	4	09Y494
2	61	100.0	114	6	097947
3	61	100.0	128	4	09Y6V5
4	61	100.0	129	6	097948
5	53	86.9	97	11	09Z0K2
6	53	86.9	115	11	09Z0K1
7	53	86.9	130	11	09Z0K0
8	41	67.2	207	1	09HLV7
9	39	63.9	786	5	024014
10	39	63.9	803	5	024012
11	38	62.3	205	5	020174
12	38	62.3	235	5	09YBW4
13	38	62.3	257	10	09SUN5
14	38	62.3	293	10	049561
15	38	62.3	496	13	09PV88
16	38	62.3	500	13	09DE99
17	38	62.3	3722	2	098T91
18	38	62.3	3722	2	094873
19	37	60.7	138	2	084949

20	37	60.7	249	1	09V2N2	09v2n2 pyrococcus
21	36	59.0	177	5	09BPN9	09bpn9 caenorhabdi
22	36	59.0	236	5	09NEW8	09new8 caenorhabdi
23	36	59.0	352	12	086283	086283 unidentified
24	36	59.0	373	10	023876	023876 oryza sativ
25	36	59.0	477	3	09UM05	09um05 clavispora
26	36	59.0	550	5	094130	094130 caenorhabdi
27	36	59.0	629	5	045273	045273 caenorhabdi
28	36	59.0	869	2	09F634	09f634 stigmatella
29	35	57.4	128	11	099N14	099n14 mus musculu
30	35	57.4	206	5	061761	061761 caenorhabdi
31	35	57.4	218	2	09LSY0	09lsy0 streptomyce
32	35	57.4	296	10	09LVZ6	09lvz6 arabidopsis
33	35	57.4	297	2	09HV29	09hv29 pseudomonas
34	35	57.4	347	10	040035	040035 hordeum vul
35	35	57.4	424	10	048648	048648 adiantum ca
36	35	57.4	494	2	09C117	09c117 lactococc
37	35	57.4	497	2	09A0V7	09a0v7 streptococ
38	35	57.4	509	12	065191	065191 african swi
39	35	57.4	521	5	018014	018014 caenorhabdi
40	35	57.4	681	5	09G0T4	09g0t4 leishmania
41	35	57.4	682	11	09EST2	09es12 cavia porce
42	35	57.4	832	2	P74619	P74619 synchocyst
43	35	57.4	1043	5	09XTZ0	09xtz0 caenorhabdi
44	35	57.4	1278	4	09UPP5	09upp5 homo sapien
45	35	57.4	1611	10	09SDB6	09sdb6 arabidopsis
46	35	57.4	1736	10	023025	023025 arabidopsis
47	35	56.6	216	10	09CAM3	09cam3 arabidopsis
48	34	55.7	154	11	09JK11	09jk11 mus pahari
49	34	55.7	162	13	P70014	P70014 xenopus lae
50	34	55.7	167	2	09X8G5	09x8g5 streptomyce
51	34	55.7	216	10	09ZSX5	09zxs5 zea mays (m
52	34	55.7	253	2	034788	034788 streptococ
53	34	55.7	266	12	056868	056868 gallia herp
54	34	55.7	270	5	09GUG0	09gug0 caenorhabdi
55	34	55.7	304	6	09GXM6	09gxm6 macaca fasc
56	34	55.7	306	2	09JXY6	09jxy6 neisseria m
57	34	55.7	316	5	076902	076902 drosophila
58	34	55.7	318	2	09JYV5	09jyv5 neisseria m
59	34	55.7	355	8	09M081	09m081 physarum po
60	34	55.7	359	10	082469	082469 mesembryant
61	34	55.7	393	10	049132	049132 diospyros k
62	34	55.7	405	2	09Z5W4	09z5w4 pseudomonas
63	34	55.7	410	8	021172	021172 galapagnus
64	34	55.7	415	3	013352	013352 magnaporthe
65	34	55.7	502	11	006884	006884 rattus norv
66	34	55.7	583	10	041486	041486 solanum tub
67	34	55.7	628	10	09XIC7	09xic7 arabidopsis
68	34	55.7	646	10	09C792	09c792 arabidopsis
69	34	55.7	737	2	09A926	09a926 caulobacter
70	34	55.7	738	5	09W5X2	09w5x2 drosophila
71	34	55.7	1487	5	09Y062	09y062 drosophila
72	34	55.7	1487	5	09VG18	09vg18 drosophila
73	34	55.7	1970	5	09VQU8	09vqu8 drosophila
74	34	54.1	71	2	09JUN9	09jun9 neisseria m
75	34	54.1	101	1	058860	058860 pyrococcus
76	34	54.1	102	11	09D6D2	09d6d2 mus musculu
77	34	54.1	103	10	09XJ71	09xj71 cucumis sat
78	33	54.1	130	8	080033	080033 exoneurella
79	33	54.1	131	8	080034	080034 brunasappia
80	33	54.1	136	8	079124	079124 brunasappia
81	33	54.1	131	8	079125	079125 brunasappia
82	33	54.1	131	8	079126	079126 exoneurella
83	33	54.1	151	8	099834	099834 ophraella c
84	33	54.1	156	4	09G462	09g462 diadassa co
85	33	54.1	159	4	09HB06	09hb06 homo sapien
86	33	54.1	161	11	09GCV9	09gcv9 mus musculu
87	33	54.1	192	8	09G7A3	09g7a3 brevineura
88	33	54.1	192	8	09G798	09g798 xylocopa bo
89	33	54.1	197	8	09G782	09g782 xylocopa va
90	33	54.1	198	8	09G7A2	09g7a2 xylocopa mi
91	33	54.1	198	8	09G7A1	09g7a1 xylocopa tr
92	33	54.1	198	8	09G799	09g799 xylocopa vi

239	33	54.1	413	8	09B4K1	09b4k1 diadastia tu	312	32	52.5	299	1	028568	028568 archaeoglob
240	33	54.1	413	8	09B4J9	09b4j9 diadastia ri	313	32	52.5	299	1	028888	028888 archaeoglob
241	33	54.1	413	8	09B4J7	09b4j7 diadastia au	314	32	52.5	299	1	028859	028859 archaeoglob
242	33	54.1	413	8	09B4J6	09b4j6 diadastia ri	315	32	52.5	299	1	029835	029835 archaeoglob
243	33	54.1	413	8	09B4J4	09b4j4 diadastia pi	316	32	52.5	305	10	09C6A2	09c6a2 arabidopsi
244	33	54.1	413	8	09B4J0	09b4j0 diadastia va	317	32	52.5	305	10	09C6A2	09c6a2 bradyrhizob
245	33	54.1	413	8	09B1L9	09b1l9 diadastia ma	318	32	52.5	313	5	09LNU2	09lnu2 arabidopsi
246	33	54.1	413	8	09B1L2	09b1l2 diadastia ni	319	32	52.5	313	10	076920	076920 drosophila
247	33	54.1	413	8	09B1G0	09b1g0 diadastia ni	320	32	52.5	327	2	09R8K9	09r8k9 delnoco
248	33	54.1	413	8	09B1G0	09b1g0 diadastia ni	321	32	52.5	331	2	087922	087922 yersinia in
249	33	54.1	413	8	09B0V7	09b0v7 diadastia pa	322	32	52.5	338	2	09AHG0	09ahg0 fusobacteri
250	33	54.1	413	8	09B0N8	09b0n8 diadastia me	323	32	52.5	345	2	09I1S0	09i1s0 pseudomonas
251	33	54.1	413	8	09B0M6	09b0m6 diadastia sp	324	32	52.5	357	1	028862	028862 archaeoglob
252	33	54.1	414	8	09B4O1	09b4o1 alepidoscel	325	32	52.5	361	1	057936	057936 pyrococcus
253	33	54.1	416	2	09RVA2	09rva2 delnoco	326	32	52.5	368	5	017992	017992 caenorhabdi
254	33	54.1	418	2	054651	054651 streptococ	327	32	52.5	370	10	09SUR1	09sur1 arabidopsi
255	33	54.1	433	4	09BSU8	09bsu8 homo sapien	328	32	52.5	381	10	09RFW2	09rfw2 arabidopsi
256	33	54.1	439	8	09MFK9	09mfk9 acalymma vl	329	32	52.5	384	2	09K3I1	09k3i1 streptomyce
257	33	54.1	440	8	09MFK8	09mfk8 acalymma bl	330	32	52.5	400	2	09KYG1	09kyg1 streptomyce
258	33	54.1	440	8	09MFK7	09mfk7 diabrotica	331	32	52.5	402	5	021056	021056 caenorhabdi
259	33	54.1	440	8	09MFK6	09mfk6 diabrotica	332	32	52.5	402	5	09NEO0	09neo0 caenorhabdi
260	33	54.1	440	8	09MFK5	09mfk5 diabrotica	333	32	52.5	419	2	09PUO0	09puo0 chlamydia m
261	33	54.1	440	8	09MFK4	09mfk4 diabrotica	334	32	52.5	419	2	09HTV1	09htv1 pseudomonas
262	33	54.1	440	8	09MFK3	09mfk3 diabrotica	335	32	52.5	419	4	09H7H6	09h7h6 homo sapien
263	33	54.1	440	8	09MFK2	09mfk2 diabrotica	336	32	52.5	426	2	09HXI4	09hxi4 pseudomonas
264	33	54.1	440	8	09MFK1	09mfk1 diabrotica	337	32	52.5	432	2	09PND9	09pnd9 campylobact
265	33	54.1	440	8	09MEK0	09mek0 diabrotica	338	32	52.5	433	2	09ZSL0	09zsl0 leptospira
266	33	54.1	440	8	09MEF9	09mef9 diabrotica	339	32	52.5	445	2	F74224	F74224 synechocyst
267	33	54.1	440	8	09MEJ9	09mej9 diabrotica	340	32	52.5	445	2	F74224	F74224 synechocyst
268	33	54.1	440	8	09MEJ8	09mej8 diabrotica	341	32	52.5	464	2	056885	056885 yersinia en
269	33	54.1	440	8	09MEJ7	09mej7 diabrotica	342	32	52.5	464	2	084498	084498 chlamydia t
270	33	54.1	440	8	09MEJ6	09mej6 diabrotica	343	32	52.5	464	2	09Z7U4	09z7u4 chlamydia p
271	33	54.1	444	12	P88924	P88924 kaposi's sa	344	32	52.5	478	2	09R8K8	09r8k8 yersinia en
272	33	54.1	454	3	09UOK2	09uok2 schizosacch	345	32	52.5	484	5	021761	021761 caenorhabdi
273	33	54.1	495	2	099W86	099w86 staphylococ	346	32	52.5	484	10	09FEF6	09fef6 arabidopsi
274	33	54.1	512	11	061745	061745 mus musculu	347	32	52.5	508	13	013254	013254 gallus gall
275	33	54.1	512	11	061364	061364 mus musculu	348	32	52.5	513	4	09UFE1	09ufe1 homo sapien
276	33	54.1	528	8	09B9I3	09b9i3 waterstonie	349	32	52.5	518	5	017616	017616 caenorhabdi
277	33	54.1	546	10	09SKL1	09skl1 arabidopsi	350	32	52.5	522	12	09WHJ1	09whj1 walleye ept
278	33	54.1	566	4	09HEA8	09hea8 homo sapien	351	32	52.5	539	2	09FAH8	09fah8 porphyromon
279	33	54.1	573	11	09QXW2	09qxw2 mus musculu	352	32	52.5	567	10	09SVL5	09svl5 arabidopsi
280	33	54.1	712	5	09VNR5	09vnr5 drosophila	353	32	52.5	579	2	09K474	09k474 streptomyce
281	33	54.1	711	2	09S517	09s517 staphylococ	354	32	52.5	612	2	09X7Y5	09x7y5 streptomyce
282	33	54.1	712	10	080890	080890 arabidopsi	355	32	52.5	614	2	052516	052516 pseudomonas
283	33	54.1	734	5	09BHZ0	09bhz0 leishmania	356	32	52.5	614	5	022708	022708 caenorhabdi
284	33	54.1	745	3	P79086	P79086 collettotric	357	32	52.5	617	2	09JZ26	09jz26 neisseria m
285	33	54.1	755	10	09LXM7	09lxm7 arabidopsi	358	32	52.5	628	2	09JUZ1	09ju21 neisseria m
286	33	54.1	1106	2	09EV03	09ev03 erwina chr	359	32	52.5	637	10	080625	080625 arabidopsi
287	33	54.1	1357	12	089328	089328 rice ragged	360	32	52.5	667	5	09Y117	09y117 drosophila
288	33	54.1	1741	5	046095	046095 drosophila	361	32	52.5	673	5	09VW10	09vw10 drosophila
289	33	54.1	1741	5	09W517	09w517 drosophila	362	32	52.5	700	10	09LFM2	09lfm2 arabidopsi
290	32.5	53.3	97	5	09V8C5	09v8c5 drosophila	363	32	52.5	768	11	088797	088797 raltus norv
291	32	52.5	87	12	09B675	09b675 simlan cyto	364	32	52.5	84.1	5	09U6X3	09u6x3 drosophila
292	32	52.5	132	2	09EZM6	09ezm6 staphylococ	365	32	52.5	922	11	09OXJ2	09oxj2 mus musculu
293	32	52.5	133	2	099748	099748 staphylococ	366	32	52.5	925	11	09OZE4	09oze4 mus musculu
294	32	52.5	154	11	09R129	09r129 raltus norv	367	32	52.5	1016	4	043147	043147 homo sapien
295	32	52.5	155	11	09R132	09r132 raltus norv	368	32	52.5	1039	5	023567	023567 caenorhabdi
296	32	52.5	155	11	09R131	09r131 raltus norv	369	32	52.5	1197	11	09ZOR5	09zor5 mus musculu
297	32	52.5	155	11	09R127	09r127 raltus norv	370	32	52.5	1307	2	09MX71	09mx71 acetobacter
298	32	52.5	157	4	013092	013092 homo sapien	371	32	52.5	1415	2	09HVI8	09hvi8 pseudomonas
299	32	52.5	168	11	09DPD6	09dpd6 mus musculu	372	32	52.5	1503	5	09V6P4	09v6p4 drosophila
300	32	52.5	180	2	055966	055966 synechocyst	373	32	52.5	1651	5	045176	045176 caenorhabdi
301	32	52.5	198	12	09B674	09b674 simlan cyto	374	32	52.5	1658	11	09ZOR6	09zor6 mus musculu
302	32	52.5	210	2	034947	034947 bacillus su	375	32	52.5	1718	5	062603	062603 trypanosoma
303	32	52.5	219	10	09AVT2	09avt2 picea abies	376	32	52.5	1817	5	019931	019931 caenorhabdi
304	32	52.5	220	2	052941	052941 calochrix v	377	32	52.5	2157	11	09ZLR1	09zlr1 mus musculu
305	32	52.5	225	2	09RVM8	09rvm8 delnoco	378	32	52.5	2161	12	09R1F1	09r1f1 meleagridd h
306	32	52.5	255	4	09BZ16	09bzt6 homo sapien	379	32	52.5	2164	12	09R1F1	09r1f1 meleagridd h
307	32	52.5	264	12	083481	083481 tobacco mos	380	32	52.5	2195	3	002822	002822 saccharomyc
308	32	52.5	286	10	09C738	09c738 arabidopsi	381	32	52.5	2204	12	099FV6	099fv6 porcine tes
309	32	52.5	288	10	09R2F8	09r2f8 delnoco	382	32	52.5	2502	12	099AV6	099av6 porcine rep
310	32	52.5	288	2	09RV34	09rv34 delnoco	383	32	52.5	2503	12	09YN02	09yn02 porcine rep
311	32	52.5	289	5	09VB79	09vb79 drosophila	384	32	52.5	2503	12	09WJB2	09wjb2 porcine rep

385	32	52.5	2503	12	Q9ENK6	Q9enK6 porcine rep	458	31	50.8	409	2	Q9x668	Q9x668 staphylococ
386	32	52.5	2503	12	Q9E8M0	Q9e8M0 porcine rep	459	31	50.8	409	5	Q9BK22	Q9BK22 caenorhabd1
387	32	52.5	2503	12	Q99136	Q99136 porcine rep	460	31	50.8	411	2	Q992T2	Q992T2 streptococ
388	32	52.5	2503	12	Q999U6	Q999U6 porcine rep	461	31	50.8	415	2	Q33471	Q33471 pseudomonas
389	32	52.5	3956	12	Q9DLM9	Q9dLM9 porcine rep	462	31	50.8	415	2	Q50214	Q50214 pseudomonas
390	32	52.5	3960	12	Q9DLE1	Q9dLE1 porcine rep	463	31	50.8	415	2	Q33494	Q33494 pseudomonas
391	32	52.5	3960	12	Q9DLE0	Q9dLE0 porcine rep	464	31	50.8	420	3	Q9C1B5	Q9C1B5 fusarid sp
392	32	52.5	3960	12	Q9DLN8	Q9dLN8 porcine rep	465	31	50.8	425	2	P95472	P95472 pseudomonas
393	31	50.8	77	10	Q41157	Q41157 rubus hispi	466	31	50.8	465	10	Q9LRT3	Q9LRT3 arabidopsis
394	31	50.8	79	2	Q32020	Q32020 bacillus su	467	31	50.8	465	10	Q9FVY4	Q9FVY4 arabidopsis
395	31	50.8	83	5	Q9U7Z9	Q9U7Z9 hesperocida	468	31	50.8	465	10	Q9ZMR4	Q9ZMR4 arabidopsis
396	31	50.8	112	6	Q9N1T9	Q9n1T9 canis fam11	469	31	50.8	472	13	Q9J342	Q9J342 gallus gall
397	31	50.8	126	1	Q92899	Q92899 archaeoglob	470	31	50.8	476	2	Q9JY27	Q9JY27 neisseria m
398	31	50.8	131	8	Q79123	Q79123 ceratina au	471	31	50.8	477	2	Q32354	Q32354 corynebacte
399	31	50.8	133	3	Q94586	Q94586 schizosacch	472	31	50.8	477	2	Q9Z474	Q9Z474 corynebacte
400	31	50.8	136	10	Q9SN73	Q9sn73 arabidopsis	473	31	50.8	479	5	Q17697	Q17697 caenorhabd1
401	31	50.8	138	10	Q04222	Q04222 helianthus	474	31	50.8	479	5	Q9MUZ1	Q9MUZ1 coleletoric
402	31	50.8	159	2	Q9JYV2	Q9jYV2 neisseria m	475	31	50.8	481	13	Q9MD53	Q9MD53 brachydanio
403	31	50.8	163	2	Q9RL62	Q9RL62 streptomyce	476	31	50.8	488	12	Q9WT03	Q9WT03 human herpe
404	31	50.8	176	2	Q9RZR2	Q9rZR2 deinococcus	477	31	50.8	496	8	Q34175	Q34175 cepaea nemo
405	31	50.8	180	5	Q9U249	Q9u249 caenorhabd1	478	31	50.8	504	5	Q9VFM0	Q9VFM0 drosophila
406	31	50.8	186	5	Q9YAF7	Q9yaf7 drosophila	479	31	50.8	508	13	Q9PU44	Q9PU44 gallus gall
407	31	50.8	189	8	Q63003	Q63003 blindia acu	480	31	50.8	512	3	Q9UQZ1	Q9UQZ1 coleletoric
408	31	50.8	190	10	Q9MB83	Q9mb83 nepenthes a	481	31	50.8	517	13	Q9DG54	Q9DG54 brachydanio
409	31	50.8	191	10	Q9MB80	Q9mb80 nepenthes a	482	31	50.8	517	13	Q980C7	Q980C7 brachydanio
410	31	50.8	192	10	Q9FS59	Q9fs59 trifolium ur	483	31	50.8	524	4	Q9BTT6	Q9BTT6 homo sapien
411	31	50.8	192	10	Q9FS58	Q9fs58 trifolium ur	484	31	50.8	527	5	Q9VJK5	Q9VJK5 drosophila
412	31	50.8	193	10	Q9C9H1	Q9c9H1 arabidopsis	485	31	50.8	529	2	P74332	P74332 synecocyst
413	31	50.8	197	4	Q9HAC0	Q9nac0 homo sapien	486	31	50.8	532	5	Q23296	Q23296 caenorhabd1
414	31	50.8	198	8	Q9G7A0	Q9g7A0 xylocopa au	487	31	50.8	537	5	Q9VP64	Q9VP64 drosophila
415	31	50.8	198	10	Q9MB84	Q9mb84 nepenthes a	488	31	50.8	538	5	Q25416	Q25416 leishmania
416	31	50.8	201	10	Q9MB81	Q9mb81 nepenthes a	489	31	50.8	546	1	Q9HLE7	Q9HLE7 thermoplas
417	31	50.8	206	1	Q50104	Q50104 pyrococcus	490	31	50.8	547	4	Q9SV07	Q9SV07 homo sapien
418	31	50.8	206	9	Q9G0F6	Q9g0F6 roseophaga	491	31	50.8	547	4	Q9NV09	Q9NV09 homo sapien
419	31	50.8	216	5	Q20623	Q20623 caenorhabd1	492	31	50.8	547	4	Q9BTR2	Q9BTR2 homo sapien
420	31	50.8	218	12	Q9DHN1	Q9dhn1 yaba-like d	493	31	50.8	558	10	Q9C9H4	Q9C9H4 arabidopsis
421	31	50.8	219	2	Q9JXY9	Q9jxy9 neisseria m	494	31	50.8	566	10	Q9LXN3	Q9LXN3 saccharomyc
422	31	50.8	226	5	Q45753	Q45753 caenorhabd1	495	31	50.8	583	3	Q08961	Q08961 arabidopsis
423	31	50.8	226	10	Q22614	Q22614 kostelezky	496	31	50.8	593	10	Q9FLB0	Q9FLB0 arabidopsis
424	31	50.8	242	12	Q9WNC4	Q9wnG4 tobacco mos	497	31	50.8	596	12	Q9YMR0	Q9YMR0 lymantria d
425	31	50.8	245	10	Q9AVQ7	Q9avq7 sesbania ro	498	31	50.8	607	13	Q9W715	Q9W715 oncorhynch
426	31	50.8	245	10	Q9AVQ4	Q9avq4 sesbania ro	499	31	50.8	607	13	Q9PW89	Q9PW89 salvelinu
427	31	50.8	249	4	Q9H8W4	Q9h8W4 homo sapien	500	31	50.8	632	6	Q9N1P6	Q9N1P6 canis fam11
428	31	50.8	252	10	Q9M6N6	Q9m6N6 hordeum vul	501	31	50.8	649	4	Q9P215	Q9P215 homo sapien
429	31	50.8	258	5	Q9VHT3	Q9vht3 drosophila	502	31	50.8	656	5	Q9N342	Q9N342 caenorhabd1
430	31	50.8	263	5	Q9U2T5	Q9u2T5 caenorhabd1	503	31	50.8	661	6	Q9GLE5	Q9GLE5 bos taurus
431	31	50.8	266	5	Q96202	Q96202 plasmodium	504	31	50.8	667	10	Q9ZS01	Q9ZS01 arabidopsis
432	31	50.8	266	10	Q9M4N2	Q9m4N2 medicago tr	505	31	50.8	678	2	P73509	P73509 synecocyst
433	31	50.8	271	2	Q9RXY2	Q9rxy2 deinococcus	506	31	50.8	678	10	Q9SG80	Q9SG80 arabidopsis
434	31	50.8	286	6	Q9GLZ3	Q9GLZ3 macaca fasc	507	31	50.8	679	11	Q9FG18	Q9FG18 arabidopsis
435	31	50.8	316	12	Q68400	Q68400 human cytom	508	31	50.8	687	11	Q9DRB0	Q9DRB0 mus musculu
436	31	50.8	320	10	Q9CAH5	Q9cah5 arabidopsis	509	31	50.8	687	11	Q9P244	Q9P244 homo sapien
437	31	50.8	330	10	Q9ZRX2	Q9zrx2 trifolium ae	510	31	50.8	700	4	Q9N2U0	Q9N2U0 caenorhabd1
438	31	50.8	333	10	Q9ZS77	Q9zS77 hordeum vul	511	31	50.8	704	5	Q9P5U8	Q9P5U8 neurospora
439	31	50.8	335	10	Q9SE65	Q9seG5 caenorhabd1	512	31	50.8	735	3	Q9P195	Q9P195 leishmania
440	31	50.8	337	5	Q45279	Q45279 caenorhabd1	513	31	50.8	745	5	Q9U158	Q9U158 leishmania
441	31	50.8	338	2	P73085	P73085 synecocyst	514	31	50.8	762	6	Q9TUK0	Q9TUK0 sus scrofa
442	31	50.8	345	10	Q9LS32	Q9LS32 physcomitire	515	31	50.8	763	6	Q9TUK1	Q9TUK1 sus scrofa
443	31	50.8	348	5	Q9WVG7	Q9wvg7 drosophila	516	31	50.8	763	11	Q9R101	Q9R101 spermophilu
444	31	50.8	349	5	Q9RPM1	Q9rpm1 pseudomonas	517	31	50.8	775	2	Q9Z879	Q9Z879 chlamydia p
445	31	50.8	355	5	Q22383	Q22383 caenorhabd1	518	31	50.8	775	2	Q9JS20	Q9JS20 chlamydia p
446	31	50.8	358	4	Q9UG73	Q9UG73 homo sapien	519	31	50.8	797	2	Q9XU17	Q9XU17 caenorhabd1
447	31	50.8	371	2	Q9Z897	Q9z897 chlamydia p	520	31	50.8	807	2	Q9A950	Q9A950 caulobacter
448	31	50.8	372	4	Q9H9X4	Q9H9X4 homo sapien	521	31	50.8	808	2	Q87758	Q87758 klebsiella
449	31	50.8	377	3	Q74794	Q74794 schizosacch	522	31	50.8	865	5	Q18395	Q18395 drosophila
450	31	50.8	379	2	Q9KDI5	Q9KDI5 bacillus ha	523	31	50.8	865	5	Q9N998	Q9N998 leishmania
451	31	50.8	379	2	Q99T14	Q99T14 staphylococ	524	31	50.8	866	5	Q9BNW9	Q9BNW9 drosophila
452	31	50.8	385	1	Q9YAV4	Q9Yav4 aeropyrum p	525	31	50.8	925	4	Q95786	Q95786 homo sapien
453	31	50.8	391	2	Q9KTV2	Q9KTV2 vibrio chol	526	31	50.8	948	5	Q9U304	Q9U304 caenorhabd1
454	31	50.8	398	4	Q9NT04	Q9nt04 homo sapien	527	31	50.8	958	10	Q9AYP6	Q9AYP6 victia faba
455	31	50.8	399	4	Q9HAH7	Q9nah7 homo sapien	528	31	50.8	997	5	Q01858	Q01858 caenorhabd1
456	31	50.8	400	4	Q9UDX4	Q9udX4 homo sapien	529	31	50.8	1019	3	Q9P774	Q9P774 schizosacch
457	31	50.8	400	11	Q9Z1J8	Q9z1J8 rattus norv	530	31	50.8	1118	10	Q9LJS9	Q9LJS9 arabidopsis

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531 31 50.8 1139 5 076601 076601 caenorhabdi
532 31 50.8 1164 4 09H1S5 09H1S5 homo sapien
533 31 50.8 1170 2 09A1R8 09A1R8 erysipelothe
534 31 50.8 1222 10 09SVW6 09SVW6 arabidopsis
535 31 50.8 1265 5 09NCL9 09NCL9 culic quing
536 31 50.8 1323 10 09MOM2 09MOM2 arabidopsis
537 31 50.8 1377 13 09DDN5 09DDN5 xenopus lae
538 31 50.8 1454 5 010463 010463 caenorhabdi
539 31 50.8 1669 11 09QZS0 09QZS0 mus musculu
540 31 50.8 1765 11 088457 088457 rattus norv
541 31 50.8 1765 11 09R053 09R053 mus musculu
542 31 50.8 1765 11 09JMD4 09JMD4 mus musculu
543 31 50.8 1840 11 061818 061818 mus musculu
544 31 50.8 1963 5 09VSK5 09VSK5 drosophila
545 31 50.8 1964 10 09LIM2 09LIM2 arabidopsis
546 31 50.8 1966 5 09NMX6 09NMX6 drosophila
547 31 50.8 2051 5 09NMX9 09NMX9 anopheles g
548 31 50.8 2454 3 09UVP2 09UVP2 emericeella
549 31 50.8 2454 3 09UVP6 09UVP6 emericeella
550 31 50.8 3033 12 09Q9B0 09Q9B0 hepatitis c
551 31 50.8 6815 5 091704 091704 drosophila
552 31 50.8 16215 5 09NFS3 09NFS3 drosophila
553 30.5 50.0 445 2 09KPB7 09KPB7 vibrio chol
554 30.5 50.0 574 2 09K9B5 09K9B5 bacillus ha
555 30.5 50.0 603 5 09N9A4 09N9A4 caenorhabdi
556 30.5 50.0 1423 5 09W1A0 09W1A0 drosophila

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ALIGNMENTS

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RESULT 1
09Y494 PRELIMINARY; PRT; 72 AA.
AC 09Y494;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, AND BRAIN;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT Identification of a Delta isoform of preprotachykinin mRNA in Human
RT Mononuclear Phagocytes and Lymphocytes.
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF050657; AAC15703.1;
DR InterPro: IPR002040; Tachykinin.
DR InterPro: IPR003580; Protachykinin.
DR Pfam: PF02202; Tachykinin; 1
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
DR SMART: SM00203; TK; 2.
FT SMART 1
FT NON_TER 72
FT SEQUENCE 72 AA; 8274 MW; 2C02B2BA41EAD16 CRC64;
SQ

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Query Match 100.0%; Score 61; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 RPKPOFFGLM 11
Db 23 RPKPOFFGLM 33
RESULT 2
097947 PRELIMINARY; PRT; 114 AA.
ID 097947

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AC 097947;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ 1.
OS Tupia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupala.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Heitland A., Maegert H.J., Krueffner M., Forsmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z50785; CAA90648.1;
DR InterPro: IPR002040; Tachykinin.
DR InterPro: IPR003580; Protachykinin.
DR Pfam: PF02202; Tachykinin; 1
DR PRODOM: PD005598; Protachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
DR SMART: SM00203; TK; 2.
FT CHAIN 58
FT CHAIN 72
FT CHAIN 92
FT CHAIN 83
FT CHAIN 92
FT SEQUENCE 114 AA; 13281 MW; B439C3D27FD47CAB CRC64;
SQ

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Query Match 100.0%; Score 61; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 RPKPOFFGLM 11
Db 58 RPKPOFFGLM 68

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RESULT 3
09Y6V5 PRELIMINARY; PRT; 128 AA.
AC 09Y6V5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE WOGSC:H_DJ0841B21.1 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalicki J., Angell S.;
RT "The sequence of Homo sapiens PAC clone DJ0841B21."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC004140; AAC02754.1;
DR InterPro: IPR002040; Tachykinin.
DR InterPro: IPR003580; Protachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
DR SMART: SM00203; TK; 1.
FT SMART 1
FT SEQUENCE 128 AA; 14770 MW; 0F8D61774AEC1CA CRC64;
SQ

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Query Match 100.0%; Score 61; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 RPKPOFFGLM 11
Db 11 RPKPOFFGLM 11

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Db 58 RRPQOOFGLM 68
RESULT 4
097948
ID 097948 PRELIMINARY; PRT: 129 AA.
AC 097948;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Tupia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Helldand A., Maegert H.J., Kruboeffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: 250786; CAA90649.1; -
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR ProDom: PD005598; Protachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
FT SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

Query Match 100.0%; Score 61; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRPQOOFGLM 11
Db 58 RRPQOOFGLM 68

RESULT 5
ID 0920K2 PRELIMINARY; PRT: 97 AA.
AC 0920K2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DELTA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PBRIDGE WHITE; TISSUE-BRAIN;
RA Helldand A., Maegert H.J., Kruboeffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: 250782; CAA90645.1; -
DR InterPro: IPR003580; Protachykinin.
DR ProDom: PD005598; Protachykinin; 1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;
SQ SEQUENCE 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 97;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RRPQOOFGLM 11

Db 58 RRPQOOFGLM 68
RESULT 6
0920K1
ID 0920K1 PRELIMINARY; PRT: 115 AA.
AC 0920K1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PBRIDGE WHITE; TISSUE-BRAIN;
RA Helldand A., Maegert H.J., Kruboeffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: 250783; CAA90646.1; -
DR InterPro: IPR002040; Tachykinin.
DR ProDom: PD005598; Protachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 98 92 NEUROKININ A.
SQ SEQUENCE 115 AA; 13190 MW; 39EFBE8CB847174 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 115;
Best Local Similarity 90.9%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RRPQOOFGLM 11
Db 58 RRPQOOFGLM 68

RESULT 7
ID 0920K0 PRELIMINARY; PRT: 130 AA.
AC 0920K0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PBRIDGE WHITE; TISSUE-BRAIN;
RA Helldand A., Maegert H.J., Kruboeffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: 250784; CAA90647.1; -
DR InterPro: IPR002040; Tachykinin.
DR ProDom: PD005598; Protachykinin; 1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 98 92 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 130 AA; 14850 MW; C4B2F55B6A60A7C0 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 130;
Best Local Similarity 90.9%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
1111111111

DB 58 RPKPOQFFGLM 68

RESULT 8

Q9HLV7 PRELIMINARY; PRT; 207 AA.

AC Q9HLV7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN TA0086.
GN TA0086.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
OC Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Granel W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Friseman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL: AL445063; CAC11234.1; -
DR InterPro: IPR001279; Beta_lactam_mct.
DR Pfam: PF00753; lactamase_B.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 22741 MW; 60136f482EB2A94D CRC64;

Query Match 67.2%; Score 41; DB 1; Length 207;
Best Local Similarity 70.0%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQFFGLM 11
1111111111

DB 100 PKRPSFFGRM 109

RESULT 9

Q24014 PRELIMINARY; PRT; 786 AA.

AC Q24014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE GI-LIKE ORF'S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RX MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
both belong to the ddp1 plasmid family.";
RL Plasmid 31:121-130(1994).
DR EMBL: U00176; AAC14374.1; -
SQ SEQUENCE 786 AA; 90191 MW; 2167146E1F012003 CRC64;

Query Match 63.9%; Score 39; DB 5; Length 786;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10

DB 717 KPEPIQFFGI 726

RESULT 10

Q24012 PRELIMINARY; PRT; 803 AA.

AC Q24012;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE GI-LIKE ORF'S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RX MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
both belong to the ddp1 plasmid family.";
RL Plasmid 31:121-130(1994).
DR EMBL: U00175; AAC14372.1; -
SQ SEQUENCE 803 AA; 91385 MW; 219F8272FA16FACD CRC64;

Query Match 63.9%; Score 39; DB 5; Length 803;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
1111111111

DB 734 KPEPIQFFGI 743

RESULT 11

Q20174 PRELIMINARY; PRT; 205 AA.

AC Q20174;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE COSMID F38E9.
GN F38E9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showmken R.,
Smaildon S., Smith A., Sonhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterson R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Wu X., Gatung S.,
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U46668; AAA93346.1; -
SQ SEQUENCE 205 AA; 23000 MW; B99FB37DB706ECOD CRC64;
Query Match 62.3%; Score 38; DB 5; Length 205;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 RPKQOFG 8
1111111
Db 151 RPKQOFG 157
RESULT 12
Q9VBM4 PRELIMINARY; PRT; 235 AA.
AC Q9VBM4
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG13653 PROTEIN.
GN CG13653
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galles R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bonos P.V., Borman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Clawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou J.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hsiao L.D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaisli D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidani-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-Z., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2135-2195(2000).
DR EMBL: AE003751; AAF56413.1; -
DR FLYbase: FBgn039288; CG13653.
SQ SEQUENCE 235 AA; 27051 MW; F99BDB455BA7A3E CRC64;

Query Match 62.3%; Score 38; DB 5; Length 235;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKQOFG 10
1111111
Db 85 RPKQOFG 94
RESULT 13
Q9SUN5 PRELIMINARY; PRT; 257 AA.
AC Q9SUN5
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PURNATIVE SNRNP PROTEIN.
GN Pp13.90 OR AT4G20440.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL080253; CAB45810.1; -
DR EMBL: AL161553; CAB79044.1; -
DR InterPro: IPR002965; P_t1ch-extensn.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
DR PRINTS: PR01217; PRICHEXTENS.
SQ SEQUENCE 257 AA; 27140 MW; D931178BCBC51B5 CRC64;
Query Match 62.3%; Score 38; DB 10; Length 257;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKQOFG 9
1111111
Db 189 RPKQOFG 197
RESULT 14
Q49561 PRELIMINARY; PRT; 293 AA.
AC Q49561
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GIBBERELLIN 20-OXIDASE - LIKE PROTEIN (GIBBERELLIN 20-OXIDASE-LIKE
PROTEIN).
GN F737.140 OR AT4G21200.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
 RA Bancroft I., Mewes H.W., Mayer K., Schueller C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL021960; CAIL7539.1; -;
 DR EMBL: AL161554; CAB79120.1; -;
 DR Mendel: 27589; Arath; 2972; 27589.
 DR InterPro: IPR002419; Fe_asc_oxidored.
 DR Pfam: PF00671; Fe_Asc_oxidored; 1.
 SO SEQUENCE 293 AA; 34050 MW; 5138093F136DF66 CRC64;

Query Match 62.3%; Score 38; DB 10; Length 293;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFFGLM 11
 111 : 111
 Db 159 PKPVEYGLM 168

RESULT 15
 Q9PVE8 PRELIMINARY; PRT; 496 AA.
 AC Q9PVE8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME P450 3A30.
 GN CYP3A30.
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 OX NCBI_TaxID=8078;
 RN [1]
 RP SEQUENCE OF 313-436 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE-97382427; PubMed-9240431;
 RA Celander M., Stegeman J.J.;
 RT "Isolation of a cytochrome P450 3A cDNA sequence (CYP3A30) from the
 RT marine teleost Fundulus heteroclitus and phylogenetic analyses of
 RT CYP3A genes.";
 RL Blochem. Biophys. Res. Commun. 236:306-312(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Celander M., Hegelund-Myrback T., Stegeman J.J.;
 RT "Cloning and sequencing of the complete coding region of cytochrome
 RT P450 3A30 (CYP3A30) from the marine teleost Fundulus heteroclitus.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL: AF105068; AAF14117.1; -;
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Eletion transport; Endoplasmic reticulum; Heme; Membrane; Microsome;

KW Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 496 AA; 57051 MW; 40CFB23D75F4A4EB CRC64;

Query Match 62.3%; Score 38; DB 13; Length 496;
 Best Local Similarity 70.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGLM 11
 111 : 111
 Db 40 PKPVEFGTM 49

RESULT 16
 Q9DE99 PRELIMINARY; PRT; 500 AA.
 AC Q9DE99;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME P450 3A.
 GN CYP3A.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MEDAKA;
 RA Kullman S.W., Hamm J.T., Hinton D.E.;
 RT "Identification and Characterization of a cDNA Encoding Cytochrome
 RT P450 3A from the Fresh Water Teleost Oryzias latipes.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL: AF105018; AAG35209.1; -;
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Heme; Monooxygenase; Oxidoreductase.
 SO SEQUENCE 500 AA; 57381 MW; EB0A8479601CE8C7 CRC64;

Query Match 62.3%; Score 38; DB 13; Length 500;
 Best Local Similarity 70.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGLM 11
 111 : 111
 Db 41 PKPVEFGTM 50

RESULT 17
 Q9RT91 PRELIMINARY; PRT; 502 AA.
 AC Q9RT91;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME P450 3A40.
 GN CYP3A40.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kullman S.W., Hinton D.E.;
 RT "Identification of multiple isozymes of cytochrome P450 3A from the

RT fresh water teleost medaka: Characterization and ontogeny."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF251272; AAK37960.1; -
SQ SEQUENCE 502 AA; 57707 MW; 1E9FE38B21CED1D8 CRC64;

Query Match 62.3%; Score 38; DB 13; Length 502;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOOFFGLM 11
||| ||| |
Db 41 RKPVPFFGLM 50

RESULT 18
P94873 PRELIMINARY; PRT; 3722 AA.
ID P94873
AC P94873;
DT 01-MAY-1997 (TRIMBLrel. 03, Created)
DR 01-MAY-1997 (TRIMBLrel. 03, Last sequence update)
DE 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)
DE ALPHA-AMINOADIPYL-CYSTEINYL-VALINE SYNTHETASE.
GN PCAB.
OS Lysobacter lactamgenus.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Lysobacter.
OX NCBI_TaxID=39596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK90;
RX MEDLINE=96275943; PubMed=8737573;
RA Kimura H., Miyashita H., Sumino Y.;
RT "Organization and expression in *Pseudomonas putida* of the gene cluster
involved in cephalosporin biosynthesis from *Lysobacter lactamgenus*
TK90".
RT Appl. Microbiol. Biotechnol. 45:490-501(1996).
RL EMBL: D50308; BAA08846.1; -
DR HSSP: P14687; 1AMU.
DR InterPro: IPR002106; AA_trna_ligase_II.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR000977; DNA_ligase.
DR InterPro: IPR001242; DDF4.
DR InterPro: IPR00379; Est_III_thioest_actsite.
DR InterPro: IPR003880; Phosphonat_attach.
DR InterPro: IPR001031; Thioesterase.
DR Pfam: PF00501; AMP-binding; 3.
DR Pfam: PF00668; Condensation; 3.
DR Pfam: PF00550; PP-binding; 3.
DR Pfam: PF00975; Thioesterase; 1.
DR PROSITE: PS00179; AA-trna_ligase_II_1; UNKNOWN_1.
DR PROSITE: PS00075; ACP_DOMAIN; 3.
DR PROSITE: PS00455; AMP BINDING; 1.
DR PROSITE: PS00657; DNA_LIGASE_A1; UNKNOWN_2.
DR PROSITE: PS00012; PHOSPHONATETHEINE; UNKNOWN_2.
KW Phosphonatetheine.
SQ SEQUENCE 3722 AA; 411611 MW; 3597B3483463809B CRC64;

Query Match 62.3%; Score 38; DB 2; Length 3722;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGLM 11
||| :| | |
Db 1412 RKPDEFGLV 1421

RESULT 19
O84949 PRELIMINARY; PRT; 138 AA.
ID O84949
AC O84949;
DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE SSEE.
GN SSEE.
OS Salmomella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmomella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLJ344;
RA Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;
RT "Macrophage-dependent induction of the *Salmomella* pathogenicity island
2 type III secretion system and its role in intracellular survival."
RL Mol. Microbiol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=99000132; PubMed=9786193;
RA Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G.,
RA Vazquez-Torres A., Gleeson C., Fang F.C., Holden D.W.;
RT "Genes encoding putative effector proteins of the type III secretion
system of *Salmomella* pathogenicity island 2 are required for bacterial
RT virulence and proliferation in macrophages."
RL Mol. Microbiol. 30:163-174(1998).
DR EMBL: AF020808; AAC28883.1; -
DR EMBL: AJ24892; CAA12189.1; -
SQ SEQUENCE 138 AA; 16266 MW; 4712D484CB8440E3 CRC64;

Query Match 60.7%; Score 37; DB 2; Length 138;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RKPPOFFGLM 11
:|: ||| | | |
Db 60 OPRPOLFHL 70

RESULT 20
O9V2N2 PRELIMINARY; PRT; 249 AA.
ID O9V2N2
AC O9V2N2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 29.2 KDA PROTEIN.
GN PAB2321.
GN Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution."
RT submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248283; CAB48966.1; -
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 249 AA; 29212 MW; 392F2EC61C84D6FD CRC64;

Query Match 60.7%; Score 37; DB 1; Length 249;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RKPPOFFGL 10
| | | :| | | |
Db 124 RIKPEKFFGI 133

RESULT 21

09BPN9
ID 09BPN9 PRELIMINARY: PRT: 177 AA.
AC 09BPN9
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN Y92H12BR.2.
GN Y92H12BR.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC087232; AAK09077.1; -; A2B3104976B88E5E CRC64;
SQ SEQUENCE 177 AA: 21018 MW: A2B3104976B88E5E CRC64;

Query Match 59.0%; Score 36; DB 5; Length 177;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
DB 68 RPKPROF 74

RESULT 22
ID 09NEM8 PRELIMINARY: PRT: 236 AA.
AC 09NEM8
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Y11B2A.16 PROTEIN.
GN Y11B2A.16.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sulston J.E.;
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: AL132904; CAC35845.1; -;
SQ SEQUENCE 236 AA: 26444 MW: 344BBE28A01C5431 CRC64;

Query Match 59.0%; Score 36; DB 5; Length 236;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RPKPOOF 8
DB 15 RPKPSFF 21

RESULT 23
ID 086283 PRELIMINARY: PRT: 352 AA.
AC 086283
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REOVIRUS SP. 1.24KB RNA SEGMENT.
OS unidentified.
OC unclassified.
OX NCBI_TaxID=32644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95313344; PubMed=7793063;
RA Bigot Y., Drezon J.M., Sizaret P.Y., Rabouille A., Hamelin M.H.,
Periquet G.;
RT "The genome segments of DpRV, a commensal reovirus of the wasp
Diatromus pulchellus (Hymenoptera).";
RL Virology 210:109-119(1995).
DR EMBL: X82046; CAA57562.1; -;
SQ SEQUENCE 352 AA: 39977 MW: 79F3DF03F0FE8939 CRC64;

Query Match 59.0%; Score 36; DB 12; Length 352;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFGL 10
DB 35 RPARPRFGL 44

RESULT 24
ID 023876 PRELIMINARY: PRT: 373 AA.
AC 023876
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PCF2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE; TISSUE=MERISTEMATIC TISSUE;
RX MEDLINE=97480096; PubMed=9338963;
RA Kosugi S., Ohashi Y.;
RT "PCF1 and PCF2 specifically bind to cis elements in the rice
proliferating cell nuclear antigen gene.";
RL Plant Cell 9:1607-1619(1997).
DR EMBL: D87261; BAA23143.1; -;
DR Mendel; 24192; Oryza; 3166; 24192.
SQ SEQUENCE 373 AA: 38529 MW: 111C093A043F8B2E CRC64;

Query Match 59.0%; Score 36; DB 10; Length 373;
Best Local Similarity 54.5%; Pred. No. 79;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 11
DB 55 KRPVPEFFGCM 65

RESULT 25
ID 09UW05 PRELIMINARY: PRT: 477 AA.
AC 09UW05

DT 01-MAY-2000 (TRIMBLREL. 13, Created)
 DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)
 DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
 DE SPM12 TRANSCRIPTION FACTOR HOMOLOG.
 CN CLS12.
 OS Clavispora lusitanae.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Metschnikowiaceae; Clavispora.
 OX NCBI_Taxid=36911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 42720;
 RA Young L., Lorenz M., Heitman J.;
 RT "A STE12 homolog is required for mating but dispensable for
 filamentation in *Candida lusitanae*."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF175524; AAD51741.1; -
 DR InterPro: IPR003120; STE.
 DR Pfam: PF02200; STE; 1.
 DR SMART: SM00424; STE; 1.
 SO SEQUENCE 477 AA; 54716 MW; FFBCAF29FMAAB542 CRC64;

QY 2 PKPOOFFGL 10
 Db 384 PPPAOFYGL 392

Query Match 59.0%; Score 36; DB 3; Length 477;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 26
 Q94130 PRELIMINARY; PRT; 550 AA.
 ID 094130;
 AC 094130;
 DT 01-FEB-1997 (TREMBLREL. 02, Created)
 DT 01-FEB-1997 (TREMBLREL. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE M89 PROTEIN PRECURSOR.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=96291396; PubMed=8689684;
 RA Porter J.A., Ekker S.C., Park W.-J., von Kessler D.P., Young K.E.,
 Chen C.-H., Ma Y., Woods A.S., Cotter R.J., Koonin E.V., Beachy P.A.;
 RT "Hedgehog patterning activity: role of a lipophilic modification
 mediated by the carboxy-terminal autoprocessing domain."
 RL Cell 86:21-34(1996).
 CC -1- PPM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
 CC EMBL: U61237; AAB17542.1; -
 DR InterPro: IPR001767; HInt.
 DR InterPro: IPR003586; HIntC.
 DR InterPro: IPR003587; HIntN.
 DR Pfam: PF01079; HInt; 1.
 DR SMART: SM00305; HIntC; 1.
 DR SMART: SM00306; HIntN; 1.
 KW Signal; Glycoprotein.
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 2C 550 M89 PROTEIN.
 FT CHAIN 2C 550 M89 PROTEIN N-PRODUCT (BY SIMILARITY).
 FT CHAIN 341 340 M89 PROTEIN C-PRODUCT (BY SIMILARITY).
 FT DNA_BIND 333 403 HMG BOX.
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 550 AA; 62100 MW; 2CDB81A0178E5B5B CRC64;

Query Match 59.0%; Score 36; DB 5; Length 550;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFF 8
 Db 301 QPPPOOFF 308

RESULT 27
 ID 045273 PRELIMINARY; PRT; 629 AA.
 AC 045273;
 DT 01-JUN-1998 (TREMBLREL. 06, Created)
 DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE C29F3.2 PROTEIN.
 GN C29F3.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Lalister N., Latreille P.,
 Ra Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 Thelery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 Watson A., Weinstock L., Wilkinson-Spratt J., Wollman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
 elegans*."
 RL Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA White S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z81043; CAB02804.1; -
 DR EMBL: AL023813; CAB02804.1; JOINED.
 DR EMBL: AL023813; CAA19424.1; -
 DR EMBL: Z81043; CAA19424.1; JOINED.
 DR InterPro: IPR001767; HInt.
 DR InterPro: IPR003586; HIntC.
 DR InterPro: IPR003587; HIntN.
 DR Pfam: PF01079; HInt; 1.
 DR SMART: SM00305; HIntC; 1.
 DR SMART: SM00306; HIntN; 1.
 SO SEQUENCE 629 AA; 71349 MW; 4D812B872AD5FE43 CRC64;

Query Match 59.0%; Score 36; DB 5; Length 629;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFF 8
 Db 380 QPPPOOFF 387

RESULT 28
 Q9F634

ID Q9F634 PRELIMINARY; PRT; 869 AA.
 AC Q9F634;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MXCH.
 GN MXCH.
 OS Stigmatella aurantiaca.
 CC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 CC Myxococcales; Cystobacterineae; Cystobacteraceae; Stigmatella.
 OX NCBI_TaxID=41;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SG A15;
 RX PubMed-11029592;
 RA Sliakowski B., Kunze B., Nordstiek G., Blocker H., Hoile G., Muller R.;
 RT "The myxochellin iron transport regulon of the myxobacterium
 ST Stigmatella aurantiaca Sg a15.";
 RL Eur. J. Biochem. 267:6476-6485(2000).
 DR EMBL: AF299336; AAG31132.1; -
 SQ SEQUENCE 869 AA; 95371 MW; 34102ELAD6AD33E1 CRC64;

Query Match 59.0%; Score 36; DB 2; Length 869;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PRPQPF 9
 1:1:111
 DB 637 PRPDEF 644

RESULT 29
 Q99N14 PRELIMINARY; PRT; 128 AA.
 AC Q99N14;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PREPROTACHKININ C.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Lu L., Furlonger C., Gillian W., Paige C.J.;
 RT "Hemokinin is a hemopoietic-specific tachykinin that regulates B
 lymphopoiesis.";
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF235035; AAK15025.1; -
 SQ SEQUENCE 128 AA; 13937 MW; FED91DCAB39CB444 CRC64;

Query Match 57.4%; Score 35; DB 11; Length 128;
 Best Local Similarity 54.5%; Pred. No. 40;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RRPQPF 11
 1:1:11111
 DB 56 RSRTRQFYGLM 66

RESULT 30
 O61761 PRELIMINARY; PRT; 206 AA.
 AC O61761;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE F56C3.9 PROTEIN.
 GN F56C3.9.
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Faveille A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten N., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,
 RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Stoneking T.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterson R.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF067214; AAC17009.1; -
 SQ SEQUENCE 206 AA; 24599 MW; 3F530DD3A57CD7A9 CRC64;

Query Match 57.4%; Score 35; DB 5; Length 206;
 Best Local Similarity 62.5%; Pred. No. 66;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRPQPF 8
 1:1:1111
 DB 188 KRPQPF 195

RESULT 31
 Q9L5Y0 PRELIMINARY; PRT; 218 AA.
 AC Q9L5Y0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 24.3 KDA PROTEIN.
 OS Streptomyces verticillius.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=29309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC15003;
 RA Chen M., Edwards D.J., Sanchez C., Du L., Shen B.;
 RT "N-acetyl-glucosamine biosynthesis genes in Streptomyces verticillius
 ATCC15003.";
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF245690; AAF68966.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 218 AA; 24320 MW; 085A18C6E222459F CRC64;

Query Match 57.4%; Score 35; DB 2; Length 218;
 Best Local Similarity 66.7%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KRPQPF 11
 1:1:11111

Db 104 KPSTFGILL 112

RESULT 32

Q9LVZ6 ID Q9LVZ6 PRELIMINARY; PRT; 296 AA.

AC Q9LVZ6; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

OS GENOMIC DNA, CHROMOSOME 3, p1 CLONE: MSJ11.

OC Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_Taxid=3702.

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA.

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.; Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA.

RA Nakamura Y.; MEDLINE=20277480; PubMed=10819329;

RX MEDLINE=20277480; PubMed=10819329;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty p1 and TAC clones."

RT clones."

RL DNA Res. 7:131-135(2000).

DR EMBL: AB017071; BAB02314.1; -

SQ SEQUENCE 296 AA; 32690 MM; B5BCD83423353EPE CRC64;

Query Match 57.4%; Score 35; DB 10; Length 296;

Best Local Similarity 62.5%; Pred. No. 96;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOFF 9

Db 185 PRPOFFLG 192

RESULT 33

Q9HVZ9 ID Q9HVZ9 PRELIMINARY; PRT; 297 AA.

AC Q9HVZ9; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.

OC NCBI_Taxid=287;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PAOI.

RA MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrenner P., Hickey M.J., Burkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Iarbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizler J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen.";

RT Nature 406:959-964(2000).

RL EMBL: AE004891; AAC08165.1; -

DR InterPro: IPR000620; DUF6.

DR Pfam: PF00892; DUF6; 2.

DR Hypothetical protein: Complete proteome.

SQ SEQUENCE 297 AA; 31656 MM; 55FF9F205C79B1DA CRC64;

Query Match 57.4%; Score 35; DB 2; Length 297;

Best Local Similarity 54.5%; Pred. No. 96;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKPOOFFGIL 11

Db 111 RPTPRGLFGL 121

RESULT 34

Q40055 ID Q40055 PRELIMINARY; PRT; 347 AA.

AC Q40055; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

OS HORDEIN PRECURSOR.

OC Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.

OX NCBI_Taxid=4513;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BOMI; TISSUE=IMMATURE ENDOSPERM;

RX MEDLINE=89351278; PubMed=3255313;

RA Entwistle J.;

RT "Primary structure of a C-hordein gene from barley.";

RL Carlberg Res. Commun. 53:247-258(1988).

DR EMBL: M36941; AAA92333.1; -

DR Mendel; 16774; Horvu; 2592; 16774.

FW Signal; Seed storage protein.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 347 C HORDEIN.

SQ SEQUENCE 347 AA; 40546 MM; 1E48919B2BCBC9D CRC64;

Query Match 57.4%; Score 35; DB 10; Length 347;

Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOFF 8

Db 60 PTPPOFF 66

RESULT 35

O48648 ID O48648 PRELIMINARY; PRT; 424 AA.

AC O48648; 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

OS PHYTOCHROME (FRAGMENT).

GN PHY4.

OS Adiantum capillus-veneris (Fern).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Filicophyta; Filicopsida; Filicales; Adiantaceae; Adiantum.

OX NCBI_Taxid=1818;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=POSON-ARET-1;

RA Nozue K., Kanegae T., Mada M.; J. Plant Res. 110:495-499(1997).

RL EMBL: AB003364; BAA24885.1; -

DR Mendel; 24641; Adica; 2331; 24641.

DR InterPro: IPR000014; PAS.

DR InterPro: IPR001294; Phytochrome.

DR Pfam: PF003018; GAF.

DR Pfam: PF00360; Phytochrome; 1.

DR pfam: PF00989; PAS; 1.
DR PRINTS: PR01033; PHYTOCHROME.
DR PROSITE: PS00245; PHYTOCHROME_1; 1.
DR PROSITE: PS0046; PHYTOCHROME_2; 1.
DR SMART: SM00055; GAF; 1.
DR SMART: SM00091; PAS; 1.
KW Phytochrome.
FT NON_TER 1 1
FT NON_TER 424 424
SQ SEQUENCE 424 AA; 47115 MW; 5510380FAD212E64 CRC64;

Query Match 57.4%; Score 35; DB 10; Length 424;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 11
DB 97 RPKPRKMGVL 107

RESULT 36
O9C17 PRELIMINARY; PRT; 494 AA.
AC O9C17:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6).
GN LYS.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IL403:
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis.";
RL Genome Res. 0:0-0(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC PYROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
CC TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
CC ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO AMINOACYL-TRANSFER RNA SYNTHETASES CLASS-II
CC FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL: AE006274; AK04471.1; -
DR InterPro: IPR002106; AA_TRNA_ligase_II.
DR InterPro: IPR002309; trna-synt.2.
DR InterPro: IPR002312; trna-synt.2.
DR InterPro: IPR002313; trna-synt.2.
DR pfam: PF00152; trna-synt.2; 1.
DR pfam: PF01336; trna-anti.1.
DR PRINTS: PR01042; TRNASYNTASP.
DR PRINTS: PR00982; TRNASYNTHYS.
DR PROSITE: PS00179; AA_TRNA_LIGASE_II_1; 1.
KW ATP-binding; Aminoacyl-TRNA synthetase; Complete proteome; Ligase;
KW Protein biosynthesis.
SQ SEQUENCE 494 AA; 56615 MW; 571CDA0F69ADB8 CRC64;

Query Match 57.4%; Score 35; DB 2; Length 494;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 RPKPOQFGL 10
DB 97 RPKPRKMGVL 107

DB 143 RLPKPFHGL 152

RESULT 37
O9A0V7 PRELIMINARY; PRT; 497 AA.
AC O9A0V7:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6).
GN LYS OR SPY0595.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370:
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL: AE006515; AK33574.1; -
KW Aminoacyl-TRNA synthetase; Ligase; Complete proteome;
SQ SEQUENCE 497 AA; 56599 MW; EBPDA25D5DAF92C8 CRC64;

Query Match 57.4%; Score 35; DB 2; Length 497;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 145 RLPKPFHGL 154

RESULT 38
O65191 PRELIMINARY; PRT; 509 AA.
AC O65191:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HELICASE.
GN OP509L.
OS African swine fever virus (ASFV).
OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
OC African swine fever-like viruses.
OX NCBI_TaxID=10497;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V:
RX MEDLINE=96036500; PubMed=7483270;
RA Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
RA Rodriguez J.F., Vinuela E.;
RT "Immune protection conferred by the baculovirus-related glycoprotein
RT of Thogoto virus (Orthomyxoviridae).";
RL Virology 208:249-278(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V:
RX MEDLINE=94233765; PubMed=8178480;
RA La Vega I., Gonzalez A., Blasco R., Calvo V., Vinuela E.;
RT "Nucleotide sequence and variability of the inverted terminal
RT repetitions of African swine fever virus DNA.";
RL Virology 201:152-156(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V:

RX MEDLINE=90219205; PubMed=2325203;
RA Gonzalez A., Celivo V., Almazan F., Almendral J.M., Ramirez J.C.,
La Vega I., Blasco R., Vinuela E.;
RT "Multigene families in African swine fever virus: family 360.";
RL J. Virol. 64:2073-2081(1990).
[4]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90219204; PubMed=2325202;
RA Almendral J.M., Almazan F., Blasco R., Vinuela E.;
RT "Multigene families in African swine fever virus: family 110.";
RL J. Virol. 64:2064-2072(1990).
[5]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=91134988; PubMed=1994575;
RA Camacho A., Vinuela E.;
RT "Protein p22 of African swine fever virus: an early structural protein that is incorporated into the membrane of infected cells.";
RL J. Virol. 181:251-257(1991).
[6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RA Almazan F., Murguia J.R., Rodriguez J.M., La Vega I., Vinuela E.;
RL J. Gen. Virol. 0:0-0(0).
[7]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94187118; PubMed=8139051;
RA Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
Vinuela E.;
RT "Multigene families in African swine fever virus: family 505.";
RL J. Virol. 68:2746-2751(1994).
[8]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93346971; PubMed=8393914;
RA Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E.;
RT "African swine fever virus thymidylate kinase gene: sequence and transcriptional mapping.";
RL J. Gen. Virol. 74:1633-1638(1993).
[9]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94065656; PubMed=8245848;
RA Alcamí A., Angulo A., Vinuela E.;
RT "Mapping and sequence of the gene encoding the African swine fever virus protein of M(r) 11500.";
RL J. Gen. Virol. 74:2317-2324(1993).
[10]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93277388; PubMed=8503790;
RA Munoz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
RT "Structure and expression in E. coli of the gene coding for protein p10 of African swine fever virus.";
RL Arch. Virol. 130:93-107(1993).
[11]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90357780; PubMed=2389555;
RA Blasco R., Lopez-Otin C., Munoz M., Bockamp E.O., Simon-Mateo C.,
Vinuela E.;
RT "Sequence and evolutionary relationships of African swine fever virus thymidine kinase.";
RL Virology 178:301-304(1990).
[12]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93281350; PubMed=8506138;
RA Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela E.;
RT "African swine fever virus encodes two genes which share significant homology with the two largest subunits of DNA-dependent RNA

RT polymerases.";
RL Nucleic Acids Res. 21:2423-2427(1993).
[13]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93353606; PubMed=8102411;
RA Rodriguez J.M., Yanez R.J., Almazan F., Vinuela E., Rodriguez J.F.;
RT "African swine fever virus encodes a CD2 homolog responsible for the adhesion of erythrocytes to infected cells.";
RL J. Virol. 67:5312-5320(1993).
[14]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94085774; PubMed=8262374;
RA Yanez R.J., Rodriguez J.M., Boursnell M., Rodriguez J.F., Vinuela E.;
RT "Two putative African swine fever virus helicases similar to yeast 'DEAF' pre-mRNA processing proteins and vaccinia virus ATPases D1L and D8R.";
RL Gene 134:161-174(1993).
[15]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90223993; PubMed=2327074;
RA Lopez-Otin C., Freije J.M., Parra F., Mendez E., Vinuela E.;
RT "Mapping and sequence of the gene coding for protein p12, the major capsid protein of African swine fever virus.";
RL Virology 175:477-484(1990).
[16]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94123986; PubMed=8293992;
RA Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
RT "The DNA polymerase-encoding gene of African swine fever virus: sequence and transcriptional analysis.";
RL Gene 136:103-110(1993).
[17]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93327788; PubMed=8335009;
RA Simon-Mateo C., Andres G., Vinuela E.;
RT "Polypeptide processing in African swine fever virus: a novel gene expression strategy for a DNA virus.";
RL EMBO J. 12:2977-2987(1993).
[18]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93233210; PubMed=8474154;
RA Prados F.J., Vinuela E., Alcamí A.;
RT "Sequence and characterization of the major early phosphoprotein p32 of African swine fever virus.";
RL J. Virol. 67:2475-2485(1993).
[19]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=92260660; PubMed=1583732;
RA Alcamí A., Angulo A., Lopez-Otin C., Munoz M., Freije J.M., Carrascosa A.L., Vinuela E.;
RT "Amino acid sequence and structural properties of protein p12, an African swine fever virus attachment protein.";
RL J. Virol. 66:3860-3868(1992).
[20]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93174976; PubMed=8438592;
RA Yanez R.J., Vinuela E.;
RT "African swine fever virus encodes a DNA ligase.";
RL Virology 193:531-536(1993).
[21]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93174941; PubMed=8382399;
RA Pena L., Yanez R.J., Revilla Y., Vinuela E., Salas M.L.;
RT "African swine fever virus guanylyltransferase.";

RL Virology 193:319-328(1993).
RN [22]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V;
RX MEDLINE-95159428; PubMed-7856088;
RA Simon-Mateo C., Freije J.M., Andres G., Lopez-Otin C., Vinuela E.;
RT "Mapping and sequence of the gene encoding protein p17, a major
RT African swine fever virus structural protein.";
RL Virology 206:1140-1144(1995).
RN [23]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V;
RX MEDLINE-92263807; PubMed-1316688;
RA Garcia-Beato R., Freije J.M., Lopez-Otin C., Blasco R., Vinuela E.,
RA Sals M.L.;
RT "A gene homologous to topoisomerase II in African swine fever virus.";
RL Virology 188:938-947(1992).
RN [24]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V;
RX MEDLINE-94091056; PubMed-8266720;
RA Freije J.M., Lain S., Vinuela E., Lopez-Otin C.;
RT "Nucleotide sequence of a nucleoside triphosphate phosphohydrolase
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKQOFF 8
Db 199 RRPQOFF 206

Query Match 57.4%; Score 35; DB 12; Length 509;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 39
Q18014 PRELIMINARY; PRT; 521 AA.
AC Q18014;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN C15C7.1.
GN C15C7.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
RX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Leimbach D.;
RT "The sequence of C. elegans cosmid C15C7.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41528; AAK3917.1.;
DR InterPro; IPR000727; T_SNARE.
DR SMART; SM00397; T_SNARE; 1.
SQ SEQUENCE 521 AA; 58924 MW; 7E52486E751D48F5 CRC64;

Query Match 57.4%; Score 35; DB 5; Length 521;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKQOFF 10
Db 504 PRSAFFGI 512

RESULT 40
Q9GUT4 PRELIMINARY; PRT; 681 AA.
AC Q9GUT4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE L4270.4.
GN L4270.4.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
RX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L.,
RA McDonagh P., Stuart K., Ivens A., Worthey E.A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC012524; AAG16717.1.;
SQ SEQUENCE 681 AA; 71416 MW; 6074EAA755F16F1E CRC64;

Query Match 57.4%; Score 35; DB 5; Length 681;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFF 9
Db 223 RRPQOFF 231

RESULT 41
Q9ESL2 PRELIMINARY; PRT; 682 AA.
AC Q9ESL2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ACYL-COA SYNTHETASE 5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
RX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-SPLEEN;
RA Ohtani M., Watanabe N., Kobayashi Y.;
RT "Analysis of genes associated with the guinea pig skin delayed-type
RT hypersensitivity reaction.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049761; BAB1604.1.;
DR InterPro; IPR000873; AMP-bind.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 682 AA; 75875 MW; 0566F8CA70B016E7 CRC64;

Query Match 57.4%; Score 35; DB 11; Length 682;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQOFF 10
Db 127 KPSPDQF 136

RESULT 42

P74619 PRELIMINARY: PRT; 832 AA.
 AC P74619;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 92.9 KDA PROTEIN.
 GN SL1477.
 OS *Synechocystis* sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.
 NCBI_TaxID=1148;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
 RA Hoouuchi T., Matsuno A., Muraki A., Nakazaki N., Naro K., Okumura S.,
 RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D90916; BAA18727.1;
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 832 AA; 92864 MW; CE02AA8DAFB2B9BE CRC64;

Query Match 57.4%; Score 35; DB 2; Length 832;
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFGL 10
 Db 669 RPKQOQFGL 678

RESULT 43
 O9XT20 PRELIMINARY: PRT; 1043 AA.
 AC O9XT20;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE R03E1.1 PROTEIN.
 GN R03E1.1.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Rhabditinae; *Caenorhabditis*.
 NCBI_TaxID=6239;
 RX NCBI_TaxID=6239;
 RA McMuray A.;
 RP SEQUENCE FROM N.A.
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";
 RL Nature 368:32-38(1994).
 DR EMBL: 292837; CAB07400.1;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.

DR PRINTS: PR00320; GPROTEINBRPT.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 4.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 2.
 KW Repeat; WD repeat.
 SO SEQUENCE 1043 AA; 115073 MW; A2B6FCDDC7536DF CRC64;

Query Match 57.4%; Score 35; DB 5; Length 1043;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKQOQFGL 11
 Db 955 RPKQOQFGL 964

RESULT 44
 O9UPP5 PRELIMINARY: PRT; 1278 AA.
 AC O9UPP5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE KIA1107 PROTEIN (FRAGMENT).
 GN KIA1107.
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB029030; BAA83059.1;
 FT NON-TER 1
 SO SEQUENCE 1278 AA; 140799 MW; DE032B2C4E1BDA29 CRC64;

Query Match 57.4%; Score 35; DB 4; Length 1278;
 Best Local Similarity 60.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKQOQFGL 11
 Db 890 RPKQOQFGL 899

RESULT 45
 O9SDB6 PRELIMINARY: PRT; 1611 AA.
 AC O9SDB6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE MYOSIN HEAVY CHAIN.
 GN AT2G33240.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eustoids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RX NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RL Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RESULT 48

09JUK11 PRELIMINARY; PRT; 154 AA.
AC 09JUK11;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EOSINOPHIL-ASSOCIATED RIBONUCLEASE 2 PRECURSOR.
GN EAR2.
OS Mus pahari (Shrew mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer R.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238402; AAF67702.1.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN.1.
SQ SEQUENCE 154 AA; 17927 MW; 08F002D5B461D6 CRC64;

Query Match 55.7%; Score 34; DB 11; Length 154;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 10
|||
Db 27 RPTPSQRFGL 36

RESULT 49

P70014 PRELIMINARY; PRT; 162 AA.
AC P70014;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96112032; PubMed=8845161;
RA Freitag J., Krieger J., Strotman J., Breer H.;
RT "Two classes of olfactory receptors in Xenopus laevis.";
RL Neuron 15:1383-1392(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Freitag J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08203; CAA69385.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
FT NON_TER 1
FT 162
SQ SEQUENCE 162 AA; 18296 MW; 6F75BDFB58B34541 CRC64;

Query Match 55.7%; Score 34; DB 13; Length 162;
Best Local Similarity 60.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RPKPOQFGLM 11
|||
Db 145 PKDOFFALL 154

RESULT 50

09X8G5 PRELIMINARY; PRT; 167 AA.
AC 09X8G5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
GN SCF7.08C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
RA Klashni H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL049819; CAB42667.1;
SQ SEQUENCE 167 AA; 18565 MW; 2A54F1F879D899E2 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 167;
Best Local Similarity 55.6%; Pred. No. 81;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 9
|||
Db 18 RPEPLRFGL 26

RESULT 51

09ZSX5 PRELIMINARY; PRT; 216 AA.
AC 09ZSX5;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 23.8 KDA PROTEIN.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Song R., Liaca V., Messing J.;
RT "Analysis of a 22-kDa alpha zein cluster in maize.";

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF090446; AAD09013.1; -
KW Hypothetical protein.
SQ SEQUENCE 216 AA; 23774 MW; E49E524C2B4E227B CRC64;

Query Match 55.7%; Score 34; DB 10; Length 216;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
||||| : |||
DB 69 RPKPSRTFALV 79

RESULT 52
ID 054788 PRELIMINARY; PRT; 253 AA.
AC 054788;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TRANSPOSASE.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95189099; PubMed=7883181;
RA Hui F.M., Zhou L., Morrison D.A.;
RT "Competence for genetic transformation in Streptococcus pneumoniae:
RT organization of a regulatory locus with homology to two lactococci A
RT secretion genes.";
RL Gene 153:25-31(1995).
DR EMBL: M36180; AAA69508.1; -
DR InterPro: IPR002560; Transposase_12.
DR Pfam: PF01610; Transposase_12; 1
SQ SEQUENCE 253 AA; 30676 MW; A7832B3118D11749 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 253;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOQFGLM 11
||||| : |||
DB 162 EPEKFFGLI 170

RESULT 53
ID 056868 PRELIMINARY; PRT; 266 AA.
AC 056868;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE VIRAL Tegument PROTEIN.
GN UL49.
OS gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98080487; PubMed=9420298;
RA Ziemann K., Mettenleiter T.C., Fuchs W.;
RT "Gene arrangement within the unique long genome region of infectious
RT taryngotracheitis virus is distinct from that of other
RT alphaherpesviruses.";
RL J. Virol. 72:847-852(1997).
DR EMBL: Y14300; CAA74678.1; -
DR InterPro: IPR001917; AminoTransf_2.

DR PROSITE: PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
SQ SEQUENCE 266 AA; 30358 MW; FF0459DAE1C6F4A9 CRC64;

Query Match 55.7%; Score 34; DB 12; Length 266;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOF 7
||||| : |||
DB 28 RPKPOF 34

RESULT 54
ID 09GUG0 PRELIMINARY; PRT; 270 AA.
AC 09GUG0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN Y73B6BL.M.
GN Y73B6BL.M.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC084197; AAG23472.1; -
SQ SEQUENCE 270 AA; 30321 MW; 08F5ABA5FEFC3446 CRC64;

Query Match 55.7%; Score 34; DB 5; Length 270;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPOFF 8
||||| : |||
DB 151 PKPRTF 157

RESULT 55
ID 09GMX6 PRELIMINARY; PRT; 304 AA.
AC 09GMX6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 34.0 KDA PROTEIN (FRAGMENT).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN PARIENTAL LOBE;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DB 49 RPKSROFF 56

RESULT 58

Q9JYV5 PRELIMINARY; PRT; 318 AA.

AC Q9JYV5;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DE PUTATIVE RIBOFLAVIN KINASE/FMN ADENYLYLTRANSFERASE (EC 2.7.1.26).

GN RIBF OR NMA0621.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_Taxid=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parhill J., Achman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S., Jagsis K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;

RA Whitehead S., Spratt B.G., Barrell B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."

RL Nature 404:502-506(2000).

DR EMBL; AL162753; CAB83911.1; -.

DR InterPro: IPR002606; FAD_Synth.

DR InterPro: IPR001412; tRNA-Synt_1.

DR Pfam: PF01687; FAD_Synth; 1.

DR ProDom: PD003662; FAD_Synth; 1.

DR PROSITE: PS00178; AA-TRNA_LIGASE_I; UNKNOWN_1.

KW Transferase; Kinase; Nucleotidyltransferase; Complete proteome.

SQ SEQUENCE 318 AA; 35605 MW; 224286E1C6DA0528 CRC64;

QY 2 PKPOOFFGL 10

DB 68 PPKKFFAL 76

Query Match 55.7%; Score 34; DB 2; Length 318;

Best Local Similarity 55.6%; Pred. No. 1.6e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 59

Q9MJ81 PRELIMINARY; PRT; 355 AA.

AC Q9MJ81;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DE MITOCHONDRIAL DNA, COMPLETE GENOME.

OS Physarum polycephalum (Slime mold).

OC Mitochondrion.

OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;

OX NCBI_Taxid=5791;

RN [1]

RP SEQUENCE FROM N.A.

RA Takano H., Abe T., Sakurai R., Moriyama Y., Miyazawa Y., Nozaki H., Kawano S., Sasaki N., Kuroiwa T.;

RT "The complete DNA sequence of the mitochondrial genome of Physarum polycephalum."

RL Mol. Gen. Genet. 0:0-0(2000).

DR EMBL; AB027295; BAB08081.1; -.

KW Mitochondrion.

SEQ SEQUENCE 355 AA; 43335 MW; 5CE0AABD08D6E88F CRC64;

Query Match 55.7%; Score 34; DB 8; Length 355;

Best Local Similarity 50.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10

DB 207 KRPDPFFSL 216

RESULT 60

082469 PRELIMINARY; PRT; 359 AA.

AC 082469;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)

DE PROTEIN PHOSPHATASE-2C.

GN PP2C.

OS Mesembryanthemum crystallinum (Common ice plant).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.

OX NCBI_Taxid=3544;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LEAF;

RA Miyazaki S., Koga R., Bohnert H.J., Fukuhara T.;

RT "Cell-, tissue- and environmental response-specific expression of 10 members of the PP2C gene family in Mesembryanthemum crystallinum."

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF075580; AAC36698.1; -.

DR HSP; P35813; 1A60.

DR InterPro: IPR002222; PP2C.

DR InterPro: IPR003589; PP2C catalytic.

DR InterPro: IPR001932; PP2C domain.

DR InterPro: IPR003588; PP2C_sig.

DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00332; PP2Cc; 1.

DR SMART; SM00331; PP2C_sig; 1.

DR PROSITE; PS01032; PP2C; 1.

SQ SEQUENCE 359 AA; 39565 MW; 42CCF7092742CD6C CRC64;

QY 2 PKPOOFFGL 10

DB 84 PKPSAFYGV 92

Query Match 55.7%; Score 34; DB 10; Length 359;

Best Local Similarity 55.6%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 61

049132 PRELIMINARY; PRT; 393 AA.

AC 049132;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JAN-1999 (TREMBLrel. 09, last sequence update)

DE POLYPHENOL OXIDASE (FRAGMENT).

OS Diospyros kaki (kaki persimmon).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; Ericales; Ebenaceae; Diospyros.

OX NCBI_Taxid=35925;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FUJY;

RA Bahn S.C., Shin J.S.;

RT "Cloning and expression of PPO(Polyphenol Oxidase) cDNA in persimmon

RT (Diospyros kaki).";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF039165; AAC69365.1; -;
 DR Mendel: 33386; Dloka:1008;33386.
 DR InterPro: IPR002227; Tyrosinase.
 DR Pfam: PF00264; tyrosinase; 1.
 DR PRINTS: PR00092; TYROSINASE.
 DR PROSITE: PS00497; TYROSINASE_1; 1.
 DR PROSITE: PS00498; TYROSINASE_2; 1.
 FT NON_TER 393 393
 SQ SEQUENCE 393 AA; 45559 MW; D8CEFA2CB49B8E51 CRC64;

Query Match 55.7%; Score 34; DB 10; Length 393;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFG 9
 | | | | |
 Db 169 PCPSQFG 176

RESULT 62
 0925W4 PRELIMINARY; PRT; 405 AA.
 AC 0925W4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TOPOISOMERASE.
 CN TOP.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=142;
 RA Tsol T.V., Plotnikova E.G., Cole J.R., Guerin W.F., Bagdasarian M.,
 RA Tiedje J.M.;
 RT "Cloning, expression and nucleotide sequence of the Pseudomonas
 aeruginosa strain 142 ohb genes for oxygenolytic ortho-dehalogenation
 of halobenzoates.";
 RL Appl. Environ. Microbiol. 65:0-0(1999).
 DR EMBL: AF121970; AAD20003.1; -;
 DR InterPro: IPR000380; Protopoisomerase.
 DR Pfam: PF01396; zf-C4_Topoisom; 2.
 KW Isomerase.
 SQ SEQUENCE 405 AA; 45242 MW; 76BDCBBE52812509 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 405;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
 | | | | |
 Db 189 RPDPOQF 195

RESULT 63
 021172 PRELIMINARY; PRT; 410 AA.
 AC 021172;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Galapagus galapagensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phyllophaga; Curculionidae; Entiminae; Entimini;

OC Galapagus.
 OX NCBI_TaxID=63362;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sequence A.S., Farrell B., Salmore A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL: AF015914; AAB64294.1; -;
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 410 410
 SQ SEQUENCE 410 AA; 45420 MW; B4C17F9E7A8C698F CRC64;

Query Match 55.7%; Score 34; DB 8; Length 410;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGL 10
 | | | | |
 Db 346 PQHFFGL 352

RESULT 64
 013352 PRELIMINARY; PRT; 415 AA.
 AC 013352;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MAP KINASE MPLS.
 GN MPLS.
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GV11;
 RA Xu J.R., Hamer J.E.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF020316; AAC63682.1; -;
 DR HSSP: O16539; IMFC.
 DR InterPro: IPR000719; Euk_Kinase.
 DR InterPro: IPR003527; MAP_Kin.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferrase.
 SQ SEQUENCE 415 AA; 46992 MW; F149D728145E22A CRC64;

Query Match 55.7%; Score 34; DB 3; Length 415;

DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DB HYPOTHEMETICAL 69.4 KDA PROTEIN F23M19.11.
GN F23M19.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
RA Alatafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Hutzler L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
RT "Arabidopsis thaliana chromosome 1 BAC F23M19 sequence."
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AC007454; AAD39611.1; -.
DR HSSP: P09215; 1BDY.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00560; LRR; 4.
DR Pfam: PF00069; Jkinase; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 4.
DR SMART: SM00221; STYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 628 AA; 69402 MW; 23F6C0DC3717C74F CRC64;

Query Match 55.7%; Score 34; DB 10; Length 628;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQF 8
DB 267 RRPQEFF 274

RESULT 68
Q9C792 PRELIMINARY; PRT; 646 AA.
ID Q9C792;
AC Q9C792;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE HYPOTHEMETICAL 73.9 KDA PROTEIN.
GN F10D13_27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Alatafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dekar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzler L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kuriz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltl R., Matzali A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL: AC073178; AAG60099.1; -.
DR InterPro: IPR003864; DUF221.
DR Pfam: PF02714; DUF221; 1.
KW Hypothetical protein.
SQ SEQUENCE 646 AA; 73897 MW; DB99EE6D3D7E1D4F CRC64;

Query Match 55.7%; Score 34; DB 10; Length 646;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQF 7
DB 108 RRPQEF 114

RESULT 69
Q9A926 PRELIMINARY; PRT; 737 AA.
ID Q9A926;
AC Q9A926;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update).
DE TONB-DEPENDENT RECEPTOR, PUTATIVE.
GN CC0815.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173696; PubMed=11259647;
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005758; AAK22800.1; -.
DR TIGR: CC0815; -.
KW Receptor; Complete proteome.
SQ SEQUENCE 737 AA; 80297 MW; F09E9EAFDE6A6328 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 737;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQF 7
DB 723 RRPQEF 729


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RESULT 70
09W5X2
ID 09W5X2 PRELIMINARY: PRT: 738 AA.
AC 09W5X2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG15332 PROTEIN.
GN CG15332
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunbok B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Foster C., Gilbertson A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajani M., Kalush F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE002611; AAF45377.1;
DR FlyBase; FBgn0031088; CG15332.
SQ SEQUENCE 738 AA; 78968 MW; 2BD221B563B1639 CRC64;
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AC 09Y062;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RECO HELICASE HOMOLOG.
GN BLM OR DMBIM OR CG6920.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=99160561; PubMed=10049920;
RA Kusano K., Berres M.E., Engels W.R.;
RT "Evolution of the RECO family of helicases: A drosophila homolog,
RT Dmbim, is similar to the human bloom syndrome gene.";
RL Genetics 151:1027-1039(1999).
CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
CC -1- SIMILARITY: TO DEAD/DEAH C-TERMINAL DOMAIN.
DR EMBL; U92536; AAD4141.1; -.
RA FlyBase; FBgn0015800; blm.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_ATP_helicase.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR002121; HRDC.
DR Pfam; PF00270; DEAD_1.
DR Pfam; PF00271; helicase_C_1.
DR Pfam; PF00570; HRDC_1.
DR SMART; SM00487; DEXDC_1.
DR SMART; SM00490; HELIC_1.
DR SMART; SM00341; HRDC_1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; UNKNOWN_1.
DR ATP-binding; Helicase.
KW SEQUENCE 1487 AA; 165777 MW; 5233D770AB4A3E30 CRC64;
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Query Match 55.7%; Score 34; DB 5; Length 1487;
Best Local Similarity 54.5%; Pred. NO. 7.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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OY 1 RPKPOFFGIM 11
DB 953 RSKPQHFSGII 963
```

RESULT 72

09VG18 PRELIMINARY: PRT: 1487 AA.

AC 09VG18;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE BLM PROTEIN.

GN BLM OR CG6920.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=BERKELEY;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Query Match	55.7%	Score 34	DB 5	Length 1487	
Best Local Similarity	54.5%	Pred. No. 7.9e+02			
Matches	6	Conservative	2	Mismatches	3
				Indels	0
				Gaps	0
QY	1 RPKPQQPFGLM 11				
	1 1 1 1 1 1 1				
Db	953 RSKPQHFGSII 963				
RESULT	73				
Q9VQU8					
ID	Q9VQU8	PRELIMINARY	PRT	1970	AA.
AC	Q9VQU8				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	CG10020 PROTEIN.				
GN	CG10020.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephyroidae; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

Query Match	55.7%	Score 34	DB 54	Length 1970
Best Local Similarity	45.5%	Pred. No. 1.1e+03		
Matches	5	Conservative	4	Mismatches 2
				Indels 0
				Gaps 0
Qy	1	RPKPQPFPGLM 11		
	11	::::111:		
Db	54	RRRRRPFPGCL 64		
RESULT	74			
09JUN9				
ID	09JUN9	PRELIMINARY;	PRT;	71 AA.
AC	09JUN9			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)			
DE	HYPOTHEICAL PROTEIN NMA1216.			
GN	NMA1216.			
OS	Neisseria meningitidis (serogroup A).			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			

OX NCBI_TaxID=65699;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
 RA MEDLINE=2022556; PubMed=10761919;
 RA Parkhill J., Achman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.";
 RT Nature 404:502-506(2000).
 RL EMBL: AL162755; CAB84476.1; -;
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 71 AA; 7914 MW; 3FE90AF8F5F1B10 CRC64;
 SQ

Query Match 54.1%; Score 33; DB 2; Length 71;
 Best Local Similarity 71.4%; Pred. No. 51;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOFFG 9
 11:111
 DB 40 KPQFFG 46

RESULT 75

OS860 PRELIMINARY; PRT; 101 AA.

AC 05860: 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE HYPOTHETICAL 11.7 KDA PROTEIN PH1133.

GN PH1133.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.

OX NCBI_TaxID=53953;
 [1]

RP SEQUENCE FROM N.A.

RC STRAIN-OT3;

RA MEDLINE=98344137; PubMed=9679194;

RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

RA Masuchi Y., Shizuya H., Kikuchi H.;

RT "Complete sequence and gene organization of the genome of a hyper-

RT thermophilic archaeobacterium, *Pyrococcus horikoshii* 073.";

RL DNA Res. 5:55-76(1998).

DR EMBL: AP000005; BAA30233.1; -;

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 101 AA; 11693 MW; A07F52982B589492 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 101;
 Best Local Similarity 75.0%; Pred. No. 74;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFG 11
 11111
 DB 18 PQOFFG 25

RESULT 76

OS860 PRELIMINARY; PRT; 102 AA.

AC 096D2: 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 3526402H2IRIK PROTEIN.
 GN 3526402H2IRIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL: AK014391; BMB29318.1; -;

DR MGD: MGI:191393; 3526402H2IRIK.

SQ SEQUENCE 102 AA; 11630 MW; FCFL1033BEB0EB847 CRC64;

Query Match 54.1%; Score 33; DB 11; Length 102;
 Best Local Similarity 60.0%; Pred. No. 75;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOFFG 11
 11111
 DB 88 PKPOFFG 97

RESULT 77

OS860 PRELIMINARY; PRT; 103 AA.

AC 09XJ71: 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE CSPPK.2 (FRAGMENT).

GN CSPPK.2.

OS Cucumis sativus (Cucumber).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euroids I; Cucurbitales; Cucurbitaceae; Cucumis.

OX NCBI_TaxID=3659;
 [1]

RP SEQUENCE FROM N.A.

RC TISSUE-HYPOCOTYL;

RA MEDLINE=99033466; PubMed=9816678;

RA Chono M., Nemoto K., Yamane H., Yamaguchi I., Murofushi N.;

RT "Characterization of a protein kinase gene responsive to auxin and

RT gibberellin in cucumber hypocotyls.";

RL Plant Cell Physiol. 39:958-967(1998).

DR EMBL: AB001589; BAA82163.1; -;

FT NON_TER 103 103

SQ SEQUENCE 103 AA; 11259 MW; 02948A7EDEFD2CEA CRC64;

Query Match 54.1%; Score 33; DB 10; Length 103;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFGL 10
 ||| |||
 Db 74 PKPSDFGL 82

RESULT 78
 080033 PRELIMINARY; PRT; 130 AA.

AC 080033;
 DT 01-NOV-1998 (TREMBLERL. 08, Created)
 DT 01-NOV-1998 (TREMBLERL. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLERL. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Exoneurella lawsoni.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 NCBI_TaxID=78187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 Apidae: Allodapini): evidence from molecular and morphological data
 sets.";
 RT sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC -1- FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072661; AAC24880.1; -.
 DR InterPro: IPR000983; COX1. 1.
 DR Pfam: PF00115; COX1. 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 15339 MW; 11CFAF1F1EAE22F2 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
 || | |||
 Db 56 PQHFLGLM 63

RESULT 79
 080034 PRELIMINARY; PRT; 130 AA.

AC 080034;
 DT 01-NOV-1998 (TREMBLERL. 08, Created)
 DT 01-NOV-1998 (TREMBLERL. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLERL. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Exoneurella tridentata.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 NCBI_TaxID=78189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 Apidae: Allodapini): evidence from molecular and morphological data
 sets.";
 RT sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC -1- FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072663; AAC24882.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1. 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 15438 MW; 4B9444ABF5AC3F4F CRC64;

Query Match 54.1%; Score 33; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
 || | |||
 Db 56 PQHFLGLM 63

RESULT 80
 079124 PRELIMINARY; PRT; 131 AA.

AC 079124;
 DT 01-NOV-1998 (TREMBLERL. 08, Created)
 DT 01-NOV-1998 (TREMBLERL. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLERL. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Braunsapis unicolor.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Braunsapis.
 NCBI_TaxID=78183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 Apidae: Allodapini): evidence from molecular and morphological data
 sets.";
 RT sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC -1- FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072659; AAC24878.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1, 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 131
 FT NON_TER 1 131
 SQ SEQUENCE 131 AA; 15603 MW; F1407925903C9FE8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 DB 56 PQHFLGLM 63

RESULT 81
 ID 079125 PRELIMINARY; PRT: 131 AA.
 AC 079125;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Brevineura xanthoclypeata.
 OG Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Apoidea; Apidae; Brevineura.
 OX NCBI_TaxID=78184;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072660; AAC24879.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1, 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 131
 FT NON_TER 1 131
 SQ SEQUENCE 131 AA; 15508 MW; D5E0508AB020093F CRC64;

Query Match 54.1%; Score 33; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 DB 56 PQHFLGLM 63

RESULT 82
 ID 079126 PRELIMINARY; PRT: 131 AA.
 AC 079126;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Exoneurella eremophila.
 OG Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Apoidea; Apidae; Exoneurella.
 OX NCBI_TaxID=78186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICCYTOCHROME C.
 CC -1- CORFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072662; AAC24881.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1, 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 131
 FT NON_TER 1 131
 SQ SEQUENCE 131 AA; 15531 MW; 55B915590BDFCF85 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 DB 56 PQHFLGLM 63

RESULT 83
 ID 099834 PRELIMINARY; PRT: 151 AA.
 AC 099834;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Ophraella communis.
 OG Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phyltophaga; Chrysomeloidea; Chrysomelidae; Galerucinae;
 CC Ophraella.
 OX NCBI_TaxID=38162;
 RN [1]
 RP SEQUENCE FROM N.A.

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RX MEDLINE-99261638; PubMed-10331253;
RA Funk D.J.:
RT "Molecular systematics of cytochrome oxidase I and 16S from
RL Neochlamisus leaf beetles and the importance of sampling.";
RL Mol. Biol. Evol. 16:67-82(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER E (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF092679; AAD05540.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 151
FT SEQUENCE 151 AA; 17205 MW; 0ED59F8A4C59B2DE CRC64;
SQ
Query Match 54.1%; Score 33; DB 8; Length 151;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PQOFFGLM 11
Db 99 PQHFLGLM 106
RESULT 84
Q9G462 PRELIMINARY; PRT; 156 AA.
AC Q9G462;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Diadastia consociata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Diadastia.
OX NCB1_TaxID=70982;
RN [1]
RP SEQUENCE FROM N.A.
RA Sipes S.D., Wolf P.G.:
RT "Phylogenetic relationships in Diadastia, a group of specialist bees.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF300575; AAG48588.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.

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DR PRINTS: PRO1165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 156
FT SEQUENCE 156 AA; 18513 MW; 7F32509B13AD420B CRC64;
SQ
Query Match 54.1%; Score 33; DB 8; Length 156;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PQOFFGLM 11
Db 75 PQHFLGLM 82
RESULT 85
Q9HB06 PRELIMINARY; PRT; 159 AA.
AC Q9HB06;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 18.5 KDA PROTEIN (SIMILAR TO F-BOX AND WD-40 DOMAIN
DE PROTEIN 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.:
RT "Novel Human cDNA clones with function of inhibiting cancer cell
RT growth."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=CERVIX CARCINOMA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF217998; AAC17240.1; -.
DR EMBL: BC000850; AAH00850.1; -.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40.2.
DR SMART: SM00320; WD40.2.
DR PROSITE: PSS0082; WD_REPEATS.2; 1.
DR PROSITE: PSS0294; WD_REPEATS_REGION.1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 159 AA; 18545 MW; 2DD8FB544D00E68 CRC64;
Query Match 54.1%; Score 33; DB 4; Length 159;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOOFF 8
Db 144 RPKPRTF 151
RESULT 86
Q9CV91 PRELIMINARY; PRT; 161 AA.
AC Q9CV91;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 2300004H16RIK PROTEIN (FRAGMENT).
GN 2300004H16RIK.
OS Mus musculus (Mouse).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBL_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Iizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koshida H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 DR EMBL: AK009028; BAB26036.1; -;
 DR MGD: MGI:1913752; 2300004H6R1K.
 FT NON_TER 161
 SO SEQUENCE 161 AA; 18414 MW; 54C67BF91F6E0B17 CRC64;

Query Match 54.1%; Score 33; DB 11; Length 161;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
 111111
 Db 38 RPKPOOFF 45

RESULT 87
 09G7A3 PRELIMINARY; PRT; 192 AA.
 AC 09G7A3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Brevineura rufitarsis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Brevineura.
 OX NCBL_TaxID=135662;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRUFT43.2;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005222; AAG24230.1; -;
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 192 AA; 22364 MW; 54C417614E83D918 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 192;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 111111
 Db 116 POOFFGLM 123

RESULT 88
 09G798 PRELIMINARY; PRT; 192 AA.
 AC 09G798;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xylocopa bombylans.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xylocopa.
 OX NCBL_TaxID=135667;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=DES.BOM;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005227; AAG24235.1; -;
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 192 AA; 22133 MW; F25AF0200986BC0 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 192;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 DB 117 PQHFLGLM 124

RESULT 89

09G782 ID PRELIMINARY; PRT: 197 AA.

AC 09G782; "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Xyllocopa varipuncta.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata;

OC Apoidea; Apoidea; Xyllocopa.

OX NCBI_TaxID=135685;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NEO.VAR:

RA Lays R., Cooper S.J.B., Schwarz M.B.;

RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AY005245; AAC24251.1; -.

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PR01165; CYCOXIDASE1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 197

FT SEQUENCE 197 AA; 22799 MW; 524729587C51DEB7 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 197;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111

DB 116 PQHFLGLM 123

RESULT 90

09G7A2 ID PRELIMINARY; PRT: 198 AA.

AC 09G7A2; "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Xyllocopa micans (southern carpenter bee).

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata;

OC Apoidea; Apoidea; Xyllocopa.

OX NCBI_TaxID=135663;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SCH.MT2.

RA Lays R., Cooper S.J.B., Schwarz M.B.;

RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AY005223; AAC24231.1; -.

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PR01165; CYCOXIDASE1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 198

FT SEQUENCE 198 AA; 22749 MW; 1C18C71053A23E07 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111

DB 117 PQHFLGLM 124

RESULT 91

09G7A1 ID PRELIMINARY; PRT: 198 AA.

AC 09G7A1; "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Xyllocopa tranquebarica.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata;

OC Apoidea; Apoidea; Xyllocopa.

OX NCBI_TaxID=135664;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NYCTOI.

RA Lays R., Cooper S.J.B., Schwarz M.B.;

RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005224; AAG24232.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; CYCOXIDASE1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 198
 SQ SEQUENCE 198 AA; 22876 MW; B87C26FA7B716B78 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 1111111
 DB 117 POHFGLM 124

RESULT 92
 09G799 PRELIMINARY; PRT; 198 AA.
 AC 09G799;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa violacea.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata;
 OC Apoidea; Apidae; Xyllocopa.
 OX NCBI_TaxID=135666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X.VIOL3;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005226; AAG24234.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 198
 SQ SEQUENCE 198 AA; 22909 MW; 7B5511PCD129FE82 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 1111111
 DB 117 POHFGLM 124

RESULT 93
 09G797 PRELIMINARY; PRT; 198 AA.
 AC 09G797;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa tabaniformis tabaniformis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata;
 OC Apoidea; Apidae; Xyllocopa.
 OX NCBI_TaxID=135668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOT01;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005228; AAG24236.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 198
 SQ SEQUENCE 198 AA; 22941 MW; 517DE2848CD0A53A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 1111111
 DB 117 POHFGLM 124

RESULT 94
 09G796 PRELIMINARY; PRT; 198 AA.
 AC 09G796;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa sicheli.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCHI_Taxid=135670;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=GN.SIC2;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005230; AAG24237.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1, 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22911 MW; 3BB7A2DDDDACC3BC CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POQFGLM 11
| | | | |
DB 117 PQHFLGLM 124

RESULT 95
09G795 PRELIMINARY; PRT; 198 AA.
AC 09G795;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xyllocopa virginica virginica (common carpenter bee).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCHI_Taxid=135671;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=XO1D;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005231; AAG24238.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1, 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22892 MW; F48FB16F6A913010 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POQFGLM 11
| | | | |
DB 117 PQHFLGLM 124

RESULT 96
09G793 PRELIMINARY; PRT; 198 AA.
AC 09G793;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xyllocopa aruana.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCHI_Taxid=135674;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=KOP.TV2;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005234; AAG24240.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1, 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22932 MW; 9E20D0DF4109493C CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;

	Matches	6;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
OY	4	PQFFFLGM	11							
DB	117	PQHFLGLM	124							

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005237; AAC24243.1; -.
DR InterPro; IPR000383; COX1.
DR Pfam; PF00115; COX1, 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22950 MW; FA187D7A98E3CEBD CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 POOFGLM 11
1111111
Db 117 POHFGLM 124

RESULT 100
09G789 PRELIMINARY; PRT; 198 AA.
AC 09G789;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylocopa nigrita.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xylocopa.
OX NCBI_Taxid=135678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AFR.NIG;
RA Leys R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005238; AAC24244.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1, 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22966 MW; 67D04DC3CD21F032 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 POOFGLM 11
1111111
Db 117 POHFGLM 124

RESULT 101
09G788 PRELIMINARY; PRT; 198 AA.
AC 09G788;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylocopa flavorufa.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xylocopa.
OX NCBI_Taxid=135679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MESOTRIAL;
RA Leys R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005239; AAC24245.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1, 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 23006 MW; 2D52B4848E335E50 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 POOFGLM 11
1111111
Db 117 POHFGLM 124

RESULT 102
09G787 PRELIMINARY; PRT; 198 AA.
AC 09G787;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylocopa olivieri.

Query Match 54.1%; Score 33; DB 8; Length 198;

06 Mitochondrion.
 0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 0C Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 0C Apoidea; Apidae; Xyllocopa.
 0X NCBI_TaxID=135680;
 0N [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PRO.OLI;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005240; AAC24246.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 RW Respiratory chain; Transmembrane.
 FT NON_TER 1 198
 FT NON_TER 1 198
 SQ SEQUENCE 198 AA; 22906 MW; DC53A42DAB0B250E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 DB 117 PQHFLGLM 124

RESULT 103
 09G786 PRELIMINARY; PRT; 198 AA.
 AC 09G786;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa latipes.
 OG Mitochondrion.
 0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 0C Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 0C Apoidea; Apidae; Xyllocopa.
 0X NCBI_TaxID=135681;
 0N [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PLA.B24;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3

CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005241; AAC24247.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 RW Respiratory chain; Transmembrane.
 FT NON_TER 1 198
 FT NON_TER 1 198
 SQ SEQUENCE 198 AA; 22917 MW; A36BB24512DDB00 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 DB 117 PQHFLGLM 124

RESULT 104
 09G785 PRELIMINARY; PRT; 198 AA.
 AC 09G785;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa aculeipennis.
 OG Mitochondrion.
 0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 0C Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 0C Apoidea; Apidae; Xyllocopa.
 0X NCBI_TaxID=135682;
 0N [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOPL0.T6;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005242; AAC24248.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 RW Respiratory chain; Transmembrane.
 FT NON_TER 1 198
 FT NON_TER 1 198
 SQ SEQUENCE 198 AA; 22896 MW; 219F5F376DCDF4C6 CRC64;


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CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005246; AAC24232.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT TER 198
SQ SEQUENCE 198 AA; 22954 MW; E96ACA0C08B0E540 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 117 PQHFLGLM 124

RESULT 108
ID 09G780 PRELIMINARY; PRT; 198 AA.
AC 09G780;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xyllocopa frontalis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCBI_TaxID=135688;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ME3.FRO12;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
RT (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005248; AAC24233.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT TER 198
SQ SEQUENCE 198 AA; 22839 MW; 9949108D2FCC6662 CRC64;

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Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 117 PQHFLGLM 124

RESULT 109
ID 09A0J6 PRELIMINARY; PRT; 207 AA.
AC 09A0J6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (FRAGMENT).
GN LYSS.
OS Acinetobacter sp. M-1.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=123502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-1;
RX MEDLINE=21101882; PubMed=11160120;
RA Tani A., Ishige T., Sakai Y., Kato N.;
RT "Gene structures and regulation of the alkane hydroxylase complex in
RT Acinetobacter sp. strain M-1.";
RL J. Bacteriol. 183:1819-1823(2001).
DR EMBL: AB049412; BAB33290.1; -.
KW Aminocyl-1-trna synthetase.
KW NON_TER 207
FT TER 207
SQ SEQUENCE 207 AA; 23581 MW; EB9C6A678E484B98 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 207;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
DB 164 RPLPKFHGL 173

RESULT 110
ID 09XDK9 PRELIMINARY; PRT; 211 AA.
AC 09XDK9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PURATIVE METHYL TRANSFERASE.
OS Bacteroides fragilis.
OC Bacteria; CFB group; Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIC 9343;
RX MEDLINE=99307214; PubMed=10377135;
RA Comstock L.E., Coyne M.J., Tzianabos A.O., Pantostil A.,
RA Onderdonk A.B., Kasper D.L.;
RT "Analysis of a capsular polysaccharide biosynthesis locus of
RT Bacteroides fragilis.";
RL Infect. Immun. 67:3525-3532(1999).
DR EMBL: AF048749; AAD40706.1; -.
DR InterPro: IPR00051; SAM_bind.
DR InterPro: IPR001601; Meth-transf.
KW Transferrase.
SQ SEQUENCE 211 AA; 23732 MW; 4BDE0F71C25F850E CRC64;

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Query Match 54.1%; Score 33; DB 2; Length 211;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPOOFFGIM 11
 11:11111
 DB 16 KPSFFGIM 24

RESULT 111

O9RRR9 PRELIMINARY; PRT; 234 AA.
 AC O9RRR9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CONSERVED HYPOTHELICAL PROTEIN.
 GN DR2585.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI;
 RX MEDLINE=20036896; Pubmed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: A6002088; AAF12124.1; -.
 DR HSP: O26255; 1EJE.
 DR TIGR: DR2585; -.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 234 AA; 25176 MW; 37CEA57E6847F70 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 234;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PPOFFGIM 11
 1111111
 DB 56 PYSFFGIM 63

RESULT 112

O9CR69 PRELIMINARY; PRT; 240 AA.
 AC O9CR69;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE 2300004H16RIK PROTEIN.
 GN 2300004H16RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arai K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Cassavant T.,
 RA Fiedrichmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK019970; BAB31941.1; -.
 DR EMBL: AK012917; BAB28548.1; -.
 DR MGI: MGI:1913752; 2300004H16RIK.
 SQ SEQUENCE 240 AA; 28034 MW; 17DCB43406E5A309 CRC64;

Query Match 54.1%; Score 33; DB 11; Length 240;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
 1111111
 DB 38 RPNPOOFF 45

RESULT 113

O9TCG7 PRELIMINARY; PRT; 265 AA.
 AC O9TCG7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus farinosus.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 OX NCBI_TaxID=77575;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N., Mitchell P.L., Packer L.;
 RT "Mitochondrial DNA differentiation between two cryptic Halictus
 RT (Hymenoptera: Halictidae) species.";
 RL Ann. Entomol. Soc. Amer. 91:387-391(1998).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 CC FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF045372; AAD47364.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 265 265

SQ SEQUENCE 265 AA; 30204 MW; 05027E8D6A47DF0D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 265;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGIM 11
11 1111
DB 184 PQHFLGIM 191

RESULT 114

OYTG66 PRELIMINARY; PRT; 265 AA.
AC OYTG66;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Halictus rubicundus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
OX NCBI_TaxID=77578;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N., Mitchell P.L., Packer L.;
RT "Mitochondrial DNA differentiation between two cryptic Halictus
(Hymenoptera: Halictidae) species.";
RL Ann. Entomol. Soc. Amer. 91:387-391(1998).
RT -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF045373; AAD47365.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 265
SQ SEQUENCE 265 AA; 30295 MW; 500DA4B4EFA3F1A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 265;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGIM 11
11 1111
DB 184 PQHFLGIM 191

RESULT 115

OYTG65 PRELIMINARY; PRT; 266 AA.
AC OYTG65;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.
OS Halictus poeyi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
OX NCBI_TaxID=77577;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N., Mitchell P.L., Packer L.;
RT "Mitochondrial DNA differentiation between two cryptic Halictus
(Hymenoptera: Halictidae) species.";
RL Ann. Entomol. Soc. Amer. 91:387-391(1998).
RT -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF045376; AAD47368.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 266
SQ SEQUENCE 266 AA; 30263 MW; A9CF473DA4FD6010 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 266;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGIM 11
11 1111
DB 184 PQHFLGIM 191

RESULT 116

OYTG64 PRELIMINARY; PRT; 266 AA.
AC OYTG64;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Halictus poeyi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
OX NCBI_TaxID=77577;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N., Mitchell P.L., Packer L.;
RT "Mitochondrial DNA differentiation between two cryptic Halictus
(Hymenoptera: Halictidae) species.";
RL Ann. Entomol. Soc. Amer. 91:387-391(1998).
RT -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).

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CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF045377; AAD47369.1; -.
DR InterPro: IPR009883; COX1.
DR Pfam: PF00115; COX1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 266
SQ SEQUENCE 266 AA; 30290 MW; A9CF473DA4E74910 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 266;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQDFGLM 11
DB 184 PQHFLGLM 131

RESULT 117
Q9T2M6 PRELIMINARY; PRT; 266 AA.
AC Q9T2M6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Halictus ligatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
OX NCBI_TaxID=77576;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N., Mitchell P.L., Packer L.;
RT "Mitochondrial DNA differentiation between two cryptic Halictus
RT (Hymenoptera: Halictidae) species."
RL Ann. Entomol. Soc. Amer. 91:387-391(1998)..
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF045375; AAD47367.1; -.
DR EMBL: AF045374; AAD47366.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 266
SQ SEQUENCE 266 AA; 30308 MW; 1DCF473DA4E1E57A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 266;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 4 PQDFGLM 11
DB 184 PQHFLGLM 191

RESULT 118
O53361 PRELIMINARY; PRT; 299 AA.
ID O53361;
AC O53361;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE PUTATIVE ACID PHOSPHATASE.
GN RV3310 OR MTV016.09.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrall B.G.;
RT Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
DR EMBL: AL021841; CA017082.1; -.
DR TubercuList; RV3310; -.
KM Complete proteome.
SQ SEQUENCE 299 AA; 31807 MW; C5E8C49CF62C8BF8 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQDFGL 10
DB 181 PKPNYPGL 189

RESULT 119
Q9NE15 PRELIMINARY; PRT; 299 AA.
ID Q9NE15;
AC Q9NE15;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE HYPOTHETICAL 32.7 KDA PROTEIN.
GN I5808.12.
OS Leishmania major.
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,
RA Rajandream M.A., Barrall B.G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RX MEDLINE=9816435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;

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ID	PRELIMINARY;	PRT;	327 AA
Q9RZR1			

AC Q9R2R1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DRB0057.
OS Deinococcus radiodurans.
OG Plasmid MPl.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001826; AAF12602.1; -.
DR TIGR: DRB0057; -.
KW Plasmid; Complete proteome.
SQ SEQUENCE 327 AA; 38026 MW; 972646ABAFE4DE0 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Y 1 RPKPOFFGLM 11
| | | | | : : :
Db 297 RPKPOFFMAIL 307

RESULT 124
Q9R2J3
ID Q9R2J3 PRELIMINARY; PRT; 327 AA.
AC Q9R2J3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DRB0134.
OS Deinococcus radiodurans.
OG Plasmid MPl.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001826; AAF12606.1; -.
DR TIGR: DRB0134; -.
KW Plasmid; Complete proteome.
SQ SEQUENCE 327 AA; 38018 MW; ED4DAD9413470AC CRC64;

Query Match 54.1%; Score 33; DB 2; Length 327;

Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Y 1 RPKPOFFGLM 11
| | | | | : : :
Db 297 RPKPOFFMAIL 307

RESULT 125
Q9RY10
ID Q9RY10 PRELIMINARY; PRT; 327 AA.
AC Q9RY10;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DR0144.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001876; AAF09729.1; -.
DR TIGR: DR0144; -.
KW Complete proteome.
SQ SEQUENCE 327 AA; 37974 MW; 2B8FE12290FB169 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Y 1 RPKPOFFGLM 11
| | | | | : : :
Db 297 RPKPOFFMAIL 307

RESULT 126
Q9R3L4
ID Q9R3L4 PRELIMINARY; PRT; 327 AA.
AC Q9R3L4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DRB0005 OR DRB0102.
OS Deinococcus radiodurans.
OG Plasmid MPl.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;

RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI.":
RL Science 286:1571-1577(1999).
DR EMBL; AE001826; AAF12607.1; -.
DR EMBL; AE001826; AAF12603.1; -.
DR TIGR; DRB0005; -.
DR TIGR; DRB0102; -.
KM Plasmid: Complete proteome.
SQ SEQUENCE 327 AA; 37960 MW; 5FRCAD9AC84EB57D CRC64;

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RRPQOFGML 11
Db 297 RRPQOFGML 307

RESULT 127

O9CP29 PRELIMINARY; PRT; 334 AA.
AC O9CP29;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DPPP.
GN DPPP OR PM0237.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OC NCBITaxid=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; AE006058; AAK02321.1; -.
DR InterPro: IPR000515; BPD.transp.
DR Pfam: PF00528; BPD.transp. 1.
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBR. 1.
KM Complete proteome; Transmembrane; transport.
SQ SEQUENCE 334 AA; 37057 MW; 7979D793F7C9B1A8 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 334;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRPQOFG 8
Db 60 RRPQOFG 67

RESULT 128

O9B210 PRELIMINARY; PRT; 390 AA.
AC O9B210;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BA702N.1 (FYN-RELATED KINASE) (FRAGMENT).
GN FRK.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBITaxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL357141; CAC27542.1; -.
KM Kinase.
SQ SEQUENCE 390 AA; 44994 MW; F9C5984DEIDCD09 CRC64;

Query Match 54.1%; Score 33; DB 4; Length 390;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFGML 11
Db 344 POOFGML 351

RESULT 129

O95684 PRELIMINARY; PRT; 399 AA.
AC O95684;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE FGFR1 ONCOGENE PARTNER (FOP).
GN FOP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBITaxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99135870; PubMed=9949182;
RA Popovici C., Zhang B., Gregoire M.J., Jonveaux P.,
RA Lafage-Pochitaloff M., Birbaud D., Pebusque M.J.;
RT "The t(6;8)(q27;p11) translocation in a stem cell myeloproliferative
disorder fuses a novel gene, FOP, to fibroblast growth factor receptor
1.";
RL Blood 93:1381-1389(1999).
DR EMBL; Y18046; CAA77020.1; -.
SQ SEQUENCE 399 AA; 43064 MW; 7A4B5F627B9D272 CRC64;

Query Match 54.1%; Score 33; DB 4; Length 399;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 PRPOFGML 10
Db 261 PRPOFGML 269

RESULT 130

O9TCF5 PRELIMINARY; PRT; 405 AA.
AC O9TCF5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasiodonotum lustrans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasiodonotum.
OX NCBITaxid=88524;
RN [1]

RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999)
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER 3 (BY SIMILARITY).
 CC AND COPPER 3 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF104643; AAF14158.1; -.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1.1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1.1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 405 405
 SO SEQUENCE 405 AA; 45511 MW; 7EA7D84C2074C929 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 405;
 Best Local Similarity 75.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
 11 1 111
 Db 324 PQHFLGLM 331

RESULT 131
 Q9B4P4 PRELIMINARY; PRT; 407 AA.
 AC Q9B4P2;
 DT 01-JUN-2001 (TREMBLREL. 17, Created)
 DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
 OS Diadasiidae australis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Diadasiidae.
 OX NCBI_TaxID=143975;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stiles S.D., Wolf P.G.;
 RT "Phylogenetic relationships within Diadasiidae, a group of specialist
 bees";
 RL Submitted (ANG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF300529; AAK20573.1; -.
 KW Mitochondrion.
 FT NON_TER 1 1
 FT 407 407
 SO SEQUENCE 407 AA; 46368 MW; 8CEA48F5D9ACD9D4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 407;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
 11 1 111
 Db 326 PQHFLGLM 333

RESULT 132
 Q9XP15 PRELIMINARY; PRT; 409 AA.
 AC Q9XP15;
 DT 01-NOV-1999 (TREMBLREL. 12, Created)
 DT 01-NOV-1999 (TREMBLREL. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Apanteles canariensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Ichneumonidae; Braconidae; Microgasterinae; Apanteles.
 OX NCBI_TaxID=92962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mardulyn P., Whitfield J.B.;
 RT "Phylogenetic signal in the COI, 16S, and 28S genes for inferring
 relationships among genera of Microgasterinae (Hymenoptera;
 Braconidae): evidence of a high diversification rate in this group of
 parasitoids";
 RL Mol. Phylogenet. Evol. 0:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102703; AAD40857.1; -.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1.1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1.1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 409 409
 SO SEQUENCE 409 AA; 46433 MW; 9FF4509A5DC374FC CRC64;

Query Match 54.1%; Score 33; DB 8; Length 409;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
 11 1 111
 Db 331 PQHFLGLM 338

RESULT 133
 Q9B4P2 PRELIMINARY; PRT; 411 AA.
 AC Q9B4P2;
 DT 01-JUN-2001 (TREMBLREL. 17, Created)
 DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
 OS Diadasiidae baerli.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Diadasiidae.
 OX NCBI_TaxID=143976;
 RN [1]

RP SEQUENCE FROM N.A.
RA Sipes S.D., Wolf P.G.;
RT "Phylogenetic relationships within Diadasia, a group of specialist
bees."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF300530; AAK20575.1; -
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 411 411
SQ SEQUENCE 411 AA; 46637 MW; 3ABDAX7CEB92B6E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 411;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 332 POHFLGLM 339

RESULT 134
O9G464 PRELIMINARY; PRT; 412 AA.
ID O9G464;
AC O9G464;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Diadasia laticauda.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Diadasia.
OX NCBI_TaxID=143982;
RN [1]
RP SEQUENCE FROM N.A.
RA Sipes S.D., Wolf P.G.;
RT "Phylogenetic relationships within Diadasia, a group of specialist
bees."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF300521; AAG45968.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 412 412
SQ SEQUENCE 412 AA; 47166 MW; 63F6CFE500F74B71 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 412;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 331 POHFLGLM 338

RESULT 135
O9B4M3 PRELIMINARY; PRT; 412 AA.
ID O9B4M3;
AC O9B4M3;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
OS Melipholopsis sp. BBSL-209588.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Meliphilopsis.
OX NCBI_TaxID=143966;
RN [1]
RP SEQUENCE FROM N.A.
RA Sipes S.D., Wolf P.G.;
RT "Phylogenetic relationships within Diadasia, a group of specialist
bees."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF300549; AAK20613.1; -
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 412 412
SQ SEQUENCE 412 AA; 46994 MW; 0E6D5420BD58AC97 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 412;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 331 POHFLGLM 338

RESULT 136
O9B4K0 PRELIMINARY; PRT; 412 AA.
ID O9B4K0;
AC O9B4K0;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
OS Diadasia tuberculifrons.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Diadasia.
OX NCBI_TaxID=143992;
RN [1]
RP SEQUENCE FROM N.A.
RA Sipes S.D., Wolf P.G.;
RT "Phylogenetic relationships within Diadasia, a group of specialist
bees."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF300567; AAK20649.1; -
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 412 412
SQ SEQUENCE 412 AA; 46828 MW; 6E781E7F98B2DB38 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 412;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 331 POHFLGLM 338

RESULT 137
09TEC4 PRELIMINARY: PRT: 413 AA.
AC 09TEC4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum medipollum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88484;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103957; AAF14080.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT 413 413
SQ SEQUENCE 413 AA; 46590 MW; 52064ACD9D9D6C85 CRC64;

Query Match 54.18; Score 33; DB 8; Length 413;
Best Local Similarity 75.08; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
|||
Db 332 POHFLGLM 339

RESULT 138
09TCL2 PRELIMINARY: PRT: 413 AA.
AC 09TCL2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon kohliellus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88594;
RN [1]
RP SEQUENCE FROM N.A.

RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF102833; AAF04748.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT 413 413
SQ SEQUENCE 413 AA; 46760 MW; 2784C73AE626101 CRC64;

Query Match 54.18; Score 33; DB 8; Length 413;
Best Local Similarity 75.08; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
|||
Db 332 POHFLGLM 339

RESULT 139
09TCL1 PRELIMINARY: PRT: 413 AA.
AC 09TCL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon sericeus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88595;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF102834; AAF04749.1; -.
DR

DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46893 MW; F5D3BC2C8A998A75 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
1111111
DB 332 PQHFLGLM 339

RESULT 140
O9TCL0 PRELIMINARY; PRT; 413 AA.
AC O9TCL0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon tyleri.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88597;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasiglossus (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC -1- FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102835; AAF04750.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46813 MW; 275202431487D91 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 PQOFFGLM 11
1111111
DB 332 PQHFLGLM 339

RESULT 141
O9TCK9 PRELIMINARY; PRT; 413 AA.
AC O9TCK9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon viequesensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88597;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasiglossus (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC -1- FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102836; AAF04751.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46785 MW; A31278D249EA0992 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 PQOFFGLM 11
1111111
DB 332 PQHFLGLM 339

RESULT 142
O9TCK8 PRELIMINARY; PRT; 413 AA.
AC O9TCK8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Halictus confusus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
OX NCBI_TaxID=88589;
RN [1]

RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT *Phylogeny of the bee genus *LasioGLOSSUM* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102837; AAF04752.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PR00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46706 MW; 2756DA10ECC98A4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1111
 DB 332 PQOFFGLM 339

RESULT 143
 O9TCK7 PRELIMINARY; PRT; 413 AA.
 AC O9TCK7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus farinosus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 OX NCBI_TaxID=77575;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT *Phylogeny of the bee genus *LasioGLOSSUM* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102837; AAF04754.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PR00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46532 MW; E06C6135A9A88719 CRC64;

DR EMBL; AF102838; AAF04753.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PR00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46551 MW; 93BC11F7D9B7CA8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1111
 DB 332 PQOFFGLM 339

RESULT 144
 O9TCK6 PRELIMINARY; PRT; 413 AA.
 AC O9TCK6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus poeyi.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 OX NCBI_TaxID=77577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT *Phylogeny of the bee genus *LasioGLOSSUM* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102839; AAF04754.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PR00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46532 MW; E06C6135A9A88719 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1111

Db 332 PQHFLGLM 339

RESULT 145

09TCK3 PRELIMINARY; PRT; 413 AA.

AC 09TCK3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Halictus ligatus.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.

OX NCBI_Taxid=77576;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF102840; AAF04755.1; -

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PR01165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1

FT NON_TER 413

SO SEQUENCE 413 AA; 46573 MW; 588FF805C2D6A667 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. NO. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQHFLGLM 11

Db 332 PQHFLGLM 339

RESULT 146

09TCK4 PRELIMINARY; PRT; 413 AA.

AC 09TCK4;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Halictus poeyi.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.

OX NCBI_Taxid=77577;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF102841; AAF04756.1; -

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PR01165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1

FT NON_TER 413

SO SEQUENCE 413 AA; 46543 MW; 265AD8259F877825 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. NO. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQHFLGLM 11

Db 332 PQHFLGLM 339

RESULT 147

09TCK3 PRELIMINARY; PRT; 413 AA.

AC 09TCK3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Halictus rubicundus.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.

OX NCBI_Taxid=77578;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102842; AAF04757.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46748 MW; A11B06DC9A2ADDC CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQOFFGLM 339

RESULT 148
Q9TCK2 PRELIMINARY; PRT; 413 AA.
AC Q9TCK2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Mexalictus arizonensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Mexalictus.
OX NCBI_TaxID=85398;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102843; AAF04758.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46775 MW; C5053197EB478563 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11

DB 332 PQOFFGLM 339

RESULT 149
Q9TCK1 PRELIMINARY; PRT; 413 AA.
AC Q9TCK1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Sphecodes minor.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Sphecodes.
OX NCBI_TaxID=85399;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102844; AAF04759.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46913 MW; C0AB94DA87069F2 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQOFFGLM 339

RESULT 150
Q9TCK0 PRELIMINARY; PRT; 413 AA.
AC Q9TCK0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM convexum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.

OX NCBI_TaxID=88480;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103951; AAF14074.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KN Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46624 MW; E4392FMA4930B278 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
 |||||
 DB 332 PQHFLGLM 339

RESULT 151
 O9TCJ9 PRELIMINARY; PRT: 413 AA.
 AC O9TCJ9; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum conspicuum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88479;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103952; AAF14075.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KN Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46552 MW; AFBED43EBD1BF88 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
 |||||
 DB 332 PQHFLGLM 339

RESULT 152
 O9TCJ8 PRELIMINARY; PRT: 413 AA.
 AC O9TCJ8; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum cognatum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103953; AAF14076.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KN Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46567 MW; D24FCEE382033F3 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
1111111
Db 332 PQHFLGLM 339

RESULT 153

09TCJ7 PRELIMINARY; PRT; 413 AA.

AC 09TCJ7; 01-MAY-2000 (TREMBLEREL. 13, Created)

DT 01-MAY-2000 (TREMBLEREL. 13, last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Lasloglossum erythrum.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_Taxid=88481;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)

RL based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN

CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

FERRICCYTOCHROME C

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF103954; AAF14077.1; "

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PRO1165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1

FT SEQUENCE 413 AA; 46594 MW; 6B3DDIAC3E775BAE CRC64;

SO

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
1111111
Db 332 PQHFLGLM 339

RESULT 154

09TCJ6 PRELIMINARY; PRT; 413 AA.

AC 09TCJ6; 01-MAY-2000 (TREMBLEREL. 13, Created)

DT 01-MAY-2000 (TREMBLEREL. 13, last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Lasloglossum florale.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_Taxid=88482;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)

RL based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN

CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

FERRICCYTOCHROME C

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF103955; AAF14078.1; "

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PRO1165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1

FT SEQUENCE 413 AA; 46598 MW; EF331401C2BB0F95 CRC64;

SO

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
1111111
Db 332 PQHFLGLM 339

RESULT 155

09TCJ5 PRELIMINARY; PRT; 413 AA.

AC 09TCJ5; 01-MAY-2000 (TREMBLEREL. 13, Created)

DT 01-MAY-2000 (TREMBLEREL. 13, last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Lasloglossum lanarium.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_Taxid=88483;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)

RL based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN

CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

FERRICCYTOCHROME C

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103956; AAF14079.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46594 MW; 904A10DE4121240A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
Db 332 PQHFLGLM 339

RESULT 156

Q9TJC4 PRELIMINARY; PRT; 413 AA.
AC Q9TJC4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI;
OS Lasloglossum mirandum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88486;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103958; AAF14081.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46600 MW; 3069F02ED575037D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
Db 332 PQHFLGLM 339

RESULT 157

Q9TJC3 PRELIMINARY; PRT; 413 AA.
AC Q9TJC3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI;
OS Lasloglossum parasphecodum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88486;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103959; AAF14082.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46675 MW; E2840F36A36E9806 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
Db 332 PQHFLGLM 339

RESULT 158

Q9TJC2 PRELIMINARY; PRT; 413 AA.
AC Q9TJC2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI;
OS Lasloglossum cressonli.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxID=88489;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103963; AAF14086.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46572 MW; D71006CA01E29CC2 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 159
09TCJ1 PRELIMINARY; PRT; 413 AA.
AC 09TCJ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM cuprelicolle.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxID=88450;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103964; AAF14087.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46646 MW; 9CFE64F7E68448D6 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 160
09TCJ0 PRELIMINARY; PRT; 413 AA.
AC 09TCJ0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM gundlachii.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxID=88491;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103965; AAF14088.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46797 MW; 8E706566A052E577 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
1111111
DB 332 PQHFLGLM 339

RESULT 161

O9TC19 PRELIMINARY: PRT: 413 AA.

AC O9TC19: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT)

OS Lasloglossum hyalinum.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCB1_TaxID=88492;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN. (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL; AF103966; AAF14089.1; -

DR InterPro; IPR000883; COX1.

DR Pfam; PF00115; COX1; 1.

DR PRINTS; PR01165; CYCOXIDASE1.

DR PROSITE; PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT NON_TER 413 413

FT SEQUENCE 413 AA; 46616 MW; 80B4F5724DC71914 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
1111111
DB 332 PQHFLGLM 339

RESULT 162

O9TC19 PRELIMINARY: PRT: 413 AA.

AC O9TC19: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT)

OS Lasloglossum imitatum.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCB1_TaxID=88493;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN. (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL; AF103967; AAF14090.1; -

DR InterPro; IPR000883; COX1.

DR Pfam; PF00115; COX1; 1.

DR PRINTS; PR01165; CYCOXIDASE1.

DR PROSITE; PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT NON_TER 413 413

FT SEQUENCE 413 AA; 46754 MW; 25FF845E518E90B3 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
1111111
DB 332 PQHFLGLM 339

RESULT 163

O9TC19 PRELIMINARY: PRT: 413 AA.

AC O9TC19: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT)

OS Lasloglossum parvum.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCB1_TaxID=88494;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN. (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL; AF103967; AAF14090.1; -

DR InterPro; IPR000883; COX1.

DR Pfam; PF00115; COX1; 1.

DR PRINTS; PR01165; CYCOXIDASE1.

DR PROSITE; PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT NON_TER 413 413

FT SEQUENCE 413 AA; 46754 MW; 25FF845E518E90B3 CRC64;

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103968; AAF14091.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46646 MW; 25C3C451CEB8AAEE CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POHFLGLM 339

RESULT 164
09TC16 PRELIMINARY; PRT; 413 AA.
AC 09TC16
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum pilosum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88495;
[1]
RN SEQUENCE FROM N.A.
RP Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103969; AAF14092.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46586 MW; 9EB109D1E87B135E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POHFLGLM 339

RESULT 165
09TC15 PRELIMINARY; PRT; 413 AA.
AC 09TC15
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum rohweri.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88496;
[1]
RN SEQUENCE FROM N.A.
RP Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103970; AAF14093.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46646 MW; 542C37934BEDCDP4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POHFLGLM 339

RESULT 166
09TC14 PRELIMINARY; PRT; 413 AA.
AC 09TC14
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum tegulare.
OC Mitochondrion.

CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
CC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88497;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103971; AAF14094.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46634 MW; 97BED29E97472A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
11 1111
DB 332 PQHFLGLM 339

RESULT 167
09TC13 PRELIMINARY; PRT; 413 AA.
AC 09TC13;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE 1 (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasioglossum vierecki.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88497;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103972; AAF14095.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46533 MW; 804CD6287DFC43F5 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
11 1111
DB 332 PQHFLGLM 339

RESULT 168
09TC12 PRELIMINARY; PRT; 413 AA.
AC 09TC12;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE 1 (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasioglossum umbrilipenne.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88498;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103975; AAF14098.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46611 MW; 797998620C724B9D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
11 1 111
Db 332 PQHFLGLM 339

RESULT 169

09TCT11 PRELIMINARY; PRT; 413 AA.

DT 01-MAY-2000 (TREMBLERL. 13, Created)

DT 01-MAY-2000 (TREMBLERL. 13, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

OS Lastloglossum albidipes.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.

RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."

RL Syst. Entom. 24:0-0(1999).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

-1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

-1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

EMBL: AF103977; AAF1409.1; -.

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1; 1.

DR PRINTS: PR01165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.

FT NON_TER 1 413

FT SEQUENCE 413 AA; 46780 MW; 0CEAICE291B2BA58 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
11 1 111
Db 332 PQHFLGLM 339

RESULT 170

09TCT10 PRELIMINARY; PRT; 413 AA.

DT 01-MAY-2000 (TREMBLERL. 13, Created)

DT 01-MAY-2000 (TREMBLERL. 13, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

OS Lastloglossum albidipes.

OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.

OX NCBI_TaxID=88501;

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."

RL Syst. Entom. 24:0-0(1999).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

-1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

-1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

EMBL: AF103977; AAF1409.1; -.

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1; 1.

DR PRINTS: PR01165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.

FT NON_TER 1 413

FT SEQUENCE 413 AA; 46762 MW; 87506DFEE6D80B63 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
11 1 111
Db 332 PQHFLGLM 339

RESULT 171

09TCH9 PRELIMINARY; PRT; 413 AA.

DT 01-MAY-2000 (TREMBLERL. 13, Created)

DT 01-MAY-2000 (TREMBLERL. 13, Last sequence update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

OS Lastloglossum apistum.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.

OX NCBI_TaxID=88502;

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."

RL Syst. Entom. 24:0-0(1999).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

OS Lastloglossum c:clnclipes.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.
OX NCBI_TaxID=88505;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103981; AAF14104.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46549 MW; D338190C949874BE CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
Db 332 PQHFLGLM 339

RESULT 175
Q9TCH5 PRELIMINARY; PRT; 413 AA.
AC Q9TCH5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastloglossum comagenense.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.
OX NCBI_TaxID=88506;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3

CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103982; AAF14105.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46786 MW; F26D5CD2286DC6C8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
Db 332 PQHFLGLM 339

RESULT 176
Q9TCH4 PRELIMINARY; PRT; 413 AA.
AC Q9TCH4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastloglossum duplex.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.
OX NCBI_TaxID=88507;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103983; AAF14106.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46710 MW; EF400F726EB13989 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
|||
DB 332 POHFLGLM 339

RESULT 177
O9TCH3 PRELIMINARY; PRT; 413 AA.

AC O9TCH3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasioglossum fulvicorne.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88508;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103984; AAF14107.1; -
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413
SQ SEQUENCE 413 AA; 46820 MW; D23986B0B760199B CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
|||
DB 332 POHFLGLM 339

RESULT 178
O9TCH2 PRELIMINARY; PRT; 413 AA.

AC O9TCH2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasioglossum lineare.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88511;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

GN COI.
OS Lasioglossum laticeps.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88510;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103985; AAF14108.1; -
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413
SQ SEQUENCE 413 AA; 46644 MW; 64E59D92A8C48D69 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
|||
DB 332 POHFLGLM 339

RESULT 179
O9TCH1 PRELIMINARY; PRT; 413 AA.

AC O9TCH1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasioglossum lineare.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
OX NCBI_TaxID=88511;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum morio.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88514;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103989; AAF14113.1; -.
DR InterPro: IPR008883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46651 MW; EB0E1376047B2E9C CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQPFGLM 11
Db 332 PQPFGLM 339

RESULT 183
O9TGC7 PRELIMINARY; PRT; 413 AA.
AC O9TGC7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum nigripes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88515;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103990; AAF14113.1; -.
DR InterPro: IPR008883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46726 MW; 082E1BE63DB82472 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQPFGLM 11
Db 332 PQPFGLM 339

RESULT 184
O9TGC4 PRELIMINARY; PRT; 413 AA.
AC O9TGC4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum pauxillum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88516;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF104634; AAF14149.1; -.
DR InterPro: IPR008883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46726 MW; 082E1BE63DB82472 CRC64;

SO SEQUENCE 413 AA; 46537 MW; F9A83E9A392PC1B4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 185

09TCG3 PRELIMINARY; PRT; 413 AA.

AC 09TCG3;
DT 01-MAY-2000 (TRIMBLREL. 13, Created)
DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.

OS Lasloglossum pectorale.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_TaxID=88517;

NP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."

RL Syst. Entom. 24:0-0(1999).
-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 PROTONS;
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF104635; AAF1451.1; -
DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1; 1.

DR PRINTS: PRO1165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KM Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT NON_TER 413 413

SO SEQUENCE 413 AA; 46505 MW; B1CADF1B8BC0A59E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 186

09TCG3 PRELIMINARY; PRT; 413 AA.

AC 09TCG3;
DT 01-MAY-2000 (TRIMBLREL. 13, Created)
DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)

DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.

OS Lasloglossum pollium.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_TaxID=88518;

NP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."

RL Syst. Entom. 24:0-0(1999).
-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 PROTONS;
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF104636; AAF1451.1; -
DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1; 1.

DR PRINTS: PRO1165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1; 1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KM Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT NON_TER 413 413

SO SEQUENCE 413 AA; 46641 MW; D5674CD65A42648F CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 187

09TCG1 PRELIMINARY; PRT; 413 AA.

DT 01-MAY-2000 (TRIMBLREL. 13, Created)

DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)

DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.

OS Lasloglossum puncticolle.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_TaxID=88519;

NP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."

RL Syst. Entom. 24:0-0(1999).
-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum subtriticum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104640; AAF14155.1; -.
 DR InterPro: IPR000883; COX1.1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46747 MW; 8C54AB0B0A4128F CRC64;

 Query Match 54.18; Score 33; DB 8; Length 413;
 Best Local Similarity 75.08; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 OY 4 PQOFFGLM 11
 1111111
 Db 332 PQHFLGLM 339

 RESULT 191
 09TCEF7 PRELIMINARY; PRT; 413 AA.
 AC 09TCEF7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum truncatum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104641; AAF14156.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46665 MW; 7BC4C502C65DF1C3 CRC64;

 Query Match 54.18; Score 33; DB 8; Length 413;
 Best Local Similarity 75.08; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 OY 4 PQOFFGLM 11
 1111111
 Db 332 PQHFLGLM 339

 RESULT 192
 09TCEF6 PRELIMINARY; PRT; 413 AA.
 AC 09TCEF6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum villosulum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104642; AAF14157.1; -.
 DR InterPro: IPR000883; COX1.1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.

FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46624 MW; D4DC061F0229DC4A CRC64;

Query Match
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 || || || ||
 Db 332 PQHFLGLM 339

RESULT 193
 O9TCF4 PRELIMINARY; PRT; 413 AA.
 AC O9TCF4;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum callizonium.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88525;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104644; AAF14159.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46516 MW; 65F0037DB563C2AA CRC64;

Query Match
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 || || || ||
 Db 332 PQHFLGLM 339

RESULT 194
 O9TCF3 PRELIMINARY; PRT; 413 AA.
 AC O9TCF3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum desertum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88527;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum corticium.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88526;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104645; AAF14160.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46652 MW; C112DA8C1C043D38 CRC64;

Query Match
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 || || || ||
 Db 332 PQHFLGLM 339

RESULT 195
 O9TCF2 PRELIMINARY; PRT; 413 AA.
 AC O9TCF2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum desertum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88527;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF104646; AAF14162.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 413 AA; 46596 MW; AE84F89B5170695D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGIM 11
11 1 111
DB 332 PQHFLGLM 339

RESULT 196
O9TCE1 PRELIMINARY; PRT: 413 AA.
AC O9TCE1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastioglossum discum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastioglossum.
OX NCBI_Taxid=86528;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastioglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF104647; AAF14162.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 413 AA; 46538 MW; FBF3614973886F93 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGIM 11
11 1 111
DB 332 PQHFLGLM 339

RESULT 197
O9TCE0 PRELIMINARY; PRT: 413 AA.
AC O9TCE0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastioglossum fuscipenne.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastioglossum.
OX NCBI_Taxid=86529;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastioglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF104648; AAF14163.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 413 AA; 46668 MW; 87B42FB5498C1E81 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGIM 11
11 1 111
DB 332 PQHFLGLM 339

RESULT 198
O9TCE9 PRELIMINARY; PRT: 413 AA.

AC 09TCE9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum laevigatum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 CC -1- FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104649; AAF1464.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 413
 FT NON_TER 1 413
 SQ SEQUENCE 413 AA; 46529 MW; 561747FD6BA4F59A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY 4 POOFGLM 11
 DB 332 POHFGLM 339

RESULT 199
 ID 09TCE8 PRELIMINARY; PRT; 413 AA.
 AC 09TCE8
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum lativentre.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 CC -1- FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104650; AAF1465.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 413
 FT NON_TER 1 413
 SQ SEQUENCE 413 AA; 46334 MW; 0FA4851A84ECAD0E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY 4 POOFGLM 11
 DB 332 POHFGLM 339

RESULT 200
 ID 09TCE7 PRELIMINARY; PRT; 413 AA.
 AC 09TCE7
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum majus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88533;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 CC -1- FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104653; AAF1468.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.

KW Copper; Heme; inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA: 46508 MW: E352300D9EFA2E6 CRC64:

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. NO. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 111111
 DB 332 PQHFLGLM 339

Search completed: April 1, 2002, 16:20:04
 Job time: 150 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:29 ; Search time 23.26 Seconds
(without alignments)
36.024 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQQFFGLM 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR.68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	1	SPHO
2	61	100.0	11	1	substance P - hors
3	61	100.0	63	2	substance P - guin
4	61	100.0	72	2	tachykinin gamma C
5	61	100.0	72	2	tachykinin A gamma
6	61	100.0	97	2	preprotachykinin-A
7	61	100.0	112	2	tachykinin delta P
8	61	100.0	115	1	SPRTA
9	61	100.0	115	1	substance P alpha
10	61	100.0	129	1	SPRNG
11	61	100.0	130	1	tachykinin 1 precu
12	61	100.0	130	1	neurokinin 1 precu
13	61	100.0	130	1	substance P beta P
14	61	100.0	130	2	SPROR
15	61	100.0	130	2	neurokinin 1 precu
16	58	82.0	11	2	substance P - chlc
17	49	80.3	11	2	substance P - rain
18	48	78.7	11	2	substance P - Atla
19	44	72.1	11	2	probable substance
20	44	72.1	11	2	substance P-like P
21	44	72.1	12	2	substance P-like P
22	41	67.2	11	2	tachykinin - Afric
23	41	67.2	11	2	ranatachykinin A -
24	38	62.3	205	2	trithorax protein
25	38	62.3	257	2	hypothetical prote
26	38	62.3	293	2	small nuclear ribo
27	37	60.7	11	2	hypothetical prote
28	37	60.7	11	2	kassinin-like pept
29	37	60.7	249	2	uprololisin - frog (
					hypothetical prote

30	36	59.0	11	2	D60409
31	36	59.0	11	2	kassinin-like pept
32	36	59.0	12	2	B60409
33	36	59.0	12	2	tachykinin - Afric
34	36	59.0	12	2	S07206
35	36	59.0	321	2	A64173
36	36	59.0	373	2	T02976
37	36	59.0	629	2	T19563
38	35	57.4	728	2	E69486
39	35	57.4	133	2	A25777
40	35	57.4	206	2	T33064
41	35	57.4	297	2	A83049
42	35	57.4	347	2	T05737
43	35	57.4	474	2	T15511
44	35	57.4	494	2	E86671
45	35	57.4	512	2	A82296
46	35	57.4	832	2	S76815
47	35	57.4	1043	2	T23875
48	35	57.4	1092	2	H69071
49	35	57.4	1611	2	A84743
50	35	57.4	1736	2	F86178
51	34.5	56.6	216	2	F96657
52	34	55.7	167	2	T36290
53	34	55.7	306	2	H81036
54	34	55.7	316	2	T13601
55	34	55.7	318	2	A81982
56	34	55.7	359	2	T52337
57	34	55.7	493	2	S73890
58	34	55.7	498	1	S48058
59	34	55.7	502	2	JX0334
60	34	55.7	503	2	A40843
61	34	55.7	504	2	A22631
62	34	55.7	583	2	S30930
63	34	55.7	585	2	S34785
64	34	55.7	587	1	S33544
65	34	55.7	588	1	S33543
66	34	55.7	588	2	S30929
67	34	55.7	628	2	D86466
68	34	55.7	666	2	S56781
69	34	55.7	1799	1	S44920
70	33	54.1	71	2	G81889
71	33	54.1	101	2	G71054
72	33	54.1	234	2	F75254
73	33	54.1	282	2	T15304
74	33	54.1	299	2	E70842
75	33	54.1	320	2	H71259
76	33	54.1	327	2	A75633
77	33	54.1	327	2	C75624
78	33	54.1	327	2	E75618
79	33	54.1	327	2	C75556
80	33	54.1	327	2	B73620
81	33	54.1	404	2	A54871
82	33	54.1	416	2	F75434
83	33	54.1	454	2	T37933
84	33	54.1	502	1	D64110
85	33	54.1	505	1	SYECKT
86	33	54.1	505	1	SYECKU
87	33	54.1	505	2	I38396
88	33	54.1	505	2	E86108
89	33	54.1	505	2	F85944
90	33	54.1	512	2	I49552
91	33	54.1	521	2	A32431
92	33	54.1	546	2	F84647
93	33	54.1	712	2	T02552
94	33	54.1	755	2	T47731
95	33	54.1	1057	1	A39288
96	33	54.1	1741	2	T13610
97	32.5	53.3	325	2	S14230
98	32	52.5	11	2	S07201
99	32	52.5	180	2	S77046
100	32	52.5	210	2	A69898
101	32	52.5	225	2	G75448
102	32	52.5	263	1	S23009

kassinin-like pept
kassinin-like pept
tachykinin - Afric
kassinin - Senegal
conserved hypotnet
probable DNA bindi
hypothetical prote
translacion elonga
T-cell receptor be
hypothetical prote
hypothetical prote
probable hordein C
hypothetical prote
lysine--trNA synthet
lysyl--trNA synthet
hypothetical prote
hypothetical prote
DNA-directed DNA p
probable myosin he
hypothetical prote
hypothetical prote
probable integrat
riboflavin kinase/
hypothetical prote
FAD synthase NMA06
phosphoprotein pho
hypothetical prote
cytochrome P450 Cy
cytochrome P450 3A
cytochrome P450 3
cytochrome P450 3A
cytochrome oxidase (
catechol oxidase (
catechol oxidase (
catechol oxidase (
catechol oxidase (
hypothetical prote
hypothetical prote
ZK688.5 protein -
hypothetical prote
hypothetical prote
conserved hypotnet
hypothetical prote
probable acid phos
probable membrane
probable transposa
probable transposa
probable transposa
probable transposa
probable transposa
Gal beta-1, 3galNA
hypothetical prote
transcription acti
lysine--trNA ligas
lysine--trNA ligas
lysine--trNA ligas
protein-tyrosine k
hypothetical prote
hypothetical prote
protein-tyrosine k
cytochrome-c oxida
hypothetical prote
cellulose synthase
hypothetical prote
dorsal-ventral pat
parallel sister ch
pyruvate dehydroge
phylalemin - frog
hypothetical prote
conserved hypotnet
conserved hypotnet
insulin-like growt

103	32	52.5	271	2	B35407	tryptophan synthas
104	32	52.5	288	2	C75426	probable transposa
105	32	52.5	288	2	A75638	probable transposa
106	32	52.5	299	2	E69288	ISA0963-2 transpos
107	32	52.5	299	2	H69462	ISA0963-6 transpos
108	32	52.5	299	2	E69413	ISA0963-3 transpos
109	32	52.5	299	2	F69422	ISA0963-4 transpos
110	32	52.5	305	2	D96769	hypothetical prote
111	32	52.5	313	2	G86336	hypothetical prote
112	32	52.5	327	2	A75631	probable transposa
113	32	52.5	345	2	B83371	conserved hypotet
114	32	52.5	357	2	A69426	ISA0963-5 transpos
115	32	52.5	361	2	C71242	hypothetical prote
116	32	52.5	368	2	T15492	hypothetical prote
117	32	52.5	370	2	T05598	hypothetical prote
118	32	52.5	382	1	B64158	hypothetical prote
119	32	52.5	418	2	H72026	3',4'-dihydroxy-2'-bu
120	32	52.5	418	2	F86599	GTP cyclohydrolase
121	32	52.5	419	2	F82991	transcription term
122	32	52.5	419	2	H81667	transcription term
123	32	52.5	426	2	E83172	probable transpor
124	32	52.5	427	2	G72246	transcription term
125	32	52.5	432	2	F81320	transcription term
126	32	52.5	445	2	S73859	hypothetical prote
127	32	52.5	462	2	A42401	macrophage elastas
128	32	52.5	464	2	A71509	probable transcrip
129	32	52.5	464	2	D72058	transcription term
130	32	52.5	464	2	G86566	transcription term
131	32	52.5	469	1	KCPG1	interstitial colla
132	32	52.5	478	2	F82175	conserved hypotet
133	32	52.5	484	2	T16695	hypothetical prote
134	32	52.5	493	2	JC7205	lysine--CRNA ligas
135	32	52.5	508	2	JC6200	cholesterol monoox
136	32	52.5	513	2	T34546	hypothetical prote
137	32	52.5	515	2	F70128	transcription term
138	32	52.5	518	2	T19562	hypothetical prote
139	32	52.5	519	2	C71346	probable transcrip
140	32	52.5	532	2	T49467	related to COP1-in
141	32	52.5	567	2	T08405	hypothetical prote
142	32	52.5	612	2	T35430	probable long-chain
143	32	52.5	614	2	T25208	hypothetical prote
144	32	52.5	617	2	A81095	excinuclease ABC c
145	32	52.5	628	2	G81845	alpha-amylase ABC s
146	32	52.5	632	2	J50631	hypothetical prote
147	32	52.5	637	2	T00548	p6 protein - mous
148	32	52.5	837	2	A57542	desmocollin - bovi
149	32	52.5	896	2	T45858	hypothetical prote
150	32	52.5	1039	2	T22982	DNA-directed RNA p
151	32	52.5	1116	2	S41915	type I restriction
152	32	52.5	1163	2	D64315	formin isoform IV
153	32	52.5	1206	2	S24407	limb deformity (ld
154	32	52.5	1213	2	A41724	conserved hypotet
155	32	52.5	1415	2	C83070	formin - mouse
156	32	52.5	1468	2	S11515	vitellinogen vit-6
157	32	52.5	1651	2	B43081	hypothetical prote
158	32	52.5	1718	2	T14603	hypothetical prote
159	32	52.5	1817	2	T34249	SEC16 protein - ye
160	32	52.5	2195	2	S61103	glialdin omega-5 -
161	31	50.8	32	2	A59156	hypothetical prote
162	31	50.8	79	2	D69669	ferredoxin--thiore
163	31	50.8	97	2	UT0703	nuclear receptor p
164	31	50.8	113	2	S43435	hypothetical prote
165	31	50.8	126	2	S72785	conserved hypotet
166	31	50.8	126	2	D69293	hypothetical H1T-f
167	31	50.8	133	2	T40979	hypothetical prote
168	31	50.8	136	2	T45725	hypothetical prote
169	31	50.8	138	2	T14185	chitinase (EC 3.2.
170	31	50.8	143	2	S67619	ribosomal protein
171	31	50.8	159	2	E81982	probable phosphata
172	31	50.8	172	2	S68232	antimicrobial prote
173	31	50.8	176	2	A75624	hypothetical prote
174	31	50.8	183	2	E69286	transcription init
175	31	50.8	193	2	E96766	hypothetical prote
176	31	50.8	206	2	F71012	hypothetical prote
177	31	50.8	216	2	T22453	hypothetical prote
178	31	50.8	219	2	C81038	phosphoglycolate p
179	31	50.8	226	2	T24530	hypothetical prote
180	31	50.8	254	2	S40944	hypothetical prote
181	31	50.8	264	1	WMBVT3	30K protein - toma
182	31	50.8	264	1	WMBVL2	30K protein - toma
183	31	50.8	266	2	E71612	ribosomal protein
184	31	50.8	269	2	A26162	holocytochrome-c s
185	31	50.8	271	2	D75552	conserved hypotet
186	31	50.8	278	2	S48776	hypothetical prote
187	31	50.8	283	2	A35935	NADH dehydrogenase
188	31	50.8	304	2	G64175	hypothetical prote
189	31	50.8	320	2	D96750	unknown protein F2
190	31	50.8	323	1	PRLJHD	proteinase (EC 3.4
191	31	50.8	337	2	T19592	hypothetical prote
192	31	50.8	338	2	G69027	phosphoribosylform
193	31	50.8	338	2	S75196	hypothetical prote
194	31	50.8	355	2	T24822	hypothetical prote
195	31	50.8	371	2	C72077	conserved hypotet
196	31	50.8	371	2	F86546	hypothetical prote
197	31	50.8	377	2	T40024	probable cytochrom
198	31	50.8	379	2	D83803	tRNA-guanine trans
199	31	50.8	385	2	G72569	hypothetical prote
200	31	50.8	391	2	F82369	conserved hypotet
201	31	50.8	398	2	T46312	hypothetical prote
202	31	50.8	406	2	A35401	cytochrome P450 10
203	31	50.8	465	2	E66737	probable DEAD/DEAH
204	31	50.8	465	2	D86166	protein F21B7.12 (
205	31	50.8	466	2	E70865	trigger factor tlg
206	31	50.8	469	2	C86170	hypothetical prote
207	31	50.8	476	2	G81091	Glu-CRNA(Gln) amid
208	31	50.8	479	2	T15427	hypothetical prote
209	31	50.8	485	2	S75655	anthranilate synth
210	31	50.8	488	1	QOBEHS	alkaline exonuclea
211	31	50.8	488	2	T44030	alkaline exonuclea
212	31	50.8	488	2	T44215	lysine--tRNA ligas
213	31	50.8	488	2	S69892	cytochrome-c oxida
214	31	50.8	496	2	T11376	hypothetical prote
215	31	50.8	529	1	S76167	hypothetical prote
216	31	50.8	532	2	T27549	hypothetical prote
217	31	50.8	546	2	T19139	hypothetical prote
218	31	50.8	558	2	T16545	glycine precursor
219	31	50.8	566	2	T49988	ovule development
220	31	50.8	583	2	S65227	hypothetical prote
221	31	50.8	596	2	T30498	probable ribonucle
222	31	50.8	660	1	A28153	gelatinase A (EC 3
223	31	50.8	662	2	A42496	gelatinase A (EC 3
224	31	50.8	662	2	S34780	gelatinase A (EC 3
225	31	50.8	662	2	S70365	gelatinase A (EC 3
226	31	50.8	663	1	S46492	gelatinase A (EC 3
227	31	50.8	667	2	T01999	hypothetical prote
228	31	50.8	678	2	S77215	hypothetical prote
229	31	50.8	692	2	T13161	A-kinase anchor pr
230	31	50.8	705	2	S70691	polyribonucleotide
231	31	50.8	735	2	T49622	hypothetical prote
232	31	50.8	757	1	LIRRH	hormone-sensitiv
233	31	50.8	761	2	A53414	A-kinase anchor pr
234	31	50.8	775	2	B72074	hypothetical prote
235	31	50.8	775	2	C81594	hypothetical prote
236	31	50.8	775	2	D86549	hypothetical prote
237	31	50.8	797	2	T27518	hypothetical prote
238	31	50.8	864	2	A49070	ecdysone-inducible
239	31	50.8	922	2	T40372	trp asp repeat pro
240	31	50.8	948	2	T26417	hypothetical prote
241	31	50.8	997	2	T15243	hypothetical prote
242	31	50.8	1019	2	T50251	hypothetical coile
243	31	50.8	1139	2	T33368	hypothetical prote
244	31	50.8	1222	2	T14805	hypothetical prote
245	31	50.8	1322	2	H85202	hypothetical prote
246	31	50.8	1765	2	T42388	sodium channel alp
247	31	50.8	1840	2	T30250	GTL protein - mous
248	31	50.8	2517	2	S58380	probable RNA-direc

249	31	50.8	3712	1	YCCEVC	alpha-aminoadipyl-
250	30.5	50.0	445	2	EB2075	hypothetical prote
251	30.5	50.0	574	2	FB3991	hypothetical prote
252	30.5	50.0	2201	2	AS4774	ATP binding casset

ALIGNMENTS

RESULT 1
SPHO

Substance P - horse
C:Species: Equus caballus (domestic horse)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C:Accession: A01558
R:Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A:Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
A:Reference number: A01558
A:Accession: A01558
A:Molecule type: protein
A:Residues: 1-11 <STU>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; hormone
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 61; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 2

A60654

Substance P - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C:Accession: A60654
R:Murphy, R.
Neuropeptides 14, 105-110, 1989
A:Title: Primary amino acid sequence of guinea-pig substance P.
A:Reference number: A60654; MUID:90044685
A:Accession: A60654
A:Molecule type: protein
A:Residues: 1-11 <MUR>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 61; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 3

JC2412

tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A:Reference number: JC2411; MUID:94324969

A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 2; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 RRPQOQFFGLM 11
|||||
DB 11 RRPQOQFFGLM 21

RESULT 4

162742

tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: 162742; JC5453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: 162742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:9554261
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 100.0%; Score 61; DB 2; Length 72;

Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 RRPQOQFFGLM 11
|||||
DB 23 RRPQOQFFGLM 33

RESULT 5

JC5455

preprotachykinin-A gamma precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; 145967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5455
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <CHI>
A:Cross-references: GB:M68912; NID:9163593; PIDN:AAA30725.1; PID:9552336
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is
A:Gene: PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 100.0%; Score 61; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 23 RPKPOQFFGLM 33

RESULT 6
S12958
tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S12958; J02413
R:Harmer, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing
A:Reference number: S12958; MUID:91085565
A:Accession: S12958
A:Molecule type: mRNA
A:Residues: 1-97 <HAK>
A:Cross-references: GB:X56306; NID:956067; PIDN:CAA39752.1; PID:956068
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A:Reference number: J02411; MUID:94324969
A:Accession: J02413
A:Molecule type: mRNA
A:Residues: 48-92 <KHA>
A:Cross-references: GB:S72369; NID:9632805; PIDN:AAB31499.1; PID:9632806
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:58-68/Product: substance P #status predicted <SUP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 58 RPKPOQFFGLM 68

RESULT 7
SPRTA
substance P alpha precursor - rat
N:Alternate names: preprotachykinin alpha
N:Contains: substance P
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: B26590
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neurc
A:Reference number: A94187; MUID:87118268
A:Accession: B26590
A:Molecule type: mRNA
A:Residues: 1-112 <KRA>
A:Cross-references: GB:M4184; NID:9206329; PIDN:AAA1925.1; PID:9206330
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha f
C:Comment: The alpha form is processed to yield substance P.
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-112/Product: substance P alpha precursor #status predicted <PREA>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 58 RPKPOQFFGLM 68

RESULT 8
SPREG
substance P gamma precursor - rabbit
N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykin
N:Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
R:Maegert, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA2>
A:Cross-references: EMBL:X62994; NID:91565; PIDN:CAA44728.1; PID:91566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived fro
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein
A:Residues: 72-92 <KAG>
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
J. Neurochem. 50, 1412-1417, 1988
A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived
A:Reference number: A60200; MUID:86199570
A:Accession: A60200
A:Molecule type: protein
A:Residues: 72-92 <KA2>
C:Comment: The gamma alternatively spliced form is processed to yield substance P and
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:72-92/Product: gamma-neuropeptide K #status experimental <NPK>
F:83-92/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 58 RPKPOQFFGLM 68

RESULT 9
S47039
tachykinin I precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47039
R:Heitland, A.; Krühofer, M.; Jüergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47039
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <HEI>

A:Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
C:Superfamily: substance P precursor

Query Match 100.0%; Score 61; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOFGGLM 11
|||||
Db 58 RRPQOFGGLM 68

RESULT 10

SPRUB
neurokinin 1 precursor, beta splice form [validated] - human
M:Alternate names: neurokinin A; neurokinin alpha; neuromedin L; neuropeptide K; preprotachykinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 precursor, alpha splice form (man)
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1988 #sequence_revision 26-May-1995 #text_change 19-May-2000
C:Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270; 162
R:Harman, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Koste, R.; Curtis, A.; Goling, P.B.S. Lett. 208, 67-72, 1986
A:Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substance A:Reference number: A24805; MUID:87030957
A:Accession: A24805
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: GB:M28109; EMBL:X54469; NID:g29482; PIDN:CAA38351.1; PID:g29483
R:McGregor, G.P.; Conlon, J.M.
Peptides 11, 907-910, 1990
A:Title: Characterization of the C-terminal flanking peptide of human beta-preprotachykinin A:Reference number: A60425; MUID:91133994
A:Accession: A60425
A:Molecule type: Protein
A:Residues: 111-126 <MCG>
A:Experimental source: neuroendocrine tumor of adrenal medulla
R:Theodorsson-Norheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oeberg, K.; Jacobs Eur. J. Biochem. 166, 693-697, 1987
A:Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neurokinin A:Reference number: S00069; MUID:87275962
A:Accession: S00069
A:Molecule type: Protein
A:Residues: 98-107 <THE>
R:Kage, R.; Thim, L.; Creutzfeldt, W.; Conlon, J.M.
Biochem. J. 253, 203-207, 1988
A:Title: Post-translational processing of preprotachykinins. Isolation of protachykinin-A:Reference number: S03033; MUID:88339887
A:Accession: S03033
A:Molecule type: protein
A:Residues: 20-30 <KAG>
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse A:Reference number: JC5450; MUID:91209287
A:Accession: JC5451
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 36-73, 89-122 <CH11>
A:Cross-references: GB:M68907; NID:g190292; PIDN:AAA60160.1; PID:g553619
A:Accession: JC5450
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-86, 'P', 88-122 <CH12>
A:Cross-references: GB:M68906; NID:g190290; PIDN:AAA60159.1; PID:g553618
R:Tan, A.; Tco, H.P.
submitted to GenBank, October 1995
A:Reference number: A59269
A:Accession: A59269
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-129 <TAN>
A:Cross-references: GB:U37529; NID:g1017792; PIDN:AAA79195.1; PID:g1017793

A:Experimental source: tissue brain cortex
R:rai, J.P.; Douglas, S.D.; Rappaport, E.; Wu, J.M.; Ho, W.Z.

submitted to GenBank, February 1998
A:Description: Identification of a delta isoform of preprotachykinin mRNA in human mo
A:Reference number: A59270
A:Accession: A59270
A>Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 36-96, 'W', 116-118 <LA11>
A:Cross-references: GB:AF050658; NID:g3098594; PIDN:AAC15702.1; PID:g3098595
A:Experimental source: alpha splice form; tissue blood; tissue brain; cell type monoc
A:Accession: B59270
A>Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 36-73, 89-96, 'W', 116-122 <LA12>
A:Cross-references: GB:AF050656; NID:g3098598; PIDN:AAC15704.1; PID:g3098599
A:Experimental source: delta splice form; tissue blood; tissue brain; cell type monoc
C:Comment: This protein is processed to produce the tachykinin peptide hormones neuro
nce K).

C:Genetics:
A:Gene: GDB:TAC1; TAC2; NKNA, PPT-A
A:Cross-references: GDB:119452; OMIM:162320
A:Map position: 7q21-q22

C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SP>
F:1-96, 'W', 116-118/Product: neurokinin 1 precursor, alpha splice form #status predict
F:1-73, 89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <S
F:1-73, 89-96, 'W', 116-122/Product: neurokinin 1 precursor, alpha splice form #status p
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status experimental <NK1>
F:72-107/Product: neuropeptide K #status predicted <NK>
F:98-107/Product: neurokinin 2 #status experimental <NK2>
F:100-107/Product: neurokinin 2(3-10) #status experimental <NK23>
F:101-107/Product: neurokinin 2(4-10) #status experimental <NK24>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOFGGLM 11
|||||
Db 58 RRPQOFGGLM 68

RESULT 11

SPRUB
substance P beta precursor - rat
N:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
N:Contains: neurokinin A; substance P; substance P gamma precursor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: A37163; A26590; C26590; A25067; JC2411
R:Carter, M.S.; Krause, J.E.
J. Neurosci. 10, 2203-2214, 1990
A:Title: Structure, expression, and some regulatory mechanisms of the rat preprotachy A:Reference number: A37163; MUID:90331040
A:Accession: A37163
A:Molecule type: DNA
A:Residues: 1-130 <CAR>
A:Cross-references: GB:M34159; GB:M34160; GB:M34162; NID:g206334; PIDN:AAA41926.1; PI
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and ne A:Reference number: A94187; MUID:87118268
A:Accession: A26590
A:Molecule type: mRNA
A:Residues: 1-130 <KRA>

A:Cross-references: GB:M15191; NID:g206341; PIDN:AAA41928.1; PID:g206342; GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KR2>
A:Cross-references: GB:M34183; NID:g206343; PIDN:AAA41929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of a
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA41927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: Intestine
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the beta an
C:Comment: The beta and gamma forms are processed to yield substance P and neurokinin A
C:Genetics:
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-130/Product: substance P beta precursor #status predicted <PREB>
F:1-73, 89-130/Product: substance P gamma precursor #status predicted <PREG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:38-68/Product: substance P #status predicted <SBP>
F:98-107/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gl
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gl

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 58 RPKPOQFFGLM 68

RESULT 12
SPBOB
neurokinin 1 precursor, beta splice form [validated] - bovine
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 precu
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Feb-1984 #sequence, revision 19-Feb-1984 #text, change 16-Jun-2000
C:Accession: A05093; A01557; A01557; B25067; A61460; JC5454; I45966
R:Nawa, H.; Kotani, H.; Nakanishi, S.
Nature 312, 729-734, 1984
A:Title: Tissue-specific generation of two preprotachykinin mRNAs from one gene by alter
A:Reference number: A05093; MUID:85086245
A:Accession: A05093
A:Molecule type: DNA
A:Residues: 1-130 <NAMI>
A:Cross-references: GB:X02351; GB:M14786; NID:g655; PIDN:CAA26206.1; PID:g1197197
R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A:Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain substance P
A:Reference number: A93318; MUID:84039802
A:Accession: A01559
A:Molecule type: mRNA
A:Residues: 1-130 <NAMI>
A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A:Accession: A01557
A:Molecule type: mRNA
A:Residues: 1-96, 'M', 116-130 <NAMI>
A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763

R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of
A:Reference number: A25067; MUID:87025808
A:Accession: B25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
R:McGregor, G.P.; Kage, R.; Thim, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A:Title: Quantitation and characterization of peptides from the C-terminal flanking r
A:Reference number: A61460; MUID:90039314
A:Accession: A61460
A:Molecule type: Protein
A:Residues: 111-126 <MCG>
A:Experimental source: corpus striatum
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schultze, W.; Iyell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5454
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-120, 'A', 122 <CHI>
A:Cross-references: GB:M68911; NID:g163591; PIDN:AAA30724.1; PID:g552335
C:Comment: The protein is processed to produce neurokinin 1 (substance P) and neuroki
C:Genetics:
A:Gene: PPT-A
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status predict
F:1-73, 89-130/Product: neurokinin 1 precursor, gamma splice form #status predicted <S
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:38-68/Product: neurokinin 1 #status experimental <SBP>
F:98-107/Product: neurokinin 2 #status predicted <NEK>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CNP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 58 RPKPOQFFGLM 68

RESULT 13
S47038
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text, change 16-Jul-1999
C:Accession: S47038
R:Heiland, A.; Krühoffer, M.; Jueergen Maegerl, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47038
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <HEI>
A:Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C:Superfamily: substance P precursor

Query Match 100.0%; Score 61; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11

DB 58 RPKPOQFFGLM 68

RESULT 14
152526

neurokinin 1 precursor - mouse

N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P

N:Contents: neurokinin 1; neurokinin 2

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000

C:Accession: 152526; J05452; I62741

R:Kako, K.; Muneakata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.

Biomed. Res. 14, 253-259, 1993

A:Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and B.

A:Reference number: 152526

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: 152526

A:Molecule type: mRNA

A:Residues: 1-130 <KAK>

A:Cross-references: GB:D17584; NID:g407345; PIDN:BAA04508.1; PID:g435121

R:Chikakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.

Endocrinology 128, 2441-2448, 1991

A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse

A:Reference number: J05450; MUID:91209287

A:Accession: J05452

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 36-122 <CHT>

A:Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260

C:Gene: PPT-A

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>

F:58-68/Product: neurokinin 1 #status predicted <NK1>

F:98-107/Product: neurokinin 2 #status predicted <NK2>

F:111-126/Domain: carboxy-terminal propeptide #status predicted <CTP>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following g1

F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following g1

Query Match 100.0%; Score 61; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.0005;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11

DB 58 RPKPOQFFGLM 68

RESULT 15
JN0023

substance P - chicken

C:Species: Gallus gallus (chicken)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C:Accession: JN0023

R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: JN0023; MUID:88204263

A:Accession: JN0023

A:Molecule type: protein

A:Residues: 1-11 <CON>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 95.1%; Score 58; DB 2; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.00015;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11

DB 1 RPKPOQFFGLM 11

RESULT 16

substance P - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C:Accession: S23308

R:Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the

A:Reference number: S23186; MUID:92298992

A:Accession: S23308

A:Molecule type: protein

A:Residues: 1-11 <JEN>

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and

A>Note: substance P is derived by post-translational processing of preprotachykinin A

C:Superfamily: unassigned animal peptides

C:Keywords: neuropeptide; amidated carboxyl end; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 82.0%; Score 50; DB 2; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.0042;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11

DB 1 KRPQHOFFGLM 11

RESULT 17

substance P - Atlantic cod

C:Species: Gadus morhua (Atlantic cod)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C:Accession: S23306

R:Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the

A:Reference number: S23186; MUID:92298992

A:Accession: S23306

A:Molecule type: protein

A:Residues: 1-11 <JEN>

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and

A>Note: substance P is derived by post-translational processing of preprotachykinin A

C:Superfamily: unassigned animal peptides

C:Keywords: neuropeptide; amidated carboxyl end; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 80.3%; Score 49; DB 2; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.0064;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11

DB 1 KRPQOFGGLM 11

RESULT 18

probable substance P - smaller spotted catshark

C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999

C:Accession: S33300
R:Maugh, D.; Wang, Y.; Hazen, N.; Balmert, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A:Title: Primary structures and biological activities of substance-P-related peptides from
A:Reference number: S33300; MWID:93252508
A:Accession: S33300
A:Molecule type: protein
A:Residues: 1-11 <MANU>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and gas
A:Note: substance P is derived by post-translational processing of preprotachykinin A
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 78.7%; Score 48; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.0098;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
: | : | | | | | | | | | |
Db 1 KPRGQFFGLM 11

RESULT 19
F60409
Substance P-like peptide II - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: F60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A:Reference number: A60409; MWID:90287814
A:Accession: F60409
A:Molecule type: protein
A:Residues: 1-11 <STM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 72.1%; Score 44; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.052;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
: | : | | | | | | | | | |
Db 1 QPNPEFFGLM 11

RESULT 20
E60409
Substance P-like peptide I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: E60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A:Reference number: A60409; MWID:90287814
A:Accession: E60409
A:Molecule type: protein
A:Residues: 1-11 <STM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 72.1%; Score 44; DB 2; Length 11;

Best Local Similarity 63.6%; Pred. No. 0.052;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
: | : | | | | | | | | | |
Db 1 QPNPEFFGLM 11

RESULT 21
S10059
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambates-kassinin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C:Accession: S10059
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, 1
A:Reference number: S07436
A:Accession: S10059
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 72.1%; Score 44; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.057;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFFGLM 11
| | | | | | | | | | | |
Db 3 PKPOFFGLM 12

RESULT 22
A61033
ranatachykinin A - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C:Accession: A61033; JE0426
R:Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and 1
A:Reference number: A61033
A:Accession: A61033
A:Molecule type: protein
A:Residues: 1-11 <KAN>
R:Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and 1
A:Reference number: JE0426; MWID:91254337
A:Accession: JE0426
A:Molecule type: protein
A:Residues: 1-11 <KO2>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 67.2%; Score 41; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.19;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
: | : | | | | | | | | | |
Db 1 KPSDRFFGLM 11

RESULT 23

T13857
trithorax protein - fruit fly (*Drosophila virilis*)
C:Species: *Drosophila virilis*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13857
R:Mazo, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z17801
A:Accession: T13857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3828 <MAZ>
A:Cross-references: EMBL:Z50038; NID:g899253; PID:g899254; PIDN:CAA90349.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0014844
A:Introns: 337/3; 529/1; 721/1; 791/1; 3668/2; 3713/1; 3771/3
C:Superfamily: *Drosophila trithorax* protein
C:Keywords: DNA binding; transcription regulation; zinc finger

Query Match 67.2%; Score 41; DB 2; Length 3828;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
: : : : :
DB 618 KRPKNYFGL 627

RESULT 24
T30016
hypothetical protein F38E9.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T30016
R:Wu, X.; Gattung, S.
submitted to the EMBL Data Library, January 1996
A:Description: The sequence of *C. elegans* cosmid F38E9.
A:Reference number: Z20722
A:Accession: T30016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-205 <WU>
A:Cross-references: EMBL:U46668; PIDN:AAA93346.1; CESP:F38E9.4
C:Genetics:
A:Gene: CESP:F38E9.4

Query Match 62.3%; Score 38; DB 2; Length 205;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPOQFF 8
: : : : :
DB 151 PKPOQFF 157

RESULT 25
T10586
small nuclear ribonucleoprotein-associated protein homolog F9F13.90 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C:Accession: T10586
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16991
A:Accession: T10586
A:Molecule type: DNA
A:Residues: 1-257 <BEV>
A:Cross-references: EMBL:AL080253; GSPDB:GN00062; ATSP:F9F13.90
A:Experimental source: cultivar Columbia; BAC clone F9F13
C:Genetics:
A:Gene: ATSP:F9F13.90

A:Map position: 4
C:Superfamily: proline-rich protein

Query Match 62.3%; Score 38; DB 2; Length 257;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RRPQOQFPG 9
: : : : :
DB 189 RRPQOQFPG 197

RESULT 26
T04951
hypothetical protein F7J7.140 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
C:Accession: T04951
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15391
A:Accession: T04951
A:Molecule type: DNA
A:Residues: 1-293 <BEV>
A:Cross-references: EMBL:AL021960
A:Experimental source: cultivar Columbia; BAC clone F7J7
C:Genetics:
A:Map position: 4
A:Introns: 107/2; 214/3
A:Note: F7J7.140
C:Superfamily: 1-aminocyclopropane-1-carboxylate oxidase

Query Match 62.3%; Score 38; DB 2; Length 293;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFFGLM 11
: : : : :
DB 159 PKPSEVYGLM 168

RESULT 27
C60409
kassinin-like peptide K-II - frog (*Pseudophryne guentheri*)
C:Species: *Pseudophryne guentheri*
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C:Accession: C60409
R:Stimacov, M.; Severini, C.; De Biae, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melch
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aus
A:Reference number: A60409; MUID:90287814
A:Accession: C60409
A:Molecule type: protein
A:Residues: 1-11 <STM>
A:Note: this peptide was also found in a deamidated form
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 60.7%; Score 37; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.99;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RRPQOQFFGLM 11
: : : : :
DB 1 QPNPDERVGLM 11

RESULT 28

S07203
uperolein - frog (Uperoleia marmorata)
C:Species: Uperoleia marmorata
C>Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07203
R:Anastasi, A.; Erspamer, V.; Eudean, R.
A:Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin
A:Reference number: S07203; MUID:75131227
A:Accession: S07203
A:Molecule type: protein
A:Residues: 1-11 <ANA>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 60.7%; Score 37; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.99;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFGGLM 11
: | | : | | |
DB 1 QPDPNAFYGLM 11

RESULT 29
G75189
hypothetical protein PAB2321 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75189
R:Anonymous; Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: G75189
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <KAM>
A:Cross-references: GB:A7248283; GB:AL096836; NID:95457433; PIDN:CAB48966.1; PID:9545747
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2321

Query Match 60.7%; Score 37; DB 2; Length 249;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFGGL 10
| | | | | | | | | |
DB 124 RIKPEKFFGI 133

RESULT 30
D60409
kassinin-like peptide K-III - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: D60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A:Reference number: A60409; MUID:90287814
A:Accession: D60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 59.0%; Score 36; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFGGLM 11
: | | : | | |
DB 1 QPDPNAFYGLM 11

RESULT 31
B60409
kassinin-like peptide K-I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C:Accession: B60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melch
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aus
A:Reference number: A60409; MUID:90287814
A:Accession: B60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
A:Note: this peptide was also found in a deamidated form
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 59.0%; Score 36; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFGGLM 11
: | | : | | |
DB 1 QPDPNAFYGLM 11

RESULT 32
S07436
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambatin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C:Accession: S07436
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, 1
A:Reference number: S07436
A:Accession: S07436
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKPOQFGGLM 11
| | | : | | : | | |
DB 3 PDPDRFYGLM 12

RESULT 33
S07206
kassinin - Senegal running frog

C:Species: *Kassina senegalensis* (Senegal running frog)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Sep-2000
 C:Accession: S07206
 R:Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.
 R:Experientia 33, 857-858, 1977
 A:Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide from
 A:Reference number: S07206; MUID:77246385
 A:Accession: S07206
 A:Molecule type: protein
 A:Residues: 1-12 <ANK>
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 59.0%; Score 36; DB 2; Length 12;
 Best Local Similarity 70.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOQFGLM 11
 Db 3 PKSDQFVGLM 12

RESULT 34
 A64173
 conserved hypothetical protein H11608 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 19-May-2000
 C:Accession: A64173
 R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.
 ; Gocayne, J.D.; Scott, J.; Shriley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Furmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Guehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630
 A:Accession: A64173
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-321 <TRIG>
 A:Cross-references: GB:L42023; NID:g1574444; PIDN:AAC23252.1; PID:g1574450; TIGR:H11608
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: conserved hypothetical protein HP1443

Query Match 59.0%; Score 36; DB 2; Length 321;
 Best Local Similarity 54.5%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 Db 281 RQKPEAFEGFV 291

RESULT 35
 T02976
 probable DNA binding protein PCF2 - rice
 C:Species: *Oryza sativa* (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T02976
 R:Kosugi, S.; Ohashi, Y.
 Plant Cell 9, 1607-1619, 1997
 A:Title: PCF1 and PCF2 specifically bind to cis elements in the rice proliferating cell
 A:Reference number: Z14803; MUID:97480096
 A:Accession: T02976
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-373 <KOS>
 A:Cross-references: EMBL:D87261; NID:g2580439; PIDN:BA23143.1; PID:g2580440
 A:Experimental source: cultivar Nipponbare

Query Match 59.0%; Score 36; DB 2; Length 373;
 Best Local Similarity 54.5%; Pred. No. 52;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 Db 55 KPEPVEFGGM 65

RESULT 36
 T19563
 hypothetical protein C29F3.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T19563; T23034
 R:Matthews, L.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19142
 A:Accession: T19563
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-629 <WID>
 A:Cross-references: EMBL:Z81043; PIDN:CAB02804.1; GSPDB:GN00023; CESP:C29F3.2
 A:Experimental source: clone C29F3
 R:White, S.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z19657
 A:Accession: T23034
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-629 <WID>
 A:Cross-references: EMBL:AL023813; PIDN:CA19424.1; GSPDB:GN00023; CESP:C29F3.2
 A:Experimental source: clone H02K04
 C:Genetics:
 A:Gene: CESP:C29F3.2
 A:Map position: 5
 A:Introns: 23/1; 111/3; 177/3; 207/2; 287/1; 381/3; 399/3; 417/1; 476/2; 528/3; 537/2

Query Match 59.0%; Score 36; DB 2; Length 629;
 Best Local Similarity 75.0%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFF 8
 Db 380 OPPPOQFF 387

RESULT 37
 E69486
 translation elongation factor EF-2 (fus) homolog - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
 C:Accession: E69486
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
 Glodex, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utlacker, T.; Cotton, M.D.; Spriggs, T.; Arltach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: E69486
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-728 <KLB>
 A:Cross-references: GB:AF000972; GB:AF000782; NID:g2689295; PIDN:AA89360.1; PID:g264
 C:Superfamily: translation elongation factor 2; translation elongation factor Tu homo
 C:Keywords: GTP binding; nucleotide binding; P-loop
 F:21-150/Domain: translation elongation factor Tu homology <ETU>
 F:27-34/Region: nucleotide-binding motif A (P-loop)
 F:147-150/Region: GTP-binding NKXD motif

F:202-204/Region: GTP-binding SAK/L motif
F:33,34,70,147,148,150,202/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 59.0%; Score 36; DB 2; Length 728;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10
|||:|
Db 720 PKPEDFVGL 728

RESULT 38

A25777
T-cell receptor beta-2 chain precursor V region (MOLT-4) - human
C:Species: Homo sapiens (man)
C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 29-Aug-1997
C:Accession: A25777
R:Turnncliffe, A.; Kafford, R.; Milstein, C.; Forster, A.; Rabbitts, T.H.
Proc. Natl. Acad. Sci. U.S.A. 82, 5068-5072, 1985
A:Title: Sequence and evolution of the human T-cell antigen receptor beta-chain genes.
A:Reference number: A94053; MUID:85270467
A:Accession: A25777
A:Molecule type: mRNA
A:Residues: 1-133 <TUN>
A:Cross-references: GB:M12886
C:Genetics:
A:Gene: GDB:TCRB
A:Cross-references: 3DB:120405; OMIM:186930
A:Map position: 7q35-7q35
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 57.4%; Score 35; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOOFFG 9
||:||||
Db 118 PKNEOFFG 125

RESULT 39

T33064
hypothetical protein F56C3.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T33064
R:Stoneking, T.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid F56C3.
A:Reference number: Z21276
A:Accession: T33064
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-206 <STO>
A:Cross-references: EMBL:AF067214; PIDN:AACT1009.1; GSPDB:GN00028; CESP:F56C3.9
A:Experimental source: strain Bristol N2; clone F56C3
C:Genetics:
A:Gene: CESP:F56C3.9
A:Map position: X
A:Introns: 43/2; 87/1; 116/1; 141/2; 184/3

Query Match 57.4%; Score 35; DB 2; Length 206;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
||:|||
Db 188 KRPPOFF 195

RESULT 40

A83049
hypothetical protein PA4779 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83049
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.
Loiy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: A83049
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <STO>
A:Cross-references: GB:AE004891; GB:AE004091; NID:99951037; PIDN:AAG08165.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4779

Query Match 57.4%; Score 35; DB 2; Length 297;
Best Local Similarity 54.5%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
||:|:|
Db 111 RPRPRGLEGL 121

RESULT 41

T05737
Probable hordein C - barley
C:Species: Hordeum vulgare (barley)
C>Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Aug-1999
C:Accession: T05737
R:Entwistle, J.
Carlsberg Res. Commun. 53, 247-258, 1988
A:Title: Primary structure of a C-hordein gene from barley.
A:Reference number: Z15444; MUID:89351278
A:Accession: T05737
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-347 <ENT>
A:Cross-references: EMBL:M36941; NID:q167062; PIDN:AAA92333.1; PID:q893242
A:Experimental source: cv. Boml, immature endosperm
C:Superfamily: gliadin

Query Match 57.4%; Score 35; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOOFF 8
||:||||
Db 60 PTPPOFF 66

RESULT 42

T15511
hypothetical protein C15C7.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15511
R:Leimbach, D.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C15C7.
A:Reference number: Z18363
A:Accession: T15511
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-474 <LEI>
A:Cross-references: EMBL:U41528; NID:g1109795; PID:g1109800; PIDN:AAA83156.1; CESP:C15C7
C:Genetics:
A:Gene: CESP:C15C7.1
A:Introns: 31/3; 67/2; 106/1; 202/3; 235/3; 364/3; 410/3

Query Match 57.4%; Score 35; DB 2; Length 474;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 10
DB 457 PRPSAFGL 465

RESULT 43
E86671
lysine--tRNA ligase (EC 6.1.1.6) [imported] - Lactococcus lactis subsp. lactis (strain T
N:Alternate names: lysyl-tRNA synthetase
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: E86671
R:Boilotin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. In press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: E86671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <STO>
A:Cross-references: GB:A8005176; NID:g12723244; PIDN:AAK04471.1; GSPDB:GN00146
A:Experimental source: strain H1403
C:Genetics:
A:Gene: lysS
C:Superfamily: lysine--tRNA ligase
C:Keywords: ligase

Query Match 57.4%; Score 35; DB 2; Length 494;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 143 RPLPEKFGHL 152

RESULT 44
A82296
lysyl-tRNA synthetase, heat inducible VC0664 [imported] - Vibrio cholerae (strain N16961
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: A82296
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, R.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: A82296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <HEI>
A:Cross-references: GB:AE004152; GB:AE003852; NID:g9655096; PIDN:AAF93829.1; GSPDB:GN001
A:Experimental source: serogroup O1, strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0664
A:Map position: 1
C:Superfamily: lysine--tRNA ligase

Query Match 57.4%; Score 35; DB 2; Length 512;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 152 RPLPEKFGHL 161

RESULT 45
S76815
hypothetical protein sl11477 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76815
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S76815
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-832 <KAN>
A:Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BA18727.1; PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Synechocystis hypothetical protein sl11477

Query Match 57.4%; Score 35; DB 2; Length 832;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 669 RPDQMGFGGL 678

RESULT 46
T23875
hypothetical protein R03E1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2000
C:Accession: T23875
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19812
A:Accession: T23875
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1043 <WIL>
A:Cross-references: EMBL:Z92837; PIDN:CAB07400.1; GSPDB:GN00028; CESP:R03E1.1
A:Experimental source: clone R03E1
C:Genetics:
A:Gene: CESP:R03E1.1
A:Map position: X
A:Introns: 34/3; 92/3; 164/3; 344/3; 512/2; 558/2; 830/3; 864/3; 1003/3

Query Match 57.4%; Score 35; DB 2; Length 1043;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 11
DB 955 PRQVFFNML 964

RESULT 47
H69071
DNA-directed DNA polymerase (EC 2.7.7.7) chain 2 MTH1536 [similarity] - Methanobacter

C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Mar-2001
C:Accession: H69071
R:Smith, D.R.; Doucette-Stamm, L.A.; Delouhery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Otu, D.; Spadeford, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.
Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcn
A:Reference number: A69000; MUID:98037514
A:Accession: H69071
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1092 <MTX>
A:Cross-references: GB:AE000913; GB:AE000666; NID:g2622646; PIDN:AAB86010.1; PID:g262265
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1536
C:Superfamily: Pyrococcus furiosus DNA-directed DNA polymerase chain 2
C:Keywords: nucleotidyltransferase

Query Match 57.4%; Score 35; DB 2; Length 1092;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PKPOFFGLM 11
|||: |||
Db 932 KPEQYTGIM 940

RESULT 48
A84743
Probable myosin heavy chain [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: A84743
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nleman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: A84743
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1611 <STO>
A:Cross-references: GB:AE002093; NID:g6598338; PIDN:AAF18589.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g33240
A:Map position: 2
C:Superfamily: myosin MYO2; myosin motor domain homology

Query Match 57.4%; Score 35; DB 2; Length 1611;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFGLM 11
|||: |||
Db 1338 PQPSTFGRM 1347

RESULT 49
F86178
Hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86178
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86178
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1736 <STO>
A:Cross-references: GB:AE005172; NID:g2494118; PIDN:AAB80627.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: myosin MYO2; myosin motor domain homology

Query Match 57.4%; Score 35; DB 2; Length 1736;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFGLM 11
|||: |||
Db 1402 PQPSTFGRM 1411

RESULT 50
F96657
Hypothetical protein F16M19.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96657
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Chin, C.W.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96657
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <STO>
A:Cross-references: GB:AE005173; NID:g10092246; PIDN:AAG12661.1; GSPDB:GN00141
C:Genetics:
A:Gene: F16M19.10
A:Map position: 1

Query Match 56.6%; Score 34.5; DB 2; Length 216;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 RPKPOQ---FGL 10
|||||: |||
Db 168 RPKPQGVKVFGL 180

RESULT 51
T36290
Probable integral membrane protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36290
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21603
A:Accession: T36290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-167 <SEB>
A:Cross-references: EMBL:AL049819; PIDN:CAB42667.1; GSPDB:GN00070; SCOEDB:SCE7.08C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE7.08C

Query Match 55.7%; Score 34; DB 2; Length 167;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOOFFG 9
||| :|||
DB 18 REPPLRFYC 26

RESULT 52
H81036
riboflavin kinase/FMN adenylyltransferase NMB1834 [imported] - Neisseria meningitidis (S
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81036
R:Jettel, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: H81036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <TEM>
A:Cross-references: GB:AE002534; GB:AE002098; NID:g7227095; PIDN:AAF2169.1; PID:g722708
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1834
C:Superfamily: conserved hypothetical protein H10963

Query Match 55.7%; Score 34; DB 2; Length 306;
Best Local Similarity 55.6%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 PKPOOFFGL 10
|:|:| |
DB 56 PPKKEFFAL 64

RESULT 53
T13601
hypothetical protein 80H7.5 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13601
R:Benos, P.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17667
A:Accession: T13601
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-316 <BEN>
A:Cross-references: EMBL:AL031027; NID:e1313443; PID:e1310143; PIDN:CAA19842.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0000481
A:Note: EG:80H7.5

Query Match 55.7%; Score 34; DB 2; Length 316;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFF 8
||| :|||
DB 49 RPKSROFF 56

RESULT 54
A81982
FAD synthase NMA0621 [similarity] - Neisseria meningitidis (strain Z2491 serogroup A)
N:contains: FMN adenylyltransferase (EC 2.7.7.2); riboflavin kinase (EC 2.7.1.26)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81982
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556
A:Accession: A81982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83911.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: ribF; NMA0621
C:Superfamily: conserved hypothetical protein H10963
C:Keywords: nucleotidyltransferase; phosphotransferase

Query Match 55.7%; Score 34; DB 2; Length 318;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 PKPOOFFGL 10
|:|:| |
DB 68 PPKKEFFAL 76

RESULT 55
T52337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C:Accession: T52337
R:Miya, S.; Koga, R.; Bohmert, H.J.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999
A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcrip
A:Reference number: Z26045; MUID:99200489
A:Accession: T52337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MIY>
A:Cross-references: EMBL:AF075580; PIDN:AC36698.1
C:Genetics:
A:Gene: PP2C
C:Keywords: phosphoric monoester hydrolase

Query Match 55.7%; Score 34; DB 2; Length 359;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOOFFGL 10
||| :|||
DB 84 PKPSAFYGV 92

RESULT 56
S73890
hypothetical protein yers1 homolog A65_orf493 - Mycoplasma pneumoniae (strain ATCC 293
N:Alternate names: hypothetical protein A65_orf493
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342

C>Date: 27-Feb-1997 #sequence,revision 25-Apr-1997 #text_change 17-Mar-2000
C:Accession: S73890
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkil, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*
A:Reference number: S73327; MUID:97105885
A:Accession: S73890
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-493 <HMM>
A:Cross-references: EMBL:AE000056; GB:U00089; NID:91674263; PIDN:AA96212.1; PID:9167426
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Gene: ysr1
A:Genetic code: SGC3
C:Superfamily: hypothetical protein ymda

Query Match 55.7%; Score 34; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 11
|||
Db 281 PKLHFFEL 290

RESULT 57
S48058
cytochrome P450 CYP3A1 - black swallowtail
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Papilio polyxenes (black swallowtail)
C>Date: 10-Sep-1999 #sequence,revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S48058; A46367
R:Papalpong, H.; Barenbaum, M.R.; Schuler, M.A.
Nucleic Acids Res. 22, 3210-3217, 1994
A:Title: Transcriptional regulation of the Papilio polyxenes CYP6B1 gene.
A:Reference number: S48058; MUID:94344788
A:Accession: S48058
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-498 <2RA>
A:Cross-references: EMBL:Z29624; NID:9520879; PIDN:CA82732.1; PID:9520880
R:Chen, M.B.; Schuler, M.A.; Barenbaum, M.R.
Proc. Natl. Acad. Sci. U.S.A. 89, 10920-10924, 1992
A:Title: A host-inducible cytochrome P-450 from a host-specific caterpillar: molecular
A:Reference number: A46367; MUID:93066355
A:Accession: A46367
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-23, 'N', 25-154, 'NS', 157-498 <COH>
A:Cross-references: GB:M80828; NID:9160763; PIDN:AAA29789.1; PID:9160764
A>Note: sequence extracted from NCBI backbone (NCBIN:118719, NCBI:P:118720)
C:Genetics:
A:Introns: 445/1
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:300-465/Domain: cytochrome P450 homology <P45>
F:443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 34; DB 1; Length 498;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 9
|||
Db 34 PKPVFFEG 41

RESULT 58
JX0334
cytochrome P450 3A RU33 - rat

N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Mar-1994 #sequence,revision 28-Oct-1994 #text_change 28-Jul-2000
C:Accession: JX0334; S39797
R:Komori, M.; Oda, Y.
J. Biochem. 116, 114-120, 1994
A:Title: A major glucocorticoid-inducible P450 in rat liver is not P450 3A1.
A:Reference number: JX0334; MUID:95096005
A:Accession: JX0334
A:Molecule type: mRNA
A:Residues: 1-502 <KOM>
A:Cross-references: GB:D29967; NID:9479038; PIDN:BA06233.1; PID:9479039
A:Experimental source: Liver
R:Kirita, S.; Matsubara, T.
Arch. Biochem. Biophys. 307, 253-258, 1993
A:Title: cDNA cloning and characterization of a novel member of steroid-induced cytochrome
A:Reference number: S39797; MUID:94099605
A:Accession: S39797
A:Molecule type: mRNA
A:Residues: 1-106, 'D', 108-502 <KIR>
A:Cross-references: EMBL:DJ3912; NID:9220835; PIDN:BA03008.1; PID:9220836; GB:X96721
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; monooxygenase; oxidoreductase;
F:301-463/Domain: cytochrome P450 homology <P45>
F:441/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 502;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 9
|||
Db 41 PKPLFFEG 48

RESULT 59
A40843
cytochrome P450 3 - golden hamster
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 27-Mar-1992 #sequence,revision 27-Mar-1992 #text_change 28-Jul-2000
C:Accession: A40843
R:Teixeira, J.; Gil, G.
J. Biol. Chem. 266, 21030-21036, 1991
A:Title: Cloning, expression, and regulation of lithocholic acid 6beta-hydroxylase.
A:Reference number: A40843; MUID:92041973
A:Accession: A40843
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <TEI>
A:Cross-references: GB:M73992
C:Genetics:
A:Gene: CYP3A10
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase
F:302-464/Domain: cytochrome P450 homology <P45>
F:442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 503;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 9
|||
Db 41 PKPLFFEG 48

RESULT 60
A22631
cytochrome P450 3A1, pregnenolone 16-alpha-carbonitrile-inducible - rat
N:Alternate names: testosterone 6beta-hydroxylase

N:Contains: unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 PCN1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Jul-2000
 C:Accession: A22631; PX0035; S21697; S36137; S27107; S30378; I59218
 R:Gonzalez, F.J.; Nebert, D.W.; Hardwick, J.P.; Kasper, C.B.
 J. Biol. Chem. 260, 7435-7441, 1985
 A:Title: Complete cDNA and protein sequence of a pregnenolone 16-alpha-carbonitrile-indu
 A:Reference number: A22631; MUID:85207783
 A:Accession: A22631
 A:Molecule type: mRNA
 A:Residues: 1-504 <GON>
 A:Cross-references: GB:M10161; NID:9203777; PID:AAA41035.1; PID:9203778
 R:Natata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
 J. Biochem. 107, 718-725, 1990
 A:Title: Purification and characterization of four catalytically active testosterone 6be
 nally related forms.
 A:Reference number: PX0032; MUID:90375438
 A:Accession: PX0035
 A:Molecule type: protein
 A:Residues: 1-26 <NAG>
 A:Experimental source: liver, Sprague-Dawley male rat
 R:Lechner, M.C.
 submitted to the EMBL Data Library, December 1991
 A:Reference number: S21697
 A:Accession: S21697
 A:Molecule type: mRNA
 A:Residues: 1-206, 'A', 208-212, 'T', 214-231, 'V', 233-504 <LEC>
 A:Cross-references: EMBL:X64401; NID:956038; PID:CAA45743.1; PID:956039
 R:Albelito, V.; Lechner, M.C.
 Arch. Biochem. Biophys. 293, 147-152, 1992
 A:Title: Cloning and characterization of a novel CYP3A1 allelic variant: Analysis of CYP
 A:Reference number: S36137; MUID:92117688
 A:Accession: S36137
 A:Molecule type: mRNA
 A:Residues: 205-206, 'A', 208-212, 'T', 214-231, 'V', 233-234 <RTB>
 A:Cross-references: EMBL:X64401
 R:Teilhada, M.B.; Pereira, T.M.; Lechner, M.C.
 Arch. Biochem. Biophys. 298, 715-725, 1992
 A:Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
 A:Reference number: S27107; MUID:93037516
 A:Accession: S27107
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 1-24 <TEU>
 A:Cross-references: EMBL:X62086
 R:Cooper, K.O.; Reik, L.M.; Jayosi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R
 Arch. Biochem. Biophys. 301, 345-354, 1993
 A:Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
 A:Reference number: S30378; MUID:93213168
 A:Accession: S30378
 A:Molecule type: protein
 A:Residues: 1-25 <COO>
 R:Burger, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2145-2149, 1992
 A:Title: Paradoxical transcriptional activation of rat liver cytochrome P-450 3A1 by dex
 to primary monolayer cultures of adult rat hepatocytes.
 A:Reference number: I59218; MUID:92196074
 A:Accession: I59218
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <BUR>
 A:Cross-references: GB:M66850; NID:9205919; PID:AAA41780.1; PID:9205920
 C:Genetics: CYP3A1; P450P
 C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
 F:303-465/Domain: cytochrome P450 homology <P45>
 F:443/Binding site: heme iron (Cys) (axial ligand) #status predicted

QY 2 PKPQDFG 9
 ||| |||
 Db 41 PKPLPFG 48
 RESULT 61
 S30930
 catechol oxidase (EC 1.10.3.1) p2 precursor - potato (fragment)
 N:Alternate names: polyphenol oxidase
 C:Species: Solanum tuberosum (potato)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
 C:Accession: S30930
 R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
 Plant Mol. Biol. 21, 59-68, 1993
 A:Title: cDNA cloning and expression of potato polyphenol oxidase.
 A:Reference number: S30929; MUID:93144692
 A:Accession: S30930
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-583 <HUN>
 C:Superfamily: catechol oxidase
 C:Keywords: chloroplast; copper; oxidoreductase
 F:1-84/Domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
 F:85-583/Product: catechol oxidase #status predicted <MAT>
 F:193,202/Binding site: copper (His) #status predicted
 F:324,328,359/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 583;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PKPQDFG 9
 ||| |||
 Db 296 PCPSQFPG 303
 RESULT 62
 S34785
 catechol oxidase (EC 1.10.3.1) precursor - potato (fragment)
 N:Alternate names: polyphenol oxidase
 C:Species: Solanum tuberosum (potato)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
 C:Accession: S34785
 R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
 submitted to the EMBL Data Library, June 1992
 A:Reference number: S34785
 A:Accession: S34785
 A:Molecule type: mRNA
 A:Residues: 1-583 <HUN>
 A:Cross-references: EMBL:M95196
 R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
 Plant Mol. Biol. 21, 59-68, 1993
 A:Title: cDNA cloning and expression of potato polyphenol oxidase.
 A:Reference number: S30929; MUID:93144692
 A:Contents: annotation
 C:Superfamily: catechol oxidase
 C:Keywords: chloroplast; copper; oxidoreductase
 F:1-83/Domain: transit peptide (chloroplast) (fragment) #status predicted <MAT>
 F:84-583/Product: catechol oxidase #status predicted
 F:193,202/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 583;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PKPQDFG 9
 ||| |||
 Db 296 PCPSQFPG 303

RESULT 63
S33544
catechol oxidase (EC 1.10.3.1) precursor [similarity] - tomato
N:Alternate names: polyphenol oxidase precursor
C:Species: Lycopersicon esculentum (tomato)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
R:Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.; St
Plant Mol. Biol. 21, 1035-1051, 1993
A:Title: Organisation of the tomato polyphenol oxidase gene family.
A:Reference number: S33539; MUID:93257620
A:Accession: S33544
A:Molecule type: DNA
A:Residues: 1-585 <NEW>
A:Cross-references: EMBL:Z12838; NID:g1403355; PIDN:CAA78300.1; PID:g22735
R:Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.; St
submitted to the EMBL Data Library, June 1992
A:Description: Organization of the tomato polyphenol oxidase gene family.
A:Reference number: S22965
A:Accession: S22970
A:Molecule type: DNA
A:Residues: 1-582; 'ELKGLYLDLDYLDKLDNFILMLITLTS' <NE2>
A:Cross-references: EMBL:Z12838
C:Superfamily: catechol oxidase
C:Keywords: oxidoreductase
F:157,206/Binding site: copper (His) #status predicted
F:329,330,361/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 1; Length 585;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOOFFG 9
1 1 1111
Db 300 PCPSQFFG 307

RESULT 64
S33543
catechol oxidase (EC 1.10.3.1) E. precursor [similarity] - tomato
N:Alternate names: polyphenoloxidase
C:Species: Lycopersicon esculentum (tomato)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
A:Accession: S33543; J01672; S22969
R:Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.; St
Plant Mol. Biol. 21, 1035-1051, 1993
A:Title: Organisation of the tomato polyphenol oxidase gene family.
A:Reference number: S33539; MUID:93257620
A:Accession: S33543
A:Molecule type: DNA
A:Residues: 1-587 <NEW>
A:Cross-references: EMBL:Z12837; NID:g1403354; PIDN:CAA78299.1; PID:g22733
R:Shahar, T.; Hentley, N.; Gutfinger, T.; Hareven, D.; Lifschitz, E.
Plant Cell 4, 135-147, 1992
A:Title: The tomato 66.3-kD polyphenoloxidase gene: molecular identification and develop
A:Reference number: J01672; MUID:92338844
A:Accession: J01672
A:Molecule type: DNA
A:Residues: 1-310; 'LWLVN', 316-409, 'V', 411-540, 'V', 542-566, 'I', 568-573, 'G', 575-587 <SHA>
A:Cross-references: GB:S40548; NID:g251894; PIDN:AMB22610.1; PID:g251895
A:Experimental source: tomato flowers cv Tiny Tim LA154
C:Genetics:
A:Gene: P2
C:Superfamily: catechol oxidase
C:Keywords: copper; oxidoreductase
F:157,206/Binding site: copper (His) #status predicted
F:328,332,363/Binding site: copper (His) #status predicted

QY 2 PKPOOFFG 9
1 1 1111
Db 300 PCPSQFFG 307

RESULT 65
S30929
catechol oxidase (EC 1.10.3.1) P1 precursor - potato (fragment)
N:Alternate names: polyphenol oxidase
C:Species: Solanum tuberosum (potato)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
C:Accession: S30929
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
Plant Mol. Biol. 21, 59-68, 1993
A:Title: cDNA cloning and expression of potato polyphenol oxidase.
A:Reference number: S30929; MUID:93144692
A:Accession: S30929
A:Molecule type: mRNA
A:Residues: 1-588 <HUN>
A:Cross-references: EMBL:S54002
C:Superfamily: catechol oxidase
C:Keywords: chloroplast; copper; oxidoreductase
F:1-88/Domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F:89-588/Product: catechol oxidase #status predicted
F:158,207/Binding site: copper (His) #status predicted
F:329,333,364/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 588;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOOFFG 9
1 1 1111
Db 301 PCPSQFFG 308

RESULT 66
S34786
catechol oxidase (EC 1.10.3.1) precursor - potato (fragment)
N:Alternate names: polyphenol oxidase
C:Species: Solanum tuberosum (potato)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
A:Accession: S34786
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
submitted to the EMBL Data Library, June 1992
A:Reference number: S34785
A:Accession: S34786
A:Molecule type: mRNA
A:Residues: 1-588 <HUN>
A:Cross-references: EMBL:M95197
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
Plant Mol. Biol. 21, 59-68, 1993
A:Title: cDNA cloning and expression of potato polyphenol oxidase.
A:Reference number: S30929; MUID:93144692
A:Accession: S30929
A:Contents: annotation
C:Superfamily: catechol oxidase
C:Keywords: chloroplast; copper; oxidoreductase
F:1-88/Domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F:89-588/Product: catechol oxidase #status predicted
F:158,207/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 1; Length 587;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 67
D86466
hypothetical protein AAD39611.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86466
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D86466
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-628 <STO>
A:Cross-references: GB:AE005172; NID:g5091623; PIDN:AA039611.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 55.7%; Score 34; DB 2; Length 628;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOF 8
DB 267 RRPPOEFF 274

RESULT 68
S56781
hypothetical protein YJL010C - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J1357
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 05-Nov-1999
C:Accession: S56781
R:To Van, D.; Perea, J.; Jacq, C.
Submitted to the Protein Sequence Database, September 1995
A:Reference number: S56776
A:Accession: S56781
A:Molecule type: DNA
A:Residues: 1-666 <DEH>
A:Cross-references: EMBL:L49285; NID:g1006722; PIDN:CAA89301.1; PID:g1006723; GSPDB:GN00
C:Genetics:
A:Gene: MIPS:YJL010C
A:Map position: 10L

Query Match 55.7%; Score 34; DB 2; Length 666;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFFGLM 11
DB 48 QPOMFFGV 56

RESULT 69
S44920
ZK688.5 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S44920
R:Wilson, R.
Submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZK688.
A:Reference number: S44913

A:Accession: S44920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1799 <WIL>
A:Cross-references: EMBL:L16621; NID:g289775; PID:g289783
C:Genetics:
A:Insertions: 40/3; 96/2; 200/2; 269/2; 357/1; 486/3; 1129/3; 1194/1; 1425/1; 1503/1; 15
F:21-96/Domain: ubiquitin homology <UBH>

Query Match 55.7%; Score 34; DB 1; Length 1799;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
DB 552 RRPPOOF 558

RESULT 70
G81889
hypothetical protein NMA1216 [imported] - Neisseria meningitidis (strain Z2491 serogr
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: G81889
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
R:Holroyd, S.; Jagsis, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556
A:Accession: G81889
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA84476.1; PID:g737
C:Genetics:
A:Experimental source: serogroup A, strain Z2491
A:Gene: NMA1216

Query Match 54.1%; Score 33; DB 2; Length 71;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
DB 40 KPERFPG 46

RESULT 71
G71054
hypothetical protein PH1133 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: G71054
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohikubo, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: G71054
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <KAN>
A:Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30233.1; PID:g3257550
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
C:Genetics:
A:Gene: PH1133
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1133

Query Match 54.1%; Score 33; DB 2; Length 101;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PKPOFFGLM 11
 ||||| :
 Db 18 PKOFFELL 25

RESULT 72

F75254
 conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: F75254
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Yamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Mc
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: F75254
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-234 <WHIT>
 A:Cross-references: GB:AE002089; GB:AE000513; NID:96460427; PIDN:AAF12124.1; PID:9646041
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2585
 A:Map position: 1

Query Match 54.1%; Score 33; DB 2; Length 234;
 Best Local Similarity 75.0%; Pred. No. 1,1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PKPOFFGLM 11
 ||||| :
 Db 56 PYSEFGLM 63

RESULT 73

T15304
 hypothetical protein B0280.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
 C:Accession: T15304
 R:Puliton, L.
 submitted to the EMBL Data Library, June 1994
 A:Description: The sequence of C. elegans cosmid B0280.
 A:Reference number: S48966
 A:Accession: T15304
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-282 <FUL>
 A:Cross-references: EMBL:U010439; NID:9500762; PID:9500771; PIDN:AAAI9088.1; CESP:B0280.1
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:B0280.10
 A:Introns: 39/3; 89/1; 119/1; 133/2; 183/1; 212/3; 243/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein B0280.10

Query Match 54.1%; Score 33; DB 2; Length 282;
 Best Local Similarity 62.5%; Pred. No. 1,4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFFG 9
 |||| :
 Db 15 PTPONFG 22

RESULT 74

E70842
 probable acid phosphatase - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: E70842

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garler, T.; Churcher, C.; Harris, D.; Gordon
 ; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, S.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70842
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-299 <COL>
 A:Cross-references: GB:AL021841; GB:AL123456; NID:93261517; PIDN:CAAI7082.1; PID:e125
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3310

Query Match 54.1%; Score 33; DB 2; Length 299;
 Best Local Similarity 66.7%; Pred. No. 1,5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFFGL 10
 |||| :
 Db 181 PKPNYFGL 189

RESULT 75

H71259
 probable membrane fusion protein - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C:Accession: H71259

R:Fraser, C.M.; Norris, S.J.; Welstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; M
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:9832770
 A:Accession: H71259
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-320 <COL>

A:Cross-references: GB:AE001264; GB:AE000520; NID:93323278; PIDN:MAC65920.1; PID:9332
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0965

Query Match 54.1%; Score 33; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 1,6e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 PKPOFFGLM 11
 |||| :
 Db 162 KPQDYFGL 170

RESULT 76

A75633
 Probable transposase - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: A75633

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 ; M.; Shen, M.; Yamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896
A:Accession: A75633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12606.1; PID:g6460902; TIGR:DRB01
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0134
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
| | | | |
| | | | |
Db 297 RPKPOQFFMAIL 307

RESULT 77
C75624
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: C75624
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: C75624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12602.1; PID:g6460898; TIGR:DRB00
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0057
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
| | | | |
| | | | |
Db 297 RPKPOQFFMAIL 307

RESULT 78
E75618
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: E75618; C75629
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75618
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>

A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12607.1; PID:g6460903; TIGR:DR
A:Experimental source: strain R1
A:Accession: C75629
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12607.1; PID:g6460903; TIGR:DR
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0005; DRB0102
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
| | | | |
| | | | |
Db 297 RPKPOQFFMAIL 307

RESULT 79
C75556
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: C75556
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: C75556
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001876; GB:AE000513; NID:g6457800; PIDN:AAF09729.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0144
A:Map position: 1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
| | | | |
| | | | |
Db 297 RPKPOQFFMAIL 307

RESULT 80
B75620
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: B75620
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: B75620
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12598.1; PID:g6460894; TIGR:DR

A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0020
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MPI

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | : :
Db 297 RMPKQPFMAVL 307

RESULT 81
A54871
Gal beta-1, 3galNac-specific GalNac alpha2, 6-sialyltransferase - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 24-Sep-1999
C:Accession: A54871
R:Kurosawa, N.; Kojima, N.; Inoue, M.; Hamamoto, T.; Tsuji, S.
J. Biol. Chem. 269, 19048-19053, 1994
A:Title: Cloning and expression of Galbeta1,3galNac-specific GalNac alpha2,6-sialyltrans
A:Reference number: A54871; MUID:94308168
A:Accession: A54871
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-404 <KUR>
A:Cross-references: GB:X77775; NID:9550104; PIDN:CA54813.1; PID:9550105
C:Superfamily: galactosyl-1,3-N-acetylgalactosaminyl-specific alpha-2,6-sialyltransferas

Query Match 54.1%; Score 33; DB 2; Length 404;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFFGL 10
| | | | | : :
Db 288 EPQKIFGL 395

RESULT 82
F75434
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75434
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, H.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.; Mc
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75434
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-416 <WHI>
A:Cross-references: GB:AE001962; GB:AE000513; NID:96458855; PIDN:AAFI0703.1; PID:9645886
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1127
A:Map position: 1

Query Match 54.1%; Score 33; DB 2; Length 416;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFFGLM 11
| | | | | : :
Db 297 RMPKQPFMAVL 307

Db 139 PTPRRLEGL 148

RESULT 83
T37933
transcription activator GCN5 homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C:Accession: T37933
R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z2175
A:Accession: T37933
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-454 <MCD>
A:Cross-references: EMBL:AL109820; PIDN:CAB52569.1; GSPDB:GN00066; SPDB:SPAC1952.05
A:Experimental source: strain 972h-; cosmid c1952
C:Genetics:
A:Gene: SPDB:SPAC1952.05
A:Map position: 1
C:Superfamily: transcription factor GCN5; bromodomain homology
F:368-423/domain: bromodomain homology <BRO>

Query Match 54.1%; Score 33; DB 2; Length 454;
Best Local Similarity 36.4%; Pred. No. 2.2e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | : :
Db 342 KRPKPFPAVL 352

RESULT 84
D64110
lysine--tRNA ligase (EC 6.1.1.6) - Haemophilus influenzae (strain Rd KW20)
N:Alternate names: lysyl-tRNA synthetase
C:Species: Haemophilus influenzae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: D64110
R:Reischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodde, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: D64110
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-502 <TRIG>
A:Cross-references: GB:U32800; GB:U42023; NID:91574133; PIDN:AAC22865.1; PID:91574141
C:Superfamily: lysine--tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 54.1%; Score 33; DB 1; Length 502;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGL 10
| | | | | : :
Db 147 RPLPKFGL 156

RESULT 85
SYCKT
lysine--tRNA ligase (EC 6.1.1.6) - Escherichia coli
N:Alternate names: lysyl-tRNA synthetase I
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 21-Nov-1997 #text_change 18-Jun-1999
C:Accession: B65073; J0401; A38066; B31325

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Colwell, R.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: B65073
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-505 <BLAT>
A:Cross-references: GB:AE000372; GB:U00096; NID:92367171; PIDN:AACT5928.1; PID:91789256;
A:Experimental source: strain K-12, substrain MG1655
R:Leveau, F.; Plateau, P.; Dessen, P.; Blanquet, S.
Nucleic Acids Res. 18, 305-312, 1990
A:Title: Homology of *lys*S and *lys*U, the two *Escherichia coli* genes encoding distinct *lys*
A:Reference number: J50401; MUID:90221811
A:Accession: J50401
A:Molecule type: DNA
A:Residues: 1-396, 398-444, 'V', 445-505 <LE1>
A:Cross-references: GB:X16542
A:Experimental source: strain EM20031
A:Accession: A38066
A:Molecule type: protein
A:Residues: 1-28 <LE2>
R:Kawakami, K.; Joensson, Y.H.; Bjoerk, G.R.; Ikeda, H.; Nakamura, Y.
Proc. Natl. Acad. Sci. U.S.A. 85, 5620-5624, 1988
A:Title: Chromosomal location and structure of the operon encoding peptide-chain-release
A:Reference number: A32651; MUID:88289768
A:Accession: B31325
A:Molecule type: DNA
A:Residues: 1-505 <KAN>
A:Cross-references: GB:J03795; NID:9146339; PIDN:AAA23959.1; PID:9146341
C:Comment: In *E. coli*, *lys*S is activated and transferred to tRNA by two distinct forms
coded by the *lys*U gene.
C:Genetics:
A:Gene: *lys*S; *hcr*
A:Map position: 62 min
C:Superfamily: *lys*S-tRNA synthetase
C:Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F:2-505/Product: *lys*S-tRNA synthetase #status predicted <MAT>

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQOFGCL 10
|||:|:|
DB 151 RPLDPKFHGL 160

RESULT 86
STECKU
A:Title: *lys*S-tRNA synthetase (EC 6.1.1.6), thermotolerant - *Escherichia coli*
N:Alternate names: *lys*Y1-tRNA synthetase II; *lys*Y1-tRNA synthetase, thermotolerant
C:Species: *Escherichia coli*
C>Date: 30-Jun-1991 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999
C:Accession: S56356; H65222; J50400; JY0093
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from 92.
A:Reference number: S56314; MUID:95334362
A:Accession: S56356
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-505 <BDU>
A:Cross-references: EMBL:U14003; NID:91263172; PIDN:AA97029.1; PID:9536974
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Colwell, R.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H65222

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-505 <BLAT>
A:Cross-references: GB:AE000485; GB:U00096; NID:91790563; PIDN:AACT7090.1; PID:917905
A:Experimental source: strain K-12, substrain MG1655
R:Leveau, F.; Plateau, P.; Dessen, P.; Blanquet, S.
Nucleic Acids Res. 18, 305-312, 1990
A:Title: Homology of *lys*S and *lys*U, the two *Escherichia coli* genes encoding distinct
A:Reference number: J50401; MUID:90221811
A:Accession: J50400
A:Molecule type: DNA
A:Residues: 1-445, 'R', 447-505 <LEV>
A:Cross-references: GB:X16542
R:Clark, R.L.; Neidhardt, F.C.
J. Bacteriol. 172, 3237-3243, 1990
A:Title: Roles of the two *lys*Y1-tRNA synthetases of *Escherichia coli*: analysis of nuc
A:Reference number: JY0093; MUID:90264318
A:Accession: JY0093
A:Molecule type: DNA
A:Residues: 1-124, 126-235, 'A', 237-257, 'HVT', 263-267, 'R', 270-350, 'R', 352-370, 'S', 372-3
A:Cross-references: GB:M30630; NID:9146688; PIDN:AAA24096.1; PID:9146689
C:Comment: In *E. coli*, *lys*S is activated and transferred to tRNA by two distinct fo
coded by the *lys*U gene.
C:Genetics:
A:Gene: *lys*U
A:Map position: 94 min
C:Superfamily: *lys*S-tRNA synthetase
C:Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F:2-505/Product: *lys*S-tRNA synthetase #status predicted <MAT>

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQOFGCL 10
|||:|:|
DB 151 RPLDPKFHGL 160

RESULT 87
I38396
A:Title: *tyrosine* kinase (EC 2.7.1.112) FRK - human
N:Alternate names: *tyr*-related kinase (FRK)
C:Species: *Homo sapiens* (man)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 04-Feb-2000
C:Accession: I38396
R:Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.
Gene 138, 247-251, 1994
A:Title: Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene
A:Reference number: I38396; MUID:94171047
A:Accession: I38396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-505 <RES>
A:Cross-references: EMBL:U00803; NID:9392887; PIDN:AAA18284.1; PID:9392888
C:Genetics:
A:Gene: GDB:FRK
A:Cross-references: GDB:355675
A:Map position: 4q35-4q35
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:49-105/Domain: SH2 homology <SH3>
F:116-208/Domain: SH2 homology <SH2>
F:332-494/Domain: protein kinase homology <KIN>
F:240-248/Region: protein kinase ATP-binding motif
F:262/Active site: *lys* #status predicted

Query Match 54.1%; Score 33; DB 2; Length 505;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
||||: :|
Db 459 PQOFFYIM 466

RESULT 88
E86108
hypothetical protein lysu [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: E86108
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E86108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE005174; NID:912519106; PIDN:AAG59329.1; GSPDB:GN00145; UWGP:257
C:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: lysu
C:Superfamily: lysine--tRNA ligase

Query Match 54.1%; Score 33; DB 2; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
|||:| :|
Db 151 RPLPDKFHGL 160

RESULT 89
F85944
hypothetical protein lysu [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85944
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE005174; NID:912519106; PIDN:AAG58018.1; GSPDB:GN00145; UWGP:242
C:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: lysu
C:Superfamily: lysine--tRNA ligase

Query Match 54.1%; Score 33; DB 2; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
|||:| :|
Db 151 RPLPDKFHGL 160

RESULT 90
I49552
protein-tyrosine kinase (EC 2.7.1.112) bak/lyk - mouse
N:Alternate names: intestinal tyrosine kinase
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Mar-2000

C:Accession: I49552; I48608
R:Oberg-Welsh, C.; Welsh, M.
Gene 152, 239-242, 1995
A:Title: Cloning of BSK, a murine FRK homologue with a specific pattern of tissue dis
A:Reference number: I49552; MUID:95137395
A:Accession: I49552

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <RES>
A:Cross-references: GB:U36132; NID:9556287; PIDN:AA65197.1; PID:9777773
R:Thyveson, M.; Albrecht, D.; Zurcher, G.; Andres, A.C.; Ziemlecki, A.
Biochem. Biophys. Res. Commun. 209, 582-589, 1995
A:Title: lyk, a novel intracellular protein tyrosine kinase differentially expressed
A:Reference number: I48608; MUID:95251656
A:Accession: I48608
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-153, 'T', 155-236, 'H', 238-512 <RE2>
A:Cross-references: EMBL:Z48757; NID:9736263; PIDN:CAA88658.1; PID:9736264
C:Genetics:
A:Gene: BSK
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C:Keywords: Arp; blocked amino end; intestine; lipoprotein; myristylation; phosphotra
F:56-112/Domain: SH3 homology <SH3>
F:123-215/Domain: SH2 homology <SH2>
F:239-501/Domain: protein kinase homology <KIN>
F:247-255/Region: protein kinase Arp-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:5/Binding site: palmitate (Cys) (covalent) #status predicted
F:269/active site: lys #status predicted

Query Match 54.1%; Score 33; DB 2; Length 512;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
||||: :|
Db 466 PQOFFYIM 473

RESULT 91
A32431
cytochrome-c oxidase (EC 1.9.3.1) chain I - honeybee mitochondrion
C:Species: mitochondrion Apis mellifera (honeybee)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 07-Dec-1999
C:Accession: A32431; A61223; S52961
R:Crozier, R.H.; Crozier, Y.C.; Mackinlay, A.G.
Mol. Biol. Evol. 6, 399-411, 1989
A:Title: The CO-I and CO-II region of honeybee mitochondrial DNA: evidence for variat
A:Reference number: A32431; MUID:90136028
A:Accession: A32431
A:Molecule type: DNA
A:Residues: 1-521 <CRO>
A:Cross-references: GB:M23409; NID:9493737; PIDN:AAA18476.1; PID:9493738
A:Note: this variant of the mitochondrial genome has a small distance between the COI
R:Corneuet, J.M.; Garnery, L.; Solignac, M.
Genetics 128, 393-403, 1991
A:Title: Putative origin and function of the intergenic region between COI and COII o
A:Reference number: A61223; MUID:91301463
A:Accession: A61223
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 338-521 <COR>
A:Note: this variant of the mitochondrial genome has a large distance between the COI
R:Crozier, R.H.; Crozier, Y.C.
Genetics 133, 97-117, 1993
A:Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence a
A:Accession: S52961
A:Molecule type: DNA
A:Residues: 1-521 <CR2>
A:Cross-references: EMBL:L06178; NID:9336279; PIDN:AAB96799.1; PID:9552440

A:Experimental source: *Apis mellifera ligustica*
A:Note: the authors did not translate the codon for residue 521
C:Genetics:
A:Gene: COI
A:Genome: mitochondrion
A:Genetic code: SGCA
C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-as
transmembrane protein
F:9-455/Domain: cytochrome-c oxidase chain I homology <COI>
F:59,376/Binding site: heme a iron (His) (axial ligands) #status predicted
F:238,288,289/Binding site: copper (His) #status predicted
F:238-242/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F:242/Binding site: oxygen (Tyr) #status predicted
F:366/Binding site: magnesium (His) (shared with chain II) #status predicted
F:374/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 54.1%; Score 33; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PKQPFGLM 11
||| |||
Db 425 PKHFLGLM 432

RESULT 92
F84647
hypothetical protein At2g25370 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84647
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: F84647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-546 <STO>
A:Cross-references: GB:AE002093; NID:g4432850; PIDN:AAD20698.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g25370
A:Map position: 2

Query Match 54.1%; Score 33; DB 2; Length 546;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOFF 8
||| |||
Db 500 PSEQFF 506

RESULT 93
T02552
cellulose synthase homolog T26B15.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C:Accession: T02552; C84734
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence.
A:Reference number: 214678
A:Accession: T02552
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-712 <ROU>
A:Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298541

A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84734
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <STO>
A:Cross-references: GB:AE002093; NID:g3298541; PIDN:AAC25935.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g32530; T26B15.9
A:Map position: 2
A:Introns: 45/2; 151/3; 193/3; 234/3; 301/3; 347/1; 407/3; 524/3

Query Match 54.1%; Score 33; DB 2; Length 712;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PKQPFGLM 11
||| |||
Db 437 PKPAPFLGM 446

RESULT 94
T47731
hypothetical protein F18021.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
C:Accession: T47731
R:Benites, V.; Wurmbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24474
A:Accession: T47731
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-755 <BEN>
A:Cross-references: EMBL:ATP18021
A:Experimental source: cultivar Columbia; BAC clone F18021
C:Genetics:
A:Map position: 3
A:Introns: 219/2; 262/3; 439/3; 485/3; 668/3; 706/3
A:Note: F18021.100
C:Superfamily: Arabidopsis thaliana hypothetical protein F18021.100

Query Match 54.1%; Score 33; DB 2; Length 755;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOFFGL 10
||| |||
Db 24 RPKRRFFGL 33

RESULT 95
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (*Drosophila melan*
C:Species: *Drosophila melanogaster*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39288
R:Shmell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The *Drosophila* dorsal-ventral patterning gene tolloid is related to human bo
A:Reference number: A39288; MUID:92034970
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306

C:Genetics:
A:Gene: FlyBase:rlj
A:Cross-references: FlyBase:Fbgn0003719
C:Superfamily: dorsal-ventral patterning protein tollold; astacin homology; Clr/Cls rep
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:116-329/Domain: astacin homology <AST>
F:352-464/Domain: Clr/Cls repeat homology <Clr1>
F:468-578/Domain: Clr/Cls repeat homology <Clr2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: Clr/Cls repeat homology <Clr3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: Clr/Cls repeat homology <Clr4>
F:900-1013/Domain: Clr/Cls repeat homology <Clr5>
F:221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 54.18; Score 33; DB 1; Length 1057;
Best Local Similarity 36.48; Pred. No. 5.2e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
: : : : :
Db 42 KQPEDFFGIL 52

RESULT 96

T13610
parallel sister chromatids protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13610
R:Murphy, L.; Harris, D.; Barrell, B.
Submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
A:Reference number: Z1768
A:Accession: T13610
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1741 <MUR>
A:Cross-references: EMBL:Z98269; NID:e1355202; PID:e1251076; PIDN:CAI10973.1
C:Genetics:
A:Cross-references: FlyBase:Fbgn0013432
A:Initons: 348/3; 1219/3; 1500/3; 1557/2; 1587/1; 1650/3
A>Note: EG:87B1.2

Query Match 54.18; Score 33; DB 2; Length 1741;
Best Local Similarity 71.48; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPOOFF 8
: : : : :
Db 92 PKPKKFF 98

RESULT 97

S14230
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) E1-beta chain [validated] - *Bacillus* sp
C:Species: *Bacillus stearothermophilus*
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: S14230; T46890
R:Hawkins, C.F.; Borges, A.; Perham, R.N.
Eur. J. Biochem. 191, 337-346, 1990
A:Title: Cloning and sequence analysis of the genes encoding the alpha and beta subunits
A:Reference number: S10796; MUID:90345939
A:Accession: S14230
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <HAN>
A:Cross-references: EMBL:X53560; NID:g40038; PIDN:CAA37629.1; PID:g40042
R:Borgers, A.; Hawkins, C.F.; Packman, L.C.; Perham, R.N.
Eur. J. Biochem. 194, 95-102, 1990

A:Title: Cloning and sequence analysis of the genes encoding the dihydrolipoamide ace
Bacillus stearothermophilus.

A:Reference number: S13838; MUID:91071217

A:Accession: T46890

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-325 <BOR>

A:Cross-references: EMBL:X53560; NID:g40038; PIDN:CAA37629.1; PID:g40042

A:Experimental source: strain NCA1503

C:Genetics:

A:Gene: pdhB

C:Function:

A:Description: EC 1.2.4.1 [validated; MUID:90345939]

C:Superfamily: pyruvate dehydrogenase (lipoamide) beta chain

C:Keywords: oxidoreductase

Query Match 53.38; Score 32.5; DB 2; Length 325;
Best Local Similarity 58.38; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 RPKPO-OPFGIL 11
: : : : :
Db 76 RPVEIDPFQFV 87

RESULT 98

S07201
physalaemin - frog (*Physalaemus fuscumaculatus*)
C:Species: *Physalaemus fuscumaculatus*
C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07201
R:Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cel, J.M.
Experientia 20, 489-490, 1964
A:Title: Structure and pharmacological actions of physalaemin, the main active polype
A:Reference number: S07201; MUID:66076612
A:Accession: S07201
A:Molecule type: protein
A:Residues: 1-11 <ERS>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 52.58; Score 32; DB 2; Length 11;
Best Local Similarity 62.58; Pred. No. 8.1;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
: : : : :
Db 4 PNKFFGLM 11

RESULT 99

S77046
hypothetical protein sl10676 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S77046
R:Kanevo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S77046
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-180 <KAN>
A:Cross-references: EMBL:BD4005; GB:AB001339; NID:g1001779; PIDN:BAI10738.1; PID:g100
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: synecocystis hypothetical protein sl10676

Query Match 52.5%; Score 32; DB 2; Length 180;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKPOQFGLM 11
DB 165 KPIRQPFELL 175

RESULT 100

Conserved hypothetical protein yoa2 - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C:Accession: A69898

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
A:Authors: Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Togonoi, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zanchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69380; MUID:98044033

A:Accession: A69898

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-210 <KUN>

A:Cross-references: GB:299114; GB:AL009126; NID:q2634230; PIDN:CAB13771.1; PID:el185351;

A:Experimental source: strain 168

C:Genetics:

A:Gene: yoa2

Query Match 52.5%; Score 32; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RKPOFGLM 11
DB 197 KPIRPFELM 205

RESULT 101

Conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: G75448

R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:2003896

A:Accession: G75448

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-225 <WHI>

A:Cross-references: GB:AE001952; GB:AE000513; NID:96458725; PIDN:AAI10575.1; PID:9645872

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR099

A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 225;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKPOQFGL 10
DB 78 RGRPQHFGL 87

RESULT 102

Insulin-like growth factor-binding protein 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S23009

R:Sneyers, M.; Kettmann, R.; Massart, S.; Renaville, R.; Burny, A.; Portetelle, D.
DNA Seq. 1, 407-408, 1991

A:Title: Cloning and characterization of a cDNA encoding the bovine insulin-like grow

A:Reference number: S23009; MUID:92119331

A:Accession: S23009

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-263 <SNE>

A:Cross-references: EMBL:X54979; NID:q435; PIDN:CA38723.1; PID:q436

A:Note: the authors translated the codon TGG for residue 30 as Cys

C:Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I rep

F:180-255/Domain: thyroglobulin type I repeat homology <THY1>

Query Match 52.5%; Score 32; DB 1; Length 263;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RKPOFGL 10
DB 253 PKQOFNL 261

RESULT 103

tryptophan synthase (EC 4.2.1.20) alpha chain - Thermus aquaticus

C:Species: Thermus aquaticus

C:Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 21-Aug-1998

C:Accession: B35407

R:Koyama, Y.; Furukawa, K.

J. Bacteriol. 172, 3490-3495, 1990

A:Title: Cloning and sequence analysis of tryptophan synthetase genes of an extreme t

to competent T. thermophilus cells.

A:Reference number: A35407; MUID:90264352

A:Accession: B35407

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-271 <KOY>

A:Cross-references: GB:M32108

C:Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homol

C:Keywords: carbon-oxygen lyase; hydro-lyase

F:17-241/Domain: tryptophan synthase alpha chain homology <TRPA>

F:47/Active site: Glu #status predicted

Query Match 52.5%; Score 32; DB 2; Length 271;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKPOFGL 10
DB 108 RPRFEL 114

RESULT 104

C75426
 Probable transposase - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: C75426
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mc
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: C75425
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-288 <WHI>
 A:Cross-references: GB:AE001968; GB:AE000513; NID:g6458930; PIDN:AAF10765.1; PID:g645893
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR196
 A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 288;
 Best Local Similarity 54.5%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQPFGLM 11
 I ::::: ::
 Db 258 RMRQPFMAVL 268

RESULT 105
 A75638
 Probable transposase - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: A75638
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mc
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: A75636
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-288 <WHI>
 A:Cross-references: GB:AE001827; NID:g6460959; PIDN:AAF12670.1; PID:g6460967; TIGR:DR00
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0029
 A:Map position: Plasmid
 A:Genome: plasmid
 A:Note: plasmid CPl

Query Match 52.5%; Score 32; DB 2; Length 288;
 Best Local Similarity 54.5%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQPFGLM 11
 I ::::: ::
 Db 258 RMRQPFMAVL 268

RESULT 106
 E69288
 ISA0963-2 transposase homolog - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: E69288
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: E69288
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-299 <KLE>
 A:Cross-references: GB:AE001083; GB:AE000782; NID:g2689406; PIDN:AAB90922.1; PID:g265

Query Match 52.5%; Score 32; DB 2; Length 299;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQPFGLM 11
 I ::::: ::
 Db 234 KIERFFGLM 242

RESULT 107
 H69462
 ISA0963-6 transposase homolog - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: H69462
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: H69462
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-299 <KLE>
 A:Cross-references: GB:AE000966; GB:AE000782; NID:g2689309; PIDN:AAB89545.1; PID:g264

Query Match 52.5%; Score 32; DB 2; Length 299;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQPFGLM 11
 I ::::: ::
 Db 234 KIERFFGLM 242

RESULT 108
 E69413
 ISA0963-3 transposase homolog - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: E69413
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: E69413
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-299 <KLE>
 A:Cross-references: GB:AE001013; GB:AE000782; NID:g2689336; PIDN:AAB89935.1; PID:g264

Query Match 52.5%; Score 32; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGLM 11
|:::|||||
Db 234 KIRFFGLM 242

RESULT 109
F69422
ISA0963-4 transposase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: F69422
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
G:Glotz, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Arltach, P.; Kaane, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343
A:Accession: F69422
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-239 <RLE>
A:Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AA89862.1; PID:g264919

Query Match 52.5%; Score 32; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGLM 11
|:::|||||
Db 234 KIRFFGLM 242

RESULT 110
D96769
hypothetical protein F9E11.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96769
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D96769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <STO>
A:Cross-references: GB:AE005173; NID:g10092421; PIDN:AA612826.1; GSPDB:GN00141
C:Genetics:
A:Gene: F9E11.2
A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 305;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPOQFFGLM 11
|:::|||||
Db 242 KPVYTRFGLM 251

RESULT 111
G86336
hypothetical protein AAF88158.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G86336
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G86336
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <STO>
A:Cross-references: GB:AE005172; NID:g9558595; PIDN:AAF88158.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 313;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFF 8
|:::|||||
Db 232 RPKPLQHF 239

RESULT 112
A75631
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: A75631
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Yamathavan, J.J.; Lam, P.; McDonald, L.; Overbeek, T.; Zalewski, C.;
Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75631
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <RHID>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12605.1; PID:g6460901; TIGR:DR
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0117
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MPI

Query Match 52.5%; Score 32; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
|:::|||||
Db 297 RPKPOFFMAVL 307

RESULT 113
B83371

conserved hypothetical protein PA2197 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83371
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lardi, K.; Lim,
.; Lory, S.; Olson, M.V.
Mature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: B83371
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <STO>
A:Cross-references: GB:AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05585.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2197

Query Match 52.5%; Score 32; DB 2; Length 345;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
I:|||||
DB 322 PEAFFGL 329

RESULT 114
A:Accession: A69426
ISA0963-5 transposase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69426
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsch, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utleback, T.; Cotton, M.D.; Spriggs, T.; Artlisch, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Moose, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343
A:Accession: A69426
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <KLE>
A:Cross-references: GB:AE001007; GB:AE000782; NID:g2689330; PIDN:AAB89836.1; PID:g264916

Query Match 52.5%; Score 32; DB 2; Length 357;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQOFFGLM 11
I:|||||
DB 292 KIERFFGLM 300

RESULT 115
C71242
hypothetical protein PH0197 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: C71242
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137
A:Accession: C71242
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-361 <KAW>
A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29266.1; PID:g3256583
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenB
A:Genetics:
A:Gene: PH0197

Query Match 52.5%; Score 32; DB 2; Length 361;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
I:|||||
DB 113 PQOFFGLM 120

RESULT 116
T15492
hypothetical protein CIAF11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15492
R:Wu, X.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid CIAF11.
A:Reference number: T18360
A:Accession: T15492
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-368 <WUX>
A:Cross-references: EMBL:U39645; NID:g1049344; PID:g1049350; PIDN:AAA80366.1; CESP:CI
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:CI4F11.5
A:introns: 42/3; 67/3; 263/2; 299/1; 329/1

Query Match 52.5%; Score 32; DB 2; Length 368;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQPF 8
I:|||||
DB 34 PKPQPF 40

RESULT 117
T05598
hypothetical protein F9D16.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T05598
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hohnsels, J.; Mewes, H.W.; Mayer, K
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15419
A:Accession: T05598
A:Molecule type: DNA
A:Residues: 1-370 <BEV>
A:Cross-references: EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:introns: 148/2; 193/3; 234/2; 272/3; 322/3
A:Note: F9D16.130

Query Match 52.5%; Score 32; DB 2; Length 370;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOFFGL 10
I:|||||

DB 272 KPQAFGL 279

RESULT 118

B64158

C:Species: Haemophilus influenzae (strain Rd KW20)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000

C/Accession: B64158

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

R:Goeyens, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman, J.

R:D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Georgiagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: B64158

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-382 <TIGR>

A:Cross-references: GB:U32759; GB:I42023; NID:g1573756; PIDN:AAC22412.1; PID:g1573761; T

C:Superfamily: best homolog was a hypothetical protein from Yersinia enterocolitica

C:Superfamily: hypothetical protein HI0753

Query Match

Best Local Similarity 52.5%; Score 32; DB 1; Length 382;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPQPFGLM 11

DB 5 KPQYIGMM 13

RESULT 119

H72026

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C/Accession: H72026; G81514

R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606

A:Accession: H72026

A:Molecule type: DNA

A:Residues: 1-418 <ARN>

A:Cross-references: GB:AE001667; GB:AE001363; NID:g4377171; PIDN:AAD19010.1; PID:g437718

A:Experimental source: strain CM1029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C:; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255

A:Accession: G81514

A:Molecule type: DNA

A:Residues: 1-418 <REA>

A:Cross-references: GB:AE002257; GB:AE002161; NID:g7189902; PIDN:AAF38775.1; PID:g718991

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: rfbA/rfbB; CP0997

C:Superfamily: riba bifunctional protein; 3,4-dihydroxy-2-butanone 4-phosphate synthase

F:19-209/Domain: 3,4-dihydroxy-2-butanone 4-phosphate synthase homology <HBPs>

Query Match

Best Local Similarity 52.5%; Score 32; DB 2; Length 418;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 PQQPFGL 10

DB 366 PKRYFGL 372

RESULT 120

F86599

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C/Accession: F86599

R:Shital, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349

A:Accession: F86599

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-418 <STO>

A:Cross-references: GB:BA000008; NID:g8979246; PIDN:BAAG9080.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: rfbA/rfbB

C:Superfamily: riba bifunctional protein; 3,4-dihydroxy-2-butanone 4-phosphate syntha

Query Match

Best Local Similarity 52.5%; Score 32; DB 2; Length 418;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 PQQPFGL 10

DB 366 PKRYFGL 372

RESULT 121

F82991

C:Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: F82991

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

oy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: F82991

A:Molecule type: DNA

A:Residues: 1-419 <STO>

A:Cross-references: GB:AE004936; GB:AE004091; NID:g9951541; PIDN:AMG08624.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: rho; PA5239

C:Superfamily: transcription termination factor rho

C:Keywords: transcription termination

Query Match

Best Local Similarity 52.5%; Score 32; DB 2; Length 419;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQPFGL 9

DB 296 KPQPFGL 302

RESULT 122

H81667

C:Species: Chlamydia muridarum, Chlamydia trachomatis MOpn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000

C/Accession: H81667

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C:; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Mofn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255
A:Accession: H81667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-419 <JET>
A:Cross-references: GB:AE002345; GB:AE002160; NID:g7190791; PIDN:AEF39581.1; PID:g719080
A:Experimental source: strain N19g (MOPn)
C:Genetics:
A:Gene: TC0778
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 419;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOFFG 9
||:||||
Db 297 KPRFFG 303

RESULT 123
E83172
Probable transporter PA3781 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83172
R:Stover, C.K.; Pham, X.O.; Errin, A.L.; Miroguchi, S.D.; Warriner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: E83172
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <STO>
A:Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AG07168.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3781
C:Superfamily: conserved hypothetical protein H11029

Query Match 52.5%; Score 32; DB 2; Length 426;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPOFFGLM 11
||:||||
Db 45 PPRFFG 52

RESULT 124
G72246
Transcription termination factor Rho - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: G72246
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316
A:Accession: G72246
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <ARN>
A:Cross-references: GB:AE001796; GB:AE000512; NID:g4982033; PIDN:AD36538.1; PID:g498203
A:Experimental source: strain MSB8

C:Genetics:
A:Gene: TML470
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 427;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOFFG 9
||:||||
Db 300 KPRFFG 306

RESULT 125
F81320
Transcription termination factor Cj1156 [Imported] - Campylobacter jejuni (strain NCTC 8639)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C:Accession: F81320
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chli C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyllet, A.; Whitehead, S.; Ba Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: A81250; MUID:20150912
A:Accession: F81320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-432 <PAR>
A:Cross-references: GB:AL139077; GB:AL11168; NID:g6968444; PIDN:CA873410.1; PID:g696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: rho; Cj1156
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 432;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOFFG 9
||:||||
Db 310 KPRFFG 316

RESULT 126
S75859
Hypothetical protein g111103 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75859
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A:Reference number: S74322; MUID:97061201
A:Accession: S75859
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-445 <KAN>
A:Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18318.1; PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: conserved hypothetical protein H11029

Query Match 52.5%; Score 32; DB 2; Length 445;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOQFGLM 11
||: ||:|
DB 55 PQRFICIM 62

RESULT 127

macrophage elastase (EC 3.4.24.-) precursor - mouse
M:Alternate names: matrix metalloproteinase 12 (MMP12)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: A42401
R:Shapiro, S.D.; Gillfin, G.L.; Gilbert, D.J.; Jenkins, N.A.; Copeland, N.G.; Welgus, H.
J. Biol. Chem. 267, 4664-4671, 1992
A:Title: Molecular cloning, chromosomal localization, and bacterial expression of a murine
A:Reference number: A42401; MUID:92165826
A:Accession: A42401
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-462 <SHA>
A:Cross-references: GB:M82831; NID:g199127; PIDN:AA39526.1; PID:g199128
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:53-256/Domain: matrix metalloproteinase homology <MMP>
F:269-462/Domain: hemopexin repeat homology <PXN>
F:215,211,215,221/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:211,215,221/Binding site: zinc, catalytic (His) (active) #status predicted
F:212/Active site: Glu #status predicted

Query Match 52.5%; Score 32; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QOQFGL 10
||: ||:|
DB 61 QOQFGL 66

RESULT 128

probable transcription termination factor - Chlamydia trachomatis (serotype D, strain UW
A11509
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 15-Oct-1999
C:Accession: A71509
R:Stephens, R.S.; Kalman, S.; Jammel, C.J.; Pan, J.; Marathe, R.; Arevind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A:Reference number: A71570; MUID:99000809
A:Accession: A71509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <ARN>
A:Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AA68091.1; PID:g332892
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 464;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
||: ||:|
DB 342 KPKRFG 348

RESULT 129

transcription termination factor Rho CP0137 [imported] - Chlamydia pneumoniae (strain

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: D72058; H81608
R:Kalman, S.; Mitchell, W.; Marathe, R.; Jammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: D72058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <ARN>
A:Cross-references: GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AA18749.1; PID:g437

A:Experimental source: strain CWD029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255
A:Accession: H81608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <REA>
A:Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AA38020.1; PID:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: rho; CP0137
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 464;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
||: ||:|
DB 342 KPKRFG 348

RESULT 130

transcription termination factor [imported] - Chlamydia pneumoniae (strain J138)
G85566
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: G85566
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: G85566
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <STO>
A:Cross-references: GB:BA000008; NID:g8978982; PIDN:BA98817.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 464;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
||: ||:|
DB 342 KPKRFG 348

RESULT 131

KCPGI
interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig

N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 15-Sep-2000
C:Accession: S15986; S13597
R:Richards, C.D.; Kafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
A:Reference number: S15986; MUID:91333421
A:Accession: S15986
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-469 <RIC>
A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed by
R:Clarke, N.J.; O'Hare, M.C.; Cavatton, T.E.; Harper, G.P.
Nucleic Acids Res. 18, 6703, 1990
A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
A:Reference number: S13597; MUID:91067477
A:Accession: S13597
A:Molecule type: mRNA
A:Residues: 25-469 <CIA>
A:Cross-references: EMBL:X54724; NID:92016; PIDN:CAA38526.1; PID:9930269
R:Li, J.; Brick, P.; Blow, D.M.
Submitted to the Brookhaven Protein Data Bank, April 1995
A:Reference number: A65568; PDB:1FBL
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
C:Comment: Procollagenase can be activated without removal of the activation peptide. St
tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
A:Note: also hydro-lyses type X collagen, serpins, and alpha-macroglobulins
C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status predicted <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PNX>
F:92-218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F:219/Active site: Glu #status predicted
F:278-466/Disulfide bonds: #status experimental

Query Match 52.5% Score 32; DB 1; Length 469;
Best Local Similarly 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QQPFGL 10
| | | | |
Db 68 QQPFGL 73

RESULT 132
F82175
conserved hypothetical protein VC1632 [Imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82175
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Yamatyan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833
A:Accession: F82175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-478 <HEI>
A:Cross-references: GB:AE004241; GB:AE003852; NID:99656142; PIDN:AAF94783.1; GSPDB:GN001
A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:
A:Gene: VC1632
A:Map position: 1

Query Match 52.5% Score 32; DB 2; Length 478;
Best Local Similarly 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQPFGLM 11
| | | | |
Db 402 RQPFGLSL 412

RESULT 133
T16695
hypothetical protein R05H11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16695
R:Pauley, A.
Submitted to the EMBL Data Library, May 1994
A:Description: The sequence of C. elegans cosmid R05H11.
A:Reference number: Z18560
A:Accession: T16695
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-484 <PAU>
A:Cross-references: EMBL:U00056; NID:9485152; PID:9485153; PIDN:AAA50725.1; CESP:R05H
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R05H11.1
A:Introns: 40/2; 122/2; 167/3; 264/2; 346/3; 380/2; 411/3; 453/3

Query Match 52.5% Score 32; DB 2; Length 484;
Best Local Similarly 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPQPFGL 10
| | | | |
Db 384 PPKPQPFNI 392

RESULT 134
JC7205
Lysine--tRNA ligase (EC 6.1.1.6) - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 17-Nov-2000
C:Accession: JC7205
R:Takita, T.; Shimizu, N.; Sukata, T.; Hashimoto, S.; Akita, E.; Yokota, T.; Esaki, N
Biosci. Biotechnol. Biochem. 64, 432-437, 2000
A:Title: Lysyl-tRNA synthetase of Bacillus stearothermophilus molecular cloning and e
A:Reference number: JC7205; MUID:20199468
A:Accession: JC7205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <TAK>
A:Cross-references: DDBJ:AB012100
C:Superfamily: Lysine--tRNA ligase
C:Keywords: ligase

Query Match 52.5% Score 32; DB 2; Length 493;
Best Local Similarly 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQPFGL 10
| | | | |
Db 141 RPKPKYHGL 150

RESULT 135

```

jc6200
cholesterol monooxygenase (side-chain-cleaving) (EC 1.14.15.6) cytochrome P450 [similari
M:Alternate names: cytochrome P450sc
C:Species: Gallus gallus (chicken)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 03-Nov-2000
C:Accession: Jc6200
R:Nomura, O.; Nakabayashi, O.; Nishimori, K.; Mizuno, S.
Gene 185, 217-222, 1997
A:Title: The cDNA cloning and transient expression of a chicken gene encoding cytochrome
A:Reference number: Jc6200; MUID:97208876
A:Accession: Jc6200
A:Molecule type: mRNA
A:Residues: 1-508 <NOM>
A:Cross-references: DDBJ:D49803; NID:q1906770; PIDN:BAAL8920.1; PID:q1906771
A:Experimental source: tissue adrenal gland
C:Genetics:
A:Gene: pscsc1
C:Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; steroid binding
F:315-474/Domain: cytochrome P450 homology <P45>
F:452/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match          52.5%; Score 32; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPOGF 7
111:111
Db 422 PKPEGF 427

RESULT 136
T34546
hypothetical protein DKFZP434B0328.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Sep-2000
C:Accession: T34546
R:Blocker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence database, October 1999
A:Reference number: Z21539
A:Accession: T34546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-513 <BLO>
A:Cross-references: EMBL:AL122051
A:Experimental source: adult testis; clone DKFZP434B0328
C:Genetics:
A:Note: DKFZP434B0328.1
C:Superfamily: protein kinase C zinc-binding repeat homology
F:200-250/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match          52.5%; Score 32; DB 2; Length 513;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOGFGLM 11
11:11111
Db 184 PKPEGFVGM 193

RESULT 137
F70128
transcription termination factor rho - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 26-Aug-1999
C:Accession: F70128; S35618; I40295
R:Praser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.

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A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943
A:Accession: F70128
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-515 <KLE>
A:Cross-references: GB:AE001133; GB:AE000783; NID:g2688120; PIDN:AAAC66619.1; PID:g268
R:Fillly, K.; Campbell, J.
Nucleic Acids Res. 21, 1040, 1993
A:Title: A Borrelia burgdorferi homolog of the Escherichia coli rho gene.
A:Reference number: S35618; MUID:93197131
A:Accession: S35618
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 97-515 <TIL>
A:Cross-references: EMBL:L07656
R:Ojalimi, C.; Davidson, B.E.; Saint Giron, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A:Title: Conservation of gene arrangement and an unusual organization of rRNA genes i
A:Reference number: I40241; MUID:95111614
A:Accession: I40295
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 142-153, 'H', 155-305, 'D', 307-331 <RES>
A:Cross-references: GB:I46347; NID:9928812; PIDN:AAA73991.1; PID:9928813
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: ATP; transcription termination
F:264-475/Domain: ATP-binding #status predicted <ATP>

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Query Match          52.5%; Score 32; DB 2; Length 515;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPQOFG 9
11:11111
Db 391 KPRKFG 397

RESULT 138
T19562
hypothetical protein C29F3.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19562
R:Mathews, L.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19142
A:Accession: T19562
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-518 <WIL>
A:Cross-references: EMBL:281043; PIDN:CAB02803.1; GSPDB:GN00023; CESP:C29F3.7
A:Experimental source: clone C29F3
C:Genetics:
A:Gene: CESP:C29F3.7
A:Map position: 5
A:Introns: 24/1; 76/3; 114/2; 351/2; 456/2

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Query Match          52.5%; Score 32; DB 2; Length 518;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQOFG 9
11:11111
Db 360 PQEFG 365

RESULT 139

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C71346
probable transcription termination factor Rho (rho) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 15-Oct-1999
C:Accession: C71346
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ullerbach, T.; Mcd
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: AT1250; MUID:98332770
A:Accession: C71346
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-519 <COL>
A:Cross-references: GB:AE001207; GB:AE00520; NID:g3322526; PIDN:AC65243.1; PID:g332252
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0254
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 519;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOFFG 9
||:||||
Db 392 KPRFFG 398

RESULT 140
T49467
related to COP1-interacting protein CIP8 [imported] - Neurospora crassa
N:Alternate names: protein B14D6.190
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C:Accession: T49467
R:Schulte, U.; Algin, V.; Hohsiesl, J.; Brandt, P.; Farciann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49467
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-532 <SCH>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.190
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:
A:Gene: NCSP:B14D6.190
A:Map position: 6
C:Superfamily: RING finger homology
P:418-468/Domain: RING finger homology <RRN>

Query Match 52.5%; Score 32; DB 2; Length 532;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPOOFFG 10
||:||||
Db 259 PSPRFFG 267

RESULT 141
T08405
hypothetical protein F18B3.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 10-Dec-1999
C:Accession: T08405
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub
submitted to the Protein Sequence Database, May 1999
A:Reference number: 216409

A:Accession: T08405
A:Molecule type: DNA
A:Residues: 1-567 <OUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.120
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.120
A:Map position: 3
A:Introns: 13/1; 31/3; 406/3
C:Superfamily: Arabidopsis hypothetical protein F19F18.80

Query Match 52.5%; Score 32; DB 2; Length 567;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOOFFG 10
||:||||
Db 375 KPEOFFNL 382

RESULT 142
T35430
probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) SC6A5.39 [similarity] - Strep
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Nov-2000
C:Accession: T35430
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parthill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, March 1999
A:Reference number: 221577
A:Accession: T35430
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-612 <OLU>
A:Cross-references: EMBL:AL049485; PIDN:CAB39723.1; GSPDB:GN00070; SCODEB:SC6A5.39
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC6A5.39
C:Superfamily: Synchocystis long-chain-fatty-acid--CoA ligase; acetate--CoA ligase h
C:Keywords: acid-thiol ligase; coenzyme A
P:73-598/Domain: acetate--CoA ligase homology <ACL>

Query Match 52.5%; Score 32; DB 2; Length 612;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOOFFG 10
||:||||
Db 276 RPAOFFGV 283

RESULT 143
T25208
hypothetical protein ZK1067.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T25208; T27687
R:Barlow, K.
submitted to the EMBL Data Library, December 1995
A:Reference number: 219995
A:Accession: T25208
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-614 <WIL>
A:Cross-references: EMBL:Z68319; PIDN:CAA92704.1; GSPDB:GN00020; CESP:ZK1067.6
A:Experimental source: clone T23G7
R:Thomas, K.
submitted to the EMBL Data Library, March 1996
A:Reference number: 220404
A:Accession: T27687
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-614 <MI2>
A:Cross-references: EMBL:270038; PIDN:CAA93887.1; GSPDB:GN00020; CESP:ZK1067.6
A:Experimental source: clone ZK1067
C:Genetics:
A:Gene: CESP:ZK1067.6
A:Map position: 2
A:introns: 146/1; 204/2; 263/1; 318/1; 397/3; 553/3

Query Match 52.5%; Score 32; DB 2; Length 614;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KPQOQF 8
||:||||:
DB 501 PQPQPF 507

RESULT 144
AB1095

exciunclease ABC chain C NMB1326 [imported] - Neisseria meningitidis (strain MC58 serogr
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: AB1095
R:Jettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Yamahyan, J.; Gill, J.; Scarlato, V.; Masiapani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: AB1095
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-617 <TE>
A:Cross-references: GB:AE002481; GB:AE002098; NID:g7226568; PIDN:AAFA1701.1; PID:g722656
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1326
C:Superfamily: exciunclease ABC chain C

Query Match 52.5%; Score 32; DB 2; Length 617;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOQF 9
||:||||:
DB 130 KPNQYFG 136

RESULT 145

exciunclease ABC subunit C NMA1540 [imported] - Neisseria meningitidis (strain Z2491 ser
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: G81845
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; MUID:20222556
A:Accession: G81845
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-628 <PAR>
A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84767.1; PID:g738018
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: UVIC; NMA1540
C:Superfamily: exciunclease ABC chain C

Query Match 52.5%; Score 32; DB 2; Length 628;
Best Local Similarity 71.4%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOQF 9
||:||||:
DB 141 KPNQYFG 147

RESULT 146
J50631

alpha-amylase (EC 3.2.1.1) precursor - Pseudomonas sp.
N:Alternate names: maltopentose-forming amylase
C:Species: Pseudomonas sp.
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 07-May-1999
C:Accession: J50631
R:Shida, O.; Takano, T.; Takagi, H.; Kadowaki, K.; Kobayashi, S.
Biosci. Biotechnol. Biochem. 56, 76-80, 1992
A>Title: Cloning and nucleotide sequence of the maltopentose-forming amylase gene fr
A:Reference number: J50631; MUID:92257012
A:Accession: J50631
A:Molecule type: DNA
A:Residues: 1-632 <SH>
A:Experimental source: strain KO-8940
A>Note: It is uncertain whether ARG for 1-Met or for 19-Met is the initiation codon
C:Comment: This enzyme hydrolyzes alpha-1,4-D-glucosidic linkages from the nonreducin
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Thermomonospora curvata alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-44/DNA: signal sequence status predicted <SIG>
F:45-632/Product: alpha-amylase #status predicted <ALP>
F:197-332/DNA: alpha-amylase core homology <AMY>

Query Match 52.5%; Score 32; DB 2; Length 632;
Best Local Similarity 62.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOQFGL 10
||:||||:
DB 270 QPSQYFGL 277

RESULT 147
T00548

hypothetical protein At2g39380 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F12L6.4
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T00548; F84816
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.
A:Reference number: Z14168
A:Accession: T00548
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-637 <ROU>
A:Cross-references: EMBL:AC004218; NID:g3355463; PID:g3355467
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: F84816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-637 <STO>
A:Cross-references: GB:AE002093; NID:g3355467; PIDN:AACT7829.1; GSPDB:GN00139

type I restriction enzyme homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997
C:Accession: D64315
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: D64315
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1163 <BUL>
A:Cross-references: GB:U67469; GB:L77117; NID:g1590890; PID:g1592264; TIGR:M0124; PID:g
C:Genetics:
A:Map position: REV123002-119511
A:Start codon: GTG

Query Match 52.5%; Score 32; DB 2; Length 1163;
Best Local Similarity 54.5%; Pred. No. 8.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPOFFGLM 11
|||:||||
DB 778 RPKPKRFGELI 788

RESULT 153
S24407
formin isoform IV - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S24407
R:Jackson-Grusby, L.; Kuo, A.; Leder, P.
Genes Dev. 6, 29-37, 1992
A:Title: A variant limb deformity transcript expressed in the embryonic mouse limb defin
A:Reference number: S24407; MUID:92112033
A:Accession: S24407
A:Molecule type: mRNA
A:Residues: 1-1206 <JMC>
A:Cross-references: EMBL:X62379; NID:g51552; PIDN:CAA44244.1; PID:g51553

Query Match 52.5%; Score 32; DB 2; Length 1206;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPKQOFF 8
||:|||
DB 1037 PEPQDF 1043

RESULT 154
A41724
limb deformity (ld) protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Mar-1993 #sequence_revision 15-Aug-1997 #text_change 10-Sep-1997
C:Accession: S24286; S38780; A41724
R:Trump, A.; Blundell, P.A.; de la Pompa, J.L.; Zeller, R.
Genes Dev. 6, 14-28, 1992
A:Title: The chicken limb deformity gene encodes nuclear proteins expressed in specific
A:Reference number: A41724; MUID:92112031
A:Accession: S24286
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1213 <TRU>
A:Cross-references: EMBL:X62681
A:Experimental source: embryo
R:Zeller, R.
submitted to the EMBL Data Library, August 1991

A:Reference number: S38780
A:Accession: S38780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-885; A', 887-1213 <ZEL>
A:Cross-references: EMBL:X62681; NID:g63567; PID:g63568
C:Comment: Mutations in this gene affect morphogenesis of both limbs and kidneys.
C:Genetics:
A:Gene: ld
C:Keywords: nucleus

Query Match 52.5%; Score 32; DB 2; Length 1213;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPKQOFF 8
||:|||
DB 1044 PEPQDF 1050

RESULT 155
C83070
conserved hypothetical protein PA4601 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83070
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: C83070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1415 <STO>
A:Cross-references: GB:AE004874; GB:AE004091; NID:g9950849; PIDN:AA07989.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4601

Query Match 52.5%; Score 32; DB 2; Length 1415;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPOFFGLM 11
|||:||||
DB 1393 RPKPAEFGML 1403

RESULT 156
S11515
formin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S11515
R:Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.
Nature 346, 850-853, 1990
A:Title: 'Formins': proteins deduced from the alternative transcripts of the limb def
A:Reference number: S11515; MUID:90363291
A:Accession: S11515
A:Molecule type: mRNA
A:Residues: 1-1468 <WOY>
A:Cross-references: EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878

Query Match 52.5%; Score 32; DB 2; Length 1468;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPKQOFF 8

Db 1299 PEPQDF 1305

RESULT 157

B43081
vitellinogen vit-6 precursor - Caenorhabditis elegans
N:Alternate names: vitellinogen ypl180
N:Contains: vitellinogen ypl15; vitellinogen ypl88
C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 26-Jan-1996 #text_change 08-Dec-2000
C:Accession: B43081; A27271; C93576; T33017; A05154; S24599
R:Spiehl, J.; Nettleton, M.; Zucker-Abrison, E.; Lea, K.; Blumenthal, T.
J. Mol. Evol. 32, 429-438, 1991
A:Title: Vitellinogen motifs conserved in nematodes and vertebrates.
A:Reference number: A43081; MUID:91251142
A:Accession: B43081
A:Molecule type: DNA
A:Residues: 1-1651 <SP11>
A:Cross-references: GB:X56213; NID:g6925; PIDN:CAA39670.1; PID:g6926
R:Spiehl, J.; Blumenthal, T.
Mol. Cell. Biol. 5, 2495-2501, 1985
A:Title: The Caenorhabditis elegans vitellinogen gene family includes a gene encoding a
A:Reference number: A93067; MUID:86284606
A:Accession: A27271
A:Molecule type: DNA
A:Residues: 1-110 <SP12>
A:Cross-references: GB:M11499; NID:g156498; PIDN:AAA28165.1; PID:g552073
R:Spiehl, J.; Denton, K.; Kirtland, S.; Cane, J.; Blumenthal, T.
Nucleic Acids Res. 13, 5283-5295, 1985
A:Title: The C. elegans vitellinogen genes: short sequence repeats in the promoter region
A:Reference number: A93576; MUID:85269643
A:Accession: C93575
A:Molecule type: DNA
A:Residues: 1-81 <SP13>
A:Cross-references: GB:X02756; NID:g6921
A:Note: The complete nucleotide sequence is not shown
R:Fullton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, G.
Submitted to the EMBL Data Library, February 1998
A:Description: The sequence of C. elegans cosmid K07H8.
A:Reference number: Z21264
A:Accession: T33017
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22, 'N', '24-205, 'E', '207-214, 'F', '216-370, 'A', '372-416, 'A', '418-633, 'N', '635-1622
A:Cross-references: EMBL:AF047559; PIDN:AAC04423.1; GSPDB:GN00022; CESP:K07H8.6
A:Experimental source: strain Bristol N2; clone K07H8
C:Comment: In Caenorhabditis, vitellinogens are synthesized by 32 cells building the int
uently taken up by the gonad.
C:Comment: The vitellinogen 6 precursor (yp180) is cleaved to yield two immunologically
C:Genetics:
A:Gene: vit-6; CESP:K07H8.6
A:Map position: 4
A:Introns: 32/2; 185/3; 1501/3; 1591/3
C:Superfamily: vitellinogen
C:Keywords: glycoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-1651/Product: vitellinogen vit-6 #status predicted <MAT>
F:252,651,1288/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 52.5%; Score 32; DB 2; Length 1651;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOFF 8
11111111
Db 1234 PKPAOYF 1240

RESULT 158
T14603
hypothetical protein - Trypanosoma cruzi

C:Species: Trypanosoma cruzi
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Sep-1999
C:Accession: T14603; T14634
R:Andersson, B.; Aslund, L.; Pettersson, U.
Submitted to the EMBL Data Library, March 1998
A:Description: 93.4 kb of complete sequence from chromosome 3 of Trypanosoma cruzi.
A:Reference number: Z18159
A:Accession: T14603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718 <AND>
A:Cross-references: EMBL:AF052832; NID:g3063540; PID:g3063541; PIDN:AAC14077.1
A:Accession: T14634
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718 <AND>
A:Cross-references: EMBL:AF052833; NID:g3063554; PID:g3063567; PIDN:AAC14102.1
C:Genetics:
A:Map position: 3

Query Match 52.5%; Score 32; DB 2; Length 1718;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFF 8
11111111
Db 142 RPKPOFF 149

RESULT 159
T34249
hypothetical protein F31D5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34249
R:Willcox, L.
Submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F31D5.
A:Reference number: Z21494
A:Accession: T34249
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1817 <M1D>
A:Cross-references: EMBL:U028941; PIDN:AAC71101.1; GSPDB:GN00020; CESP:F31D5.5
A:Experimental source: strain Bristol N2; clone F31D5
C:Genetics:
A:Gene: CESP:F31D5.5
A:Map position: 2
A:Introns: 22/2; 107/2; 199/2; 291/2; 384/2; 476/2; 566/2; 648/2; 728/2; 904/2; 1047/

Query Match 52.5%; Score 32; DB 2; Length 1817;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFGIM 11
11111111
Db 1633 PKLRFVCVM 1642

RESULT 160
S61103
SEC16 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein LPT1w; protein YL085w
C:Species: Saccharomyces cerevisiae
C>Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998
C:Accession: S61103
R:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.;
Submitted to the EMBL Data Library, August 1995
A:Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A:Reference number: S59677
A:Accession: S61103

A:Molecule type: DNA
A:Residues: 1-2195 <HML>
A:Cross-references: EMBL:U41849; NID:q1147608; PID:q1147609; MIPS:YPL085w
C:Genetics:
A:Gene: SGD:SECI6
A:Cross-references: SGD:S0006006; MIPS:YPL085w
A:Map position: 16L
C:Keywords: transmembrane protein
F:1198-1214/Domain: transmembrane #status predicted <TM>
F:1250-1266/Domain: transmembrane #status predicted <TM>

Query Match 52.5%; Score 32; DB 2; Length 2195;
Best Local Similarity 85.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPOFGL 10
DB 582 PPOFGL 588

RESULT 161
A59156
gladin omega-5 - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: A59156
R:Palosuo, K.; Alenius, H.; Varjonen, E.; Kotyluhta, M.; Mikkola, J.; Keskinen, H.; Kal
J. Allergy Clin. Immunol. 103, 912-917, 1999
A:Title: A novel wheat gladin as a cause of exercise-induced anaphylaxis.
A:Reference number: A59156; MUID:99262562
A:Accession: A59156
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-32 <PAL>
A:Experimental source: strain T1a1e; tissue wheat kernel endosperm
A:Note: seed storage protein; major allergen in wheat-dependent, exercise-induced anaphy
C:Superfamily: gliadin
C:Keywords: seed; storage protein

Query Match 50.8%; Score 31; DB 2; Length 32;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRPOGF 7
DB 25 PRPOGF 30

RESULT 162
D69969
hypothetical protein ygzE - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C:Accession: D69969
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berten
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eyring, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Faltz, D.; Faltz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallen
lech, J.; Hartwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
A:Accession: D69969

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <KUN>
A:Cross-references: GB:Z99116; GB:AI009126; NID:92634723; PID:CA14397.1; PID:926349
A:Experimental source: strain 168
C:Genetics:
A:Gene: ygzE

Query Match 50.8%; Score 31; DB 2; Length 79;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRPOFGIM 11
DB 38 PVSQWFGIL 47

RESULT 163
J07073
ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable chain - maize
N:Alternate names: ferredoxin:thioredoxin reductase chain A; ferredoxin:thioredoxin r
C:Species: Zea mays (maize)
C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
C:Accession: J07073; S74135
R:Wadate, H.; Tsugita, A.; Kizuki, K.; Schuermann, P.
Submitted to JIPID, August 1995
A:Description: Amino acid sequence of maize ferredoxin:thioredoxin reductase variable
A:Reference number: J07073
A:Accession: J07073
A:Molecule type: protein
A:Residues: 1-97 <IMW>
R:Wadate, H.; Tsugita, A.; Chow, L.P.; Kizuki, K.; Stritt-Etter, A.L.; Li, J.; Schue
Eur. J. Biochem. 241, 121-125, 1996
A:Title: Amino acid sequence of the maize ferredoxin:thioredoxin reductase variable
A:Reference number: S74135; MUID:97054599
A:Accession: S74135
A:Molecule type: protein
A:Residues: 1-52, 'C', 'S4-97' <IMW>
A:Experimental source: leaf
C:Comment: Ferredoxin:thioredoxin reductase is a [4Fe-4S] protein involved in the lig
ht-generated electron. This enzyme is composed of two dissimilar subunits, a catalyti
C:Superfamily: ferredoxin--thioredoxin reductase chain A
C:Keywords: chloroplast; heterodimer; oxidoreductase; photosynthesis

Query Match 50.8%; Score 31; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRPOGF 8
DB 77 PRPOGF 84

RESULT 164
S4335
nuclear receptor protein DR-78 - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C:Accession: S4335; S32723
R:Martin-Blanco, E.; Kornberg, T.B.
Biochim. Biophys. Acta 1216, 339-341, 1993
A:Title: DR-78, a novel Drosophila melanogaster genomic DNA fragment highly homologous
A:Reference number: S4335; MUID:94060116
A:Accession: S4335
A:Molecule type: DNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:X73045
R:Martin-Blanco, E.; Kornberg, T.B.
Submitted to the EMBL Data Library, April 1993
A:Description: DR-78, a novel Drosophila melanogaster genomic DNA fragment highly hom
A:Reference number: S32723

A:Accession: S32723
A:Molecule type: DNA
A:Residues: 1-112, 'K' <MAV>
A:Cross-references: EMBL:X73045
C:Genetics:
A:Gene: FlyBase:Elp78C
A:Cross-references: FlyBase:FBgn0004865
A:Introns: 68/3
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F:45-113/Domain: erba transforming protein homology (fragment) <ERBA>
F:47-67/Region: zinc finger CCCC motif
F:83-107/Region: zinc finger CCCC motif

Query Match 50.8%; Score 31; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 10
1: ||||
DB 15 PQQOOSYGL 23

RESULT 165

S72785
hypothetical protein B1549_F3_106 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S72785
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B1549.
A:Reference number: S72582
A:Accession: S72785
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <SMT>
A:Cross-references: EMBL:U00014; NID:g466903; PIDN:AAA50903.1; PID:g466928
C:Genetics:
A:Start codon: GTG

Query Match 50.8%; Score 31; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQ 6
|||||
DB 90 RPKPEQ 95

RESULT 166

D69293
conserved hypothetical protein AF0348 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69293
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: utteback, T.; Cotton, M.D.; Spriggs, T.; Artlisch, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343
A:Accession: D69293
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-126 <KLE>
A:Cross-references: GB:AE001080; GB:AE000782; NID:g2689403; PIDN:AAB90889.1; PID:g265028

Query Match 50.8%; Score 31; DB 2; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOQF 8
|||||
DB 25 PKPOKLF 31

RESULT 167

T40979
hypothetical HIT-family protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T40979
R:Lvine, M.; Rajandream, M.A.; Barrell, B.G.; Voicakeert, G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21961
A:Accession: T40979
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-133 <LYN>
A:Cross-references: EMBL:AL031966; PIDN:CAA21448.1; GSPDB:GN00068; SPDB:SPCC1442.14C
C:Genetics:
A:Gene: SPDB:SPCC1442.14C
A:Map position: 3
C:Superfamily: protein kinase C inhibitor; histidine triad homology

Query Match 50.8%; Score 31; DB 2; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 10
|||||
DB 99 PKPNEEYGL 107

RESULT 168

T45725
hypothetical protein F1P2.200 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
C:Accession: T45725
R:Chisme, N.; Robert, C.; Brothier, P.; Winkler, P.; Cattolico, L.; Artiguenave, F.;
submitted to the protein Sequence Database, November 1999
A:Reference number: Z23010
A:Accession: T45725
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <CHO>
A:Cross-references: EMBL:ALJ32955
A:Experimental source: cultivar Columbia; BAC clone F1P2
C:Genetics:
A:Map position: 3
A:Introns: 56/3; 79/1; 111/2
A:Note: F1P2.200
C:Superfamily: Arabidopsis thaliana hypothetical protein F1P2.200

Query Match 50.8%; Score 31; DB 2; Length 136;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQF 8
|||||
DB 23 PKPSHF 29

RESULT 169

T14185
chitinase (EC 3.2.1.14) - common sunflower (fragment)

C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14185
R:Courbou, I.; Badaoui, S.; Gentzbittel, L.; Mouzeyar, S.; Nicolas, P.
A:Submitted to the EMBL Data Library, April 1997
A:Description: RT-PCR cloning of a sunflower chitinase.
A:Reference number: Z17909
A:Accession: T14185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-138 <COU>
A:Cross-references: EMBL:U96640; NID:q2098790; PID:q2098791
C:Function:
A:Description: catalyzes hydrolysis of catalyzes hydrolysis of beta-1,4-linkages of N-A
A:Pathway: polysaccharide degradation
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 50.8%; Score 31; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKPOEFG 9
DB 44 RPKQSYFG 51

RESULT 170
S67619
ribosomal protein S16.e, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2442; protein YDL083c; protein YMR143w; r
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C:Accession: S67619; S69289; S50399; S45510
R:Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M.
A:Submitted to the Protein Sequence Database, July 1996
A:Reference number: S67608
A:Accession: S67619
A:Molecule type: DNA
A:Residues: 1-143 <WMA>
A:Cross-references: EMBL:Z74131; GSPDB:GN00004; MIPS:YDL083c; NID:g1431105; PIDN:CAA9864
A:Experimental source: strain S286C
A:Genetics: CH4
R:Badcock, K.; Churcher, C.
A:Submitted to the EMBL Data Library, December 1994
A:Reference number: S50388
A:Accession: S69289
A:Molecule type: DNA
A:Residues: 1-143 <BAD>
A:Cross-references: EMBL:Z47071
A:Genetics: CH13
A:Accession: S50399
A:Molecule type: DNA
A:Residues: 1-143 <BAM>
A:Cross-references: EMBL:Z47071; NID:g606429; PIDN:CAA67357.1; PID:g606441; GSPDB:GN0001
A:Genetics: CH13
R:Takehara, H.; Tsunashima, S.; Miyagi, M.; Warner, J.R.
J. Biol. Chem. 267, 5442-5445, 1992
A:Title: NH2-terminal acetylation of ribosomal proteins of Saccharomyces cerevisiae.
A:Reference number: S45500; MUID:92184799
A:Accession: S45510
A:Molecule type: protein
A:Residues: 2-8, 'A', '10', 'K', '12', 'R', '14', 'V', '16', 'V', '18-20', 'KN', '23-24', 'N', '26 <TAK>
C:Genetics: <CH4>
A:Gene: RPS16B; MIPS:YDL083c
A:Cross-references: MIPS:YDL083c
A:Map position: 4L
A:Introns: 8/3
C:Genetics: <CH13>
A:Gene: RPS16A; MIPS:YMR143w
A:Cross-references: MIPS:YMR143w
A:Map position: 13R

A:Introns: 8/3
C:Superfamily: Escherichia coli ribosomal protein S9
C:Keywords: acetylated amino end; blocked amino end; protein biosynthesis; ribosome
F:2-143/Product: ribosomal protein S16.e #status experimental <MAT>
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 50.8%; Score 31; DB 2; Length 143;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOEFG 9
DB 123 RPKKFG 131

RESULT 171
E81982
probable phosphatase NMA0625 [imported] - Neisseria meningitidis (strain Z2491 serogr
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: E81982
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
: Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:2022556
A:Accession: E81982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-159 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CA883915.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
A:Genetics:
A:Gene: NMA0625

Query Match 50.8%; Score 31; DB 2; Length 159;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOEFG 10
DB 82 RPKPMVFG 91

RESULT 172
S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N:Alternate names: myeloid antibacterial protein PR-39
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68232; JN0899; I47138; S19563
R:Zhao, C.; Ganz, T.; Lehnert, R.I.
FEBS Lett. 376, 130-134, 1995
A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: prop
A:Reference number: S68232; MUID:96105365
A:Accession: S68232
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-172 <ZHA>
A:Cross-references: EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g1165151
A:Experimental source: leukocytes
R:Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A:Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to t
A:Reference number: JN0899; MUID:94071853
A:Accession: JN0899
A:Molecule type: mRNA
A:Residues: 1-20, 'A', '22-172 <STO>
A:Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101
A:Experimental source: bone marrow cells
R:Gundmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.;

Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A:Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A:Reference number: 147138; MUID:95350216
A:Accession: 147138
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-23, 'T', 30-89, 'QR', 92-116, 'ND', 120-172 <GND>
A:Cross-references: EMBL:X87236; NID:9829142; PIDN:CAA60682.1; PID:91051298
R:Agarberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall
Eur. J. Biochem. 202, 849-854, 1991
A:Title: Amino acid sequence of PR-39, isolation from pig intestine of a new member of t
A:Reference number: S19563; MUID:92111534
A:Accession: S19563
A:Molecule type: protein
A:Residues: 131-169 <AGE>
A:Experimental source: intestine
C:Genetics:
A:Gene: PR39
A:Introns: 66/3; 102/3; 126/3
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial
F:1-29/Domain: signal sequence #status predicted <SIG>
F:22-129/Domain: cystatin homology <CYS>
F:30-139/Domain: propeptide #status predicted <PRO>
F:131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following 91

Query Match 50.8%; Score 31; DB 2; Length 172;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQF 8
||| ||
Db 141 RRPPEPF 148

RESULT 173
A75624
hypothetical protein DRB0054 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75624
R:Wille, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <WHI>
A:Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12635.1; PID:96460931; TIGR:DRB00
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0054
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1
C:Superfamily: Deinococcus radiodurans hypothetical protein DRB0054

Query Match 50.8%; Score 31; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
||| ||
Db 119 RPTPOFEGKI 128

RESULT 174

E69296
transcription initiation factor IID homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: E69296
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kalne, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: E69296
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1183 <KLE>
A:Cross-references: GB:AE001078; GB:AE000782; NID:92689401; PIDN:AAB90862.1; PID:9265
C:Superfamily: transcription initiation factor IID
C:Keywords: transcription initiation

Query Match 50.8%; Score 31; DB 2; Length 183;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFGLM 11
||| ||
Db 36 KPKQFGLV 44

RESULT 175
E96766
hypothetical protein F2P9_24 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96766
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E96766
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <STO>
A:Cross-references: GB:AE005173; NID:97109482; PIDN:AAF36746.1; GSPDB:GN00141
C:Genetics:
A:Gene: F2P9_24
A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 193;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPOQFGL 10
||| ||
Db 154 PRPISFMGL 162

RESULT 176
F71012
hypothetical protein PH136 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: F71012

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi, A. Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic B
A:Reference number: A71000; MUID:98344137
A:Accession: F71012
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-206 <KAM>
A:Cross-references: GB:AP000006; NID:93236133; PIDN:BAA30502.1; PID:d1031445; PID:932578
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1396

Query Match 50.8%; Score 31; DB 2; Length 206;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFEG 9
DB 76 RPOQFEG 82

RESULT 177
T22453
hypothetical protein F49E2.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
A:Accession: T22453
R:Stinson, J.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19566
A:Accession: T22453
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-216 <MIL>
A:Cross-references: EMBL:Z46267; PIDN:CAAB6423.1; GSPDB:GN00028; CESP:F49E2.4
A:Experimental source: clone F49E2
C:Genetics:
A:Gene: CESP:F49E2.4
A:Map position: X
A:introns: 28/2; 74/3; 163/3; 196/1

Query Match 50.8%; Score 31; DB 2; Length 216;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFEG 10
DB 46 RPKFAEYFGI 55

RESULT 178
C81038
phosphoglycolate phosphatase, probable NMB1830 [Imported] - Neisseria meningitidis (stra
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81038
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Yamahewyan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: C81038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <TEF>
A:Cross-references: GB:AE002532; GB:AE002098; NID:g7227078; PIDN:AAFA2165.1; PID:g722708

A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1830

Query Match 50.8%; Score 31; DB 2; Length 219;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFEG 10
DB 142 KPSPEWVFGI 151

RESULT 179
T24530
hypothetical protein T05E12.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T24530
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19904
A:Accession: T24530
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-226 <MIL>
A:Cross-references: EMBL:Z81585; PIDN:CAB04683.1; GSPDB:GN00023; CESP:T05E12.5
A:Experimental source: clone T05E12
C:Genetics:
A:Gene: CESP:T05E12.5
A:Map position: 5
A:introns: 168/2

Query Match 50.8%; Score 31; DB 2; Length 226;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 PPOQFEG 9
DB 70 POKFEG 75

RESULT 180
S40944
hypothetical protein ZK632.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C:Accession: S40944
R:Birks, M.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40933
A:Accession: S40944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <BER>
A:Cross-references: EMBL:Z22181
C:Genetics:
A:introns: 6/1; 137/1; 206/3; 241/3

Query Match 50.8%; Score 31; DB 2; Length 254;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 8
DB 49 KPKROF 56

RESULT 181
WMBVT3

30K protein - tomato mosaic virus (strain L)
C:Species: tomato mosaic virus
A:Note: host (tomato)
C>Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 16-Feb-1997
C:Accession: A04182
R:Takamatsu, N.; Ohno, T.; Meshi, T.; Okada, Y.
Nucleic Acids Res. 11, 3767-3778, 1983
A:Title: Molecular cloning and nucleotide sequence of the 30K and the coat protein cist
A:Reference number: A93473; MUID:83220776
A:Accession: A04182
A:Molecule type: genomic RNA
A:Residues: 1-264 <TAK>
C:Superfamily: tobnavirus 30K protein
C:Keywords: DNA binding

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
| | | | |
Db 233 RPKPKSF 239

RESULT 182
WMBVL2
30K protein - tomato mosaic virus (strain LII)
N:Alternate names: transport protein
C:Species: tomato mosaic virus
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Feb-1997
C:Accession: J01457
R:Calder, V.L.; Palukaitis, P.
J. Gen. Virol. 73, 165-168, 1992
A:Title: Nucleotide sequence analysis of the movement genes of resistance breaking stra
A:Reference number: J01456; MUID:92113565
A:Accession: J01457
A:Molecule type: genomic RNA
A:Residues: 1-264 <CAL>
A:Note: the authors translated the codon TGG for residue 68 as Cys
C:Comment: This protein is involved in cell-to-cell transport of the virus.
C:Superfamily: tobnavirus 30K protein
C:Keywords: DNA binding; transport protein

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
| | | | |
Db 233 RPKPKSF 239

RESULT 183
E71612
ribosomal protein r7/L12 (O0) PFB0545c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: E71612
R:Gardner, M.J.; Tetteelin, H.; Carucci, D.J.; Cummings, L.M.; Aaravind, L.; Koonin, E.V.;
Perle, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 280, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: E71612
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-266 <GAR>
A:Cross-references: GB:AE001401; GB:AE001362; NID:g3845209; PIDN:AAC71898.1; PID:g384521
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0545c

Query Match 50.8%; Score 31; DB 2; Length 266;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOOFFG 9
| | | | |
Db 136 PPSNFFG 143

RESULT 184
A26162
holocytochrome-c synthase (EC 4.4.1.17) CYC3 - yeast (Saccharomyces cerevisiae)
N:Alternate names: cytochrome c heme lyase; protein YAL039C
C:Species: Saccharomyces cerevisiae
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Nov-1999
C:Accession: A26162; S51980
R:Dumont, M.E.; Ernst, J.F.; Hampsey, D.M.; Sherman, F.
EMBO J. 6, 235-241, 1987
A:Title: Identification and sequence of the gene encoding cytochrome c heme lyase in
A:Reference number: A26162; MUID:87218469
A:Accession: A26162
A:Molecule type: DNA
A:Residues: 1-269 <DUM>
A:Cross-references: EMBL:X04776; NID:g3615; PIDN:CAA28470.1; PID:g3616
R:Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; O
submitted to the EMBL data library, August 1994
A:Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A:Reference number: S51956
A:Accession: S51980
A:Molecule type: DNA
A:Residues: 1-269 <BUS>
A:Cross-references: EMBL:U12980; NID:g1326053; PIDN:AAC04992.1; PID:g595545; GSPDB:GN
C:Genetics:
A:Gene: SGD:CYC3; MIPS:YAL039C
A:Cross-references: MIPS:YAL039C; SGD:S0000037
A:Map position: 1L
A:Genome: nuclear
C:Keywords: carbon-sulfur lyase; mitochondrion

Query Match 50.8%; Score 31; DB 2; Length 269;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 PKPOOFFG 11
| | | | |
Db 95 PPSQOMYNA 104

RESULT 185
D75552
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75552
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: D75552
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <WHI>
A:Cross-references: GB:AE001879; GB:AE000513; NID:g6457832; PIDN:AAF09759.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0172
A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 271;
 Best Local Similarity 55.6%; Pred. No. 3.1e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQF 9
 11:1111
 Db 22 RPEPQNLG 30

RESULT 186

S48776

hypothetical protein YDR087c - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein D4478; hypothetical protein YDR554.20C

C:Species: *Saccharomyces cerevisiae*

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Oct-1999

C:Accession: S48776; S49842; S39583; S55836; S67904

R:Coster, F.; Jonniaux, J.L.; Goffeau, A.

submitted to the EMBL Data Library, October 1994

A:Reference number: S48758

A:Accession: S48776

A:Molecule type: DNA

A:Residues: 1-278 <COS>

A:Cross-references: EMBL:X82086; NID:g558241; PIDN:CAA57616.1; PID:g558260

R:Richards, C.; Harris, D.E.

submitted to the EMBL Data Library, November 1994

A:Reference number: S49823

A:Accession: S49842

A:Molecule type: DNA

A:Residues: 1-278 <RRC>

A:Cross-references: EMBL:Z46796; NID:g577794; PIDN:CAA66809.1; PID:g577814

R:Essault, Y.; Blondel, M.O.; Deshaies, R.J.; Schekman, R.; Kepes, F.

EMBO J. 12, 4083-4093, 1993

A:Title: The yeast SSI1 gene is essential for secretory protein translocation and encode

A:Reference number: S39583; MUID:94038890

A:Accession: S39583

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 146-278 <ESN>

A:Cross-references: EMBL:X74499; NID:g414690; PIDN:CAA52607.1; PID:g414691

R:Coster, F.; Jonniaux, J.L.; Goffeau, A.

Yeast 11, 673-679, 1995

A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading fr

A:Reference number: S55819; MUID:96093910

A:Accession: S55836

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-278 <COM>

A:Cross-references: EMBL:X82086; NID:g558241; PIDN:CAA57616.1; PID:g558260

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

R:Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67889

A:Accession: S67904

A:Molecule type: DNA

A:Residues: 1-278 <FOU>

A:Cross-references: EMBL:Z74383; NID:g1431562; PIDN:CAA98907.1; PID:e253404; PID:g143156

A:Experimental source: strain S288C

C:Genetics:

A:Map position: 4R

Query Match 50.8%; Score 31; DB 2; Length 278;

Best Local Similarity 83.3%; Pred. No. 3.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQ 6

11:1111

Db 58 RPKPOQ 63

RESULT 187

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 31K chain precursor - *Neurospora crassa*
 C:Species: *Neurospora crassa*
 C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 23-Feb-1997
 C:Accession: A35935
 R:Videla, A.; Tropschug, M.; Werner, S.
 Biochem. Biophys. Res. Commun. 171, 1168-1174, 1990
 A:Title: Primary structure and expression of a nuclear-coded subunit of complex I hom
 A:Reference number: A35935; MUID:91024977
 A:Accession: A35935
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-283 <VID>
 C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match 50.8%; Score 31; DB 2; Length 283;
 Best Local Similarity 71.4%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
 11:1111
 Db 40 RPNPQOF 46

RESULT 188

G64175

hypothetical protein H11699 - *Haemophilus influenzae*C:Species: *Haemophilus influenzae*

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 04-Mar-2000

C:Accession: G64175; S27578

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman

; D.M.; Brandon, R.C.; Rine, L.D.; Fitchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente

A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: G64175

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-304 <TIGR>

A:Cross-references: GB:U32842; GB:L42023; NID:g1574541; PIDN:AA23345.1; PID:g1574553

A:Experimental source: strain Rd K820

R:McLaughlin, R.; Abu Kwaik, Y.; Young, R.; Spicola, S.; Apicella, M.

submitted to the EMBL Data Library, June 1992

A:Description: Characterization and sequence of the *lsg* locus from *Haemophilus influe*

A:Reference number: S27577

A:Accession: S27578

A:Molecule type: DNA

A:Residues: 1-3, 'T', 'S', '69-129', 'D', '131-219', 'C', '221-252', 'K', '254-304 <MCL>

A:Cross-references: EMBL:M94855; NID:g148931; PIDN:AAA24979.1; PID:g148933

A:Experimental source: strain A2

C:Superfamily: *Haemophilus influenzae* hypothetical protein H11699

Query Match 50.8%; Score 31; DB 2; Length 304;

Best Local Similarity 71.4%; Pred. No. 3.5e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 OOFPGM 11

11:1111

Db 25 OOFPGM 31

RESULT 189

D96750

unknown protein F28P22.22 [imported] - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: D96750

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, C.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.: Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, J.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: D96750
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1320 <STO>
 A:Cross-references: GB:AE005173; NID:g6648169; PIDN:AAF21169.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F28P22.22
 A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 320;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 PKQPF 9
 |||||
 DB 61 PKQPF 66

RESULT 190
 PRLJHD
 proteinase (EC 3.4.23.-) - squirrel monkey retrovirus SMRV-H
 C:Species: squirrel monkey retrovirus SMRV-H
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Feb-1997
 C:Accession: B31827
 R:Oda, T.; Ikeda, S.; Watanabe, S.; Hatushika, M.; Akiyama, K.; Mitsunobu, F.
 Virology 167, 468-476, 1988
 A:Title: Molecular cloning, complete nucleotide sequence, and gene structure of the pro
 A:Reference number: A31827; MUID:89073750
 A:Molecule type: DNA
 A:Residues: 1-323 <CDA>
 C:Genetics:
 A:Gene: prt
 C:Complex: homodimer
 C:Superfamily: retroviral proteinase
 C:Keywords: aspartic proteinase; homodimer; hydrolase
 F:193/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 50.8%; Score 31; DB 1; Length 323;
 Best Local Similarity 60.0%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOFGIM 11
 |||||
 DB 82 PLPPTFGIT 91

RESULT 191
 T19592
 hypothetical protein C30H6.7 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19592
 R:Mortimore, B.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19148
 A:Accession: T19592
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-337 <WIL>
 A:Cross-references: EMBL:Z81044; PIDN:CAB02813.1; GSPDB:GN00022; CESP:C30H6.7
 A:Experimental source: clone C30H6
 C:Genetics:

A:Gene: CESP:C30H6.7
 A:Map position: 4
 A:Introns: 19/2; 85/3; 120/3; 166/3; 240/2; 286/2

Query Match 50.8%; Score 31; DB 2; Length 337;
 Best Local Similarity 85.7%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQPF 9
 |||||
 DB 230 KPQPF 236

RESULT 192
 G69027
 phosphoribosylformylglycinamide cyclo-ligase - *Methanobacterium thermoautotrophicum*
 C:Species: *Methanobacterium thermoautotrophicum*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
 C:Accession: G69027
 R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.
 ; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani,
 J.; Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: fu
 A:Reference number: A69000; MUID:98037514
 A:Accession: G69027
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-338 <MTB>
 A:Cross-references: GB:AE000888; GB:AE000666; NID:g2622304; PIDN:AA85693.1; PID:g262
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MHI104
 C:Superfamily: phosphoribosylformylglycinamide cyclo-ligase; phosphoribosylformylgl
 F:4-317/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFLC>

Query Match 50.8%; Score 31; DB 2; Length 338;
 Best Local Similarity 71.4%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKQPF 8
 |||||
 DB 264 PKQPF 270

RESULT 193
 S75196
 hypothetical protein slr2043 - *Synechocystis* sp. (strain PCC 6803)
 C:Species: *Synechocystis* sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S75196
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*
 s.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S75196
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-338 <KAN>
 A:Cross-references: EMBL:D90903; GB:AB001339; NID:g1652127; PIDN:BA17110.1; PID:g165
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: adhesin B

Query Match 50.8%; Score 31; DB 2; Length 338;
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOFFGL 10
| | | | |
Db 87 PKPOQLAAL 95

RESULT 194
T24822

hypothetical protein T11A5.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T24822

R:McMurray, A. submitted to the EMBL Data Library, May 1996

A:Reference number: Z19939

A:Accession: T24822

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <MTL>

A:Cross-references: EMBL:Z72515; PIDN:CAA96683.1; GSPDB:GN00023; CESP:T11A5.3

A:Experimental source: clone T11A5

C:Genetics:

A:Gene: CESP:T11A5.3

A:Map position: 5

A:Introns: 74/2; 100/2; 151/3; 177/3; 252/2; 334/1

Query Match 50.8%; Score 31; DB 2; Length 355;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 PKPOFFGLM 11
| | | | |
Db 286 EPYQYFGIL 294

RESULT 195
C72077

conserved hypothetical protein CP0305 [imported] - *Chlamydomonas reinhardtii* (strain CWL)

C:Species: *Chlamydomonas reinhardtii*

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 28-Jul-2000

C:Accession: C72077; A81592

R:Kalmann, S.; Mitchell, W.; Marathe, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of *Chlamydomonas reinhardtii* and *C. trachomatis*.

A:Reference number: A72000; MUID:99206606

A:Accession: C72077

A:Molecule type: DNA

A:Residues: 1-371 <ARN>

A:Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:ADI8592.1; PID:g437673

A:Experimental source: strain CWL029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.

A:Reference number: A81500; MUID:20150255

A:Accession: A81592

A:Molecule type: DNA

A:Residues: 1-371 <REA>

A:Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38162.1; PID:g718923

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: YX1G_2; CP0305

C:Superfamily: conserved hypothetical protein CP0630

Query Match 50.8%; Score 31; DB 2; Length 371;
Best Local Similarity 71.4%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFF 8
| | | | |
Db 136 PPSQOFF 142

RESULT 196
F86546

hypothetical protein yx1G_2 [imported] - *Chlamydomonas reinhardtii* (strain J138)

C:Species: *Chlamydomonas reinhardtii*

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: F86546

R:Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.

A:Reference number: A86491; MUID:20330349

A:Accession: F86546

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-371 <STO>

A:Cross-references: GB:BA000008; NID:g8978820; PIDN:BA098656.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: YX1G_2

C:Superfamily: conserved hypothetical protein CP0630

Query Match 50.8%; Score 31; DB 2; Length 371;
Best Local Similarity 71.4%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFF 8
| | | | |
Db 136 PPSQOFF 142

RESULT 197
T40024

probable cytochrome c heme lyase - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40024

R:Wood, V.; Rejzandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21899

A:Accession: T40024

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-377 <MOO>

A:Cross-references: EMBL:AL031743; PIDN:CAA21104.1; GSPDB:GN00067; SPDB:SPBC26H8.12

A:Experimental source: strain 972h-; cosmid c26H8

C:Genetics:

A:Gene: SPDB:SPBC26H8.12

A:Map position: 2

Query Match 50.8%; Score 31; DB 2; Length 377;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 PKPOFFGLM 11
| | | | |
Db 224 PPSQOMYNNM 233

RESULT 198
DB3803

tRNA-guanine transglycosylase tgt [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000

C:Accession: DB3803

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a

A:Reference number: A83650; MUID:20263314

A:Accession: DB3803

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA04947.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: tgt
C:Superfamily: queuine tRNA-ribosyltransferase

Query Match 50.8%; Score 31; DB 2; Length 379;
Best Local Similarity 45.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGIM 11
||:| ||::
Db 180 RPEDQALFGII 190

RESULT 199

G72569
hypothetical protein APE1840 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: G72569
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taken
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; NID:9310339
A:Accession: G72569
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-385 <XAM>
A:Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80844.1; PID:d1044630; PID:g510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1840

Query Match 50.8%; Score 31; DB 2; Length 385;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFF 8
||||| |:
Db 254 RPKPPQLY 261

RESULT 200

F82369
conserved hypothetical protein VC0047 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82369
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; NID:20406833
A:Accession: F82369
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-391 <HEI>
A:Cross-references: GB:AE004096; GB:AE003852; NID:g9654440; PIDN:AAF93225.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0047
A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 391;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKPOQFF 8
||| |
Db 4 RPKSHFF 10

Search completed: April 1, 2002, 16:19:17
Job time: 108 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:29 ; Search time 20.12 Seconds
(without alignments)
12.303 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQOFCGLM 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 203

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	1	US-07-934-553-1 Sequence 1, Appl1
2	61	100.0	11	1	US-08-184-935-12 Sequence 12, Appl1
3	61	100.0	11	1	US-08-269-288-2 Sequence 2, Appl1
4	61	100.0	11	1	US-08-338-484-1 Sequence 1, Appl1
5	61	100.0	11	1	US-08-175-432-1 Sequence 1, Appl1
6	61	100.0	11	1	US-08-225-474-1 Sequence 1, Appl1
7	61	100.0	11	1	US-08-391-910-2 Sequence 2, Appl1
8	61	100.0	11	1	US-08-418-994-2 Sequence 2, Appl1
9	61	100.0	11	1	US-08-480-505-3 Sequence 3, Appl1
10	61	100.0	11	1	US-08-391-814-2 Sequence 2, Appl1
11	61	100.0	11	1	US-08-167-870-1 Sequence 1, Appl1
12	61	100.0	11	1	US-08-255-272-6 Sequence 6, Appl1
13	61	100.0	11	1	US-08-441-591-6 Sequence 6, Appl1
14	61	100.0	11	1	US-08-303-362A-6 Sequence 6, Appl1
15	61	100.0	11	1	US-08-462-859A-1 Sequence 1, Appl1
16	61	100.0	11	1	US-08-123-659A-1 Sequence 1, Appl1
17	61	100.0	11	1	US-08-462-415-2 Sequence 2, Appl1
18	61	100.0	11	1	US-08-463-814-2 Sequence 2, Appl1
19	61	100.0	11	1	US-08-464-247A-1 Sequence 1, Appl1
20	61	100.0	11	1	US-08-464-248A-1 Sequence 1, Appl1
21	61	100.0	11	1	US-08-444-135-2 Sequence 2, Appl1
22	61	100.0	11	1	US-08-318-391-2 Sequence 2, Appl1
23	61	100.0	11	2	US-08-796-598-11 Sequence 11, Appl1
24	61	100.0	11	2	US-08-447-175A-11 Sequence 11, Appl1
25	61	100.0	11	2	US-07-737-371E-77 Sequence 77, Appl1
26	61	100.0	11	2	US-08-848-766A-1 Sequence 1, Appl1
27	61	100.0	11	3	US-08-927-128-17 Sequence 17, Appl1

28	61	100.0	11	4	US-08-257-966-2 Sequence 2, Appl1
29	61	100.0	11	5	PCR-US95-05600-23 Sequence 23, Appl1
30	61	100.0	11	6	5441935-1 Patent No. 5441935
31	61	100.0	12	1	US-08-441-591-7 Sequence 7, Appl1
32	61	100.0	12	1	US-08-303-362A-7 Sequence 7, Appl1
33	61	100.0	12	4	US-08-505-250-27 Sequence 27, Appl1
34	61	100.0	12	4	US-08-505-250-53 Sequence 53, Appl1
35	61	100.0	12	5	PCR-US92-06532-4 Sequence 4, Appl1
36	61	100.0	12	5	PCR-US95-05600-24 Sequence 24, Appl1
37	61	100.0	20	3	US-08-890-157A-2 Sequence 2, Appl1
38	61	100.0	20	4	US-08-505-250-50 Sequence 50, Appl1
39	61	100.0	126	6	5268359-5 Patent No. 5268359
40	61	100.0	130	6	5268359-2 Patent No. 5268359
41	61	100.0	487	1	US-08-462-859A-9 Sequence 9, Appl1
42	61	100.0	487	1	US-08-123-659A-9 Sequence 9, Appl1
43	61	100.0	487	1	US-08-464-247A-9 Sequence 9, Appl1
44	61	100.0	487	1	US-08-464-248A-9 Sequence 9, Appl1
45	61	100.0	492	1	US-08-462-859A-7 Sequence 7, Appl1
46	61	100.0	492	1	US-08-123-659A-7 Sequence 7, Appl1
47	61	100.0	492	1	US-08-464-247A-7 Sequence 7, Appl1
48	61	100.0	492	1	US-08-464-248A-7 Sequence 7, Appl1
49	58	95.1	11	1	US-07-899-205-1 Sequence 1, Appl1
50	58	95.1	11	2	US-08-496-118-1 Sequence 1, Appl1
51	58	95.1	11	2	US-07-737-371E-12 Sequence 12, Appl1
52	58	95.1	11	2	US-07-737-371E-25 Sequence 25, Appl1
53	58	95.1	11	5	PCR-US92-06532-1 Sequence 1, Appl1
54	56	91.8	10	2	US-07-737-371E-9 Sequence 9, Appl1
55	56	91.8	11	1	US-08-031-325A-26 Sequence 26, Appl1
56	56	91.8	11	2	US-07-737-371E-13 Sequence 13, Appl1
57	56	91.8	11	2	US-07-737-371E-14 Sequence 14, Appl1
58	56	91.8	11	2	US-07-737-371E-16 Sequence 16, Appl1
59	56	91.8	11	2	US-07-737-371E-18 Sequence 18, Appl1
60	56	91.8	11	2	US-07-737-371E-61 Sequence 61, Appl1
61	56	91.8	11	2	US-07-737-371E-63 Sequence 63, Appl1
62	56	91.8	11	2	US-07-737-371E-64 Sequence 64, Appl1
63	56	91.8	11	2	US-08-747-137-34 Sequence 34, Appl1
64	56	91.8	11	2	US-08-505-250-34 Sequence 34, Appl1
65	56	91.8	11	1	US-08-428-488-15 Sequence 15, Appl1
66	55	90.2	11	2	US-07-737-371E-15 Sequence 15, Appl1
67	55	90.2	11	2	US-07-737-371E-17 Sequence 17, Appl1
68	55	90.2	11	2	US-07-737-371E-19 Sequence 19, Appl1
69	55	90.2	11	2	US-07-737-371E-20 Sequence 20, Appl1
70	55	90.2	11	2	US-07-737-371E-21 Sequence 21, Appl1
71	54	88.5	11	2	US-07-737-371E-22 Sequence 22, Appl1
72	54	88.5	11	2	US-07-737-371E-24 Sequence 24, Appl1
73	54	88.5	11	2	US-07-737-371E-26 Sequence 26, Appl1
74	54	88.5	11	2	US-07-737-371E-62 Sequence 62, Appl1
75	54	88.5	11	2	US-07-737-371E-65 Sequence 65, Appl1
76	54	88.5	11	2	US-07-737-371E-65 Sequence 65, Appl1
77	54	88.5	11	2	US-07-737-371E-65 Sequence 65, Appl1
78	53	86.9	11	6	5441935-3 Patent No. 5441935
79	53	86.9	11	6	5441935-8 Patent No. 5441935
80	53	86.9	11	6	5441935-8 Patent No. 5441935
81	52	85.2	11	1	US-07-737-371E-11 Sequence 11, Appl1
82	52	85.2	11	2	US-08-462-413-2 Sequence 2, Appl1
83	52	85.2	11	2	US-07-737-371E-67 Sequence 67, Appl1
84	50	82.0	11	2	US-07-737-371E-30 Sequence 30, Appl1
85	50	82.0	11	2	US-07-737-371E-32 Sequence 32, Appl1
86	50	82.0	11	2	US-08-468-514-11 Sequence 11, Appl1
87	49	80.3	9	2	US-07-737-371E-60 Sequence 60, Appl1
88	49	80.3	11	2	US-07-737-371E-55 Sequence 55, Appl1
89	49	80.3	13	1	US-07-712-828B-5 Sequence 5, Appl1
90	48	80.3	13	1	US-07-737-371E-29 Sequence 29, Appl1
91	48	78.7	11	2	US-07-737-371E-31 Sequence 31, Appl1
92	48	78.7	11	6	5441935-5 Patent No. 5441935
93	47	77.0	11	2	US-07-737-371E-33 Sequence 33, Appl1
94	47	77.0	11	2	US-07-737-371E-34 Sequence 34, Appl1
95	47	77.0	11	2	US-07-737-371E-35 Sequence 35, Appl1
96	47	77.0	11	2	US-07-737-371E-54 Sequence 54, Appl1
97	47	77.0	11	3	US-08-890-157A-4 Sequence 4, Appl1
98	46	75.4	8	2	US-07-737-371E-57 Sequence 57, Appl1
99	46	75.4	17	3	US-08-890-157A-1 Sequence 1, Appl1
100	45.5	74.6	10	4	US-09-168-548-2 Sequence 2, Appl1

101	45.5	74.6	10	6	516965-11	Patent No. 516965
102	45	73.8	11	2	US-07-737-371E-36	Sequence 36, Appl
103	45	73.8	11	6	5441935-2	Patent No. 5441935
104	44	72.1	8	2	US-07-737-371E-10	Sequence 10, Appl
105	44	72.1	9	4	US-08-505-250-29	Sequence 29, Appl
106	44	72.1	11	2	US-07-737-371E-28	Sequence 28, Appl
107	44	72.1	20	1	US-08-468-514-1	Sequence 1, Appl
108	43.5	71.3	10	1	US-08-088-322-6	Sequence 6, Appl
109	43.5	71.3	10	1	US-08-437-820-6	Sequence 6, Appl
110	42	68.9	11	2	US-07-737-371E-37	Sequence 37, Appl
111	40	65.6	7	2	US-07-737-371E-4	Sequence 4, Appl
112	40	65.6	9	4	US-08-505-250-37	Sequence 37, Appl
113	39	63.9	11	2	US-07-737-371E-3	Sequence 3, Appl
114	38	62.3	11	2	US-07-737-371E-2	Sequence 2, Appl
115	38	62.3	11	2	US-07-737-371E-38	Sequence 38, Appl
116	38	62.3	21	1	US-08-468-514-4	Sequence 4, Appl
117	37	60.7	7	2	US-07-737-371E-8	Sequence 8, Appl
118	37	60.7	8	2	US-07-737-371E-56	Sequence 56, Appl
119	36	59.0	11	2	US-07-737-371E-39	Sequence 39, Appl
120	36	59.0	12	1	US-08-428-488-18	Sequence 18, Appl
121	36	59.0	12	2	US-08-796-598-10	Sequence 10, Appl
122	36	59.0	12	2	US-08-447-175A-10	Sequence 10, Appl
123	36	59.0	12	2	US-07-737-371E-76	Sequence 76, Appl
124	35	57.4	8	4	US-08-505-250-40	Sequence 40, Appl
125	35	57.4	9	1	US-08-346-849-7	Sequence 7, Appl
126	35	57.4	9	2	US-08-293-284A-7	Sequence 7, Appl
127	35	57.4	11	2	US-07-753-909B-2	Sequence 2, Appl
128	35	57.4	11	2	US-07-737-371E-41	Sequence 41, Appl
129	35	57.4	130	4	US-08-833-876-4	Sequence 4, Appl
130	35	57.4	130	4	US-09-483-054-4	Sequence 4, Appl
131	35	57.4	474	3	US-08-978-741-8	Sequence 8, Appl
132	35	57.4	474	3	US-09-333-729A-12	Sequence 12, Appl
133	35	57.4	496	4	US-08-883-054-2	Sequence 2, Appl
134	35	57.4	496	4	US-09-483-054-2	Sequence 2, Appl
135	34	55.7	6	2	US-07-737-371E-58	Sequence 58, Appl
136	34	55.7	11	2	US-07-737-371E-40	Sequence 40, Appl
137	34	55.7	498	1	US-08-457-274A-24	Sequence 24, Appl
138	34	55.7	498	5	PCT-US95-05758-24	Sequence 24, Appl
139	34	55.7	504	1	US-08-457-274A-25	Sequence 25, Appl
140	34	55.7	504	5	PCT-US95-05758-25	Sequence 25, Appl
141	34	55.7	583	4	US-08-481-190-19	Sequence 19, Appl
142	34	55.7	583	5	PCT-US93-00869-19	Sequence 19, Appl
143	34	55.7	587	4	US-08-481-190-4	Sequence 4, Appl
144	34	55.7	587	5	PCT-US93-00869-4	Sequence 4, Appl
145	34	55.7	588	4	US-08-481-190-16	Sequence 16, Appl
146	34	55.7	588	5	PCT-US93-00869-16	Sequence 16, Appl
147	33	54.1	9	1	US-08-346-849-6	Sequence 6, Appl
148	33	54.1	9	2	US-08-293-284A-6	Sequence 6, Appl
149	33	54.1	11	2	US-08-053-451B-159	Sequence 159, Appl
150	33	54.1	138	2	US-08-480-434-63	Sequence 63, Appl
151	33	54.1	138	2	US-08-053-451B-63	Sequence 63, Appl
152	33	54.1	171	4	US-09-129-030-56	Sequence 56, Appl
153	33	54.1	324	2	US-08-793-410-30	Sequence 30, Appl
154	33	54.1	328	2	US-08-793-410-7	Sequence 7, Appl
155	33	54.1	404	2	US-08-666-367B-7	Sequence 7, Appl
156	33	54.1	505	1	US-09-143-438-7	Sequence 7, Appl
157	33	54.1	505	5	US-08-222-616-20	Sequence 20, Appl
158	33	54.1	505	1	PCT-US95-04228-20	Sequence 20, Appl
159	33	54.1	511	5	PCT-US95-05008-6	Sequence 6, Appl
160	33	54.1	711	3	US-08-949-588-2	Sequence 2, Appl
161	32.5	53.3	325	4	US-09-108-020-49	Sequence 49, Appl
162	32	52.5	6	2	US-08-430-238-15	Sequence 15, Appl
163	32	52.5	6	1	US-07-737-371E-5	Sequence 5, Appl
164	32	52.5	11	1	US-08-428-488-16	Sequence 16, Appl
165	32	52.5	11	2	US-08-796-598-7	Sequence 7, Appl
166	32	52.5	11	2	US-08-447-175A-7	Sequence 7, Appl
167	32	52.5	11	4	US-09-214-614-1	Sequence 1, Appl
168	32	52.5	54	3	US-08-967-867-4	Sequence 4, Appl
169	32	52.5	181	4	US-09-129-030-8	Sequence 8, Appl
170	32	52.5	402	4	US-09-025-578-8	Sequence 8, Appl
171	32	52.5	462	4	US-08-068-392-3	Sequence 3, Appl
172	32	52.5	462	4	US-08-396-988-3	Sequence 3, Appl
173	32	52.5	614	3	US-09-017-706-9	Sequence 9, Appl

174	32	52.5	614	3	US-09-017-706-10	Sequence 10, Appl
175 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-11</td> <td>Sequence 11, Appl</td>	32	52.5	614	3	US-09-017-706-11	Sequence 11, Appl
176 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-12</td> <td>Sequence 12, Appl</td>	32	52.5	614	3	US-09-017-706-12	Sequence 12, Appl
177 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-13</td> <td>Sequence 13, Appl</td>	32	52.5	614	3	US-09-017-706-13	Sequence 13, Appl
178 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-14</td> <td>Sequence 14, Appl</td>	32	52.5	614	3	US-09-017-706-14	Sequence 14, Appl
179 <td>31</td> <td>50.8</td> <td>8</td> <td>6</td> <td>5441935-10</td> <td>Patent No. 5441935</td>	31	50.8	8	6	5441935-10	Patent No. 5441935
180 <td>31</td> <td>50.8</td> <td>16</td> <td>4</td> <td>US-09-024-975-3</td> <td>Sequence 3, Appl</td>	31	50.8	16	4	US-09-024-975-3	Sequence 3, Appl
181 <td>31</td> <td>50.8</td> <td>26</td> <td>4</td> <td>US-08-419-066-2</td> <td>Sequence 2, Appl</td>	31	50.8	26	4	US-08-419-066-2	Sequence 2, Appl
182 <td>31</td> <td>50.8</td> <td>26</td> <td>4</td> <td>US-09-024-975-2</td> <td>Sequence 2, Appl</td>	31	50.8	26	4	US-09-024-975-2	Sequence 2, Appl
183 <td>31</td> <td>50.8</td> <td>39</td> <td>1</td> <td>US-08-162-052-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	1	US-08-162-052-1	Sequence 1, Appl
184 <td>31</td> <td>50.8</td> <td>39</td> <td>1</td> <td>US-08-310-722-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	1	US-08-310-722-1	Sequence 1, Appl
185 <td>31</td> <td>50.8</td> <td>39</td> <td>2</td> <td>US-08-419-066-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	2	US-08-419-066-1	Sequence 1, Appl
186 <td>31</td> <td>50.8</td> <td>39</td> <td>2</td> <td>US-08-728-333-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	2	US-08-728-333-1	Sequence 1, Appl
187 <td>31</td> <td>50.8</td> <td>39</td> <td>5</td> <td>US-09-024-975-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	5	US-09-024-975-1	Sequence 1, Appl
188 <td>31</td> <td>50.8</td> <td>39</td> <td>5</td> <td>PCT-US95-12080-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	5	PCT-US95-12080-1	Sequence 1, Appl
189 <td>31</td> <td>50.8</td> <td>264</td> <td>2</td> <td>US-08-553-6198-7</td> <td>Sequence 7, Appl</td>	31	50.8	264	2	US-08-553-6198-7	Sequence 7, Appl
190 <td>31</td> <td>50.8</td> <td>316</td> <td>1</td> <td>US-08-414-926A-22</td> <td>Sequence 22, Appl</td>	31	50.8	316	1	US-08-414-926A-22	Sequence 22, Appl
191 <td>31</td> <td>50.8</td> <td>316</td> <td>2</td> <td>US-08-926-822-22</td> <td>Sequence 22, Appl</td>	31	50.8	316	2	US-08-926-822-22	Sequence 22, Appl
192 <td>31</td> <td>50.8</td> <td>316</td> <td>3</td> <td>US-08-223-682-22</td> <td>Sequence 22, Appl</td>	31	50.8	316	3	US-08-223-682-22	Sequence 22, Appl
193 <td>31</td> <td>50.8</td> <td>316</td> <td>4</td> <td>US-09-527-657-22</td> <td>Sequence 22, Appl</td>	31	50.8	316	4	US-09-527-657-22	Sequence 22, Appl
194 <td>31</td> <td>50.8</td> <td>406</td> <td>6</td> <td>5212296-6</td> <td>Patent No. 5212296</td>	31	50.8	406	6	5212296-6	Patent No. 5212296
195 <td>31</td> <td>50.8</td> <td>566</td> <td>2</td> <td>US-08-533-669A-8</td> <td>Sequence 8, Appl</td>	31	50.8	566	2	US-08-533-669A-8	Sequence 8, Appl
196 <td>31</td> <td>50.8</td> <td>566</td> <td>2</td> <td>US-08-511-872-2</td> <td>Sequence 2, Appl</td>	31	50.8	566	2	US-08-511-872-2	Sequence 2, Appl
197 <td>31</td> <td>50.8</td> <td>631</td> <td>4</td> <td>US-08-448-489-17</td> <td>Sequence 17, Appl</td>	31	50.8	631	4	US-08-448-489-17	Sequence 17, Appl
198 <td>31</td> <td>50.8</td> <td>660</td> <td>3</td> <td>US-08-704-711A-18</td> <td>Sequence 18, Appl</td>	31	50.8	660	3	US-08-704-711A-18	Sequence 18, Appl
199 <td>31</td> <td>50.8</td> <td>3665</td> <td>2</td> <td>US-08-222-617A-13</td> <td>Sequence 13, Appl</td>	31	50.8	3665	2	US-08-222-617A-13	Sequence 13, Appl
200 <td>31</td> <td>50.8</td> <td>3712</td> <td>2</td> <td>US-08-222-617A-4</td> <td>Sequence 4, Appl</td>	31	50.8	3712	2	US-08-222-617A-4	Sequence 4, Appl
201 <td>31</td> <td>50.8</td> <td>3712</td> <td>2</td> <td>US-08-222-617A-25</td> <td>Sequence 25, Appl</td>	31	50.8	3712	2	US-08-222-617A-25	Sequence 25, Appl
202 <td>30.5</td> <td>50.0</td> <td>1375</td> <td>2</td> <td>US-08-665-259-26</td> <td>Sequence 26, Appl</td>	30.5	50.0	1375	2	US-08-665-259-26	Sequence 26, Appl
203 <td>30.5</td> <td>50.0</td> <td>1375</td> <td>3</td> <td>US-08-762-500-26</td> <td>Sequence 26, Appl</td>	30.5	50.0	1375	3	US-08-762-500-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-07-934-553-1
Sequence 1, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLELGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TILTON, FALLON, LUNGKUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENREISS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 2
US-08-184-935-12
Sequence 12, Application US/08184935
Patent No. 5476770
GENERAL INFORMATION:
APPLICANT: PRADELES, PHILIPPE
TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
TITLE OF INVENTION: OR HAPTEN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,935
FILING DATE: 24-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5476770man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-286-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note- "C-terminal amide"
US-08-184-935-12

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 3

US-08-269-288-2
Sequence 2, Application US/08269288
Patent No. 5491140

GENERAL INFORMATION:
APPLICANT: Bruns, Robert F.
APPLICANT: Gehlert, Donald R.
APPLICANT: Howbert, James J.
APPLICANT: Lunn, William H.W.
TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,288
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9715
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 4
US-08-338-484-1
Sequence 1, Application US/08338484
Patent No. 5494926

GENERAL INFORMATION:
APPLICANT: Owens, Andrew P.
APPLICANT: Teall, Martin R.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Robert J. No. 5494926th
STREET: 126 E. Lincoln Ave., P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
|||||
Db 1 RPKPOOFFGLM 11

RESULT 5
US-08-175-432-1
Sequence 1, Application US/08175432
Patent No. 5495047
GENERAL INFORMATION:
APPLICANT: Saarl, Walfrid S.
APPLICANT: Van Niel, Monique B.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: NORTH, ROBERT J.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: No. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
|||||
Db 1 RPKPOOFFGLM 11

RESULT 6
US-08-225-474-1
Sequence 1, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: Ige Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-225-474-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
|||||
Db 1 RPKPOOFFGLM 11

RESULT 7
US-08-391-910-2
; Sequence 2, Application US/08391910
; Patent No. 556313
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Philip A.
; TITLE OF INVENTION: HEXAMETHYLENEMINYL TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,910
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9979
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-910-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 8
US-08-418-994-2
; Sequence 2, Application US/08418994
; Patent No. 5565568
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung-Yong S.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, J. J.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: 2-ACETYLAMINOPROPANAMIDES AS TACHYKININ
; TITLE OF INVENTION: RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,994
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-8252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 9
US-08-480-505-3
; Sequence 3, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANWORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:

NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 875-0400
TELEFAX: (703) 525-3468
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Neuropeptide "Substance P"
US-08-480-505-3

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 10
US-08-391-814-2
Sequence 2, Application US/08391814
Patent No. 5607947
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,814
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-814-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 11
US-08-167-870-1
Sequence 1, Application US/08167870
Patent No. 5610183
GENERAL INFORMATION:
APPLICANT: OWENS, ANDREW P.
APPLICANT: WILLIAMS, BRIAN J.
TITLE OF INVENTION: AROMATIC COMPOUNDS, COMPOSITIONS
CONTAINING THEM AND THEIR USE IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J. NORTH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,870
FILING DATE: 17-DEC-1993
CLASSIFICATION: 544
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1151Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-7262
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-167-870-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 12
US-08-255-272-6
Sequence 6, Application US/08255272
Patent No. 5627268
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Khoury-Christianson, Anastasia
APPLICANT: M.
TITLE OF INVENTION: Production of Therapeutic Peptides in
Transgenic Animals as a Fusion with Hemoglobin
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,272
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 6794-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-255-272-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
|||||
Db 1 RPKPOFFGLM 11

RESULT 13
US-08-441-591-6
; Sequence 6, Application US/08441591
; Patent No. 5637682
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,591
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 9-SEPTEMBER-1994
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
|||||
Db 1 RPKPOFFGLM 11

RESULT 14
US-08-303-362A-6
; Sequence 6, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,362A
; FILING DATE: 9-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amine acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 15
US-08-462-859A-1
Sequence 1, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-462-859A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 16
US-08-123-659A-1
Sequence 1, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 17
US-08-462-415-2
Sequence 2, Application US/08462415
Patent No. 5670499
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Crowell, Thomas A.
APPLICANT: Gitter, Bruce D.

APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, Jeffery J.
APPLICANT: Krushinski, Joseph H.
APPLICANT: Lobb, Karen L.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: HETEROOCYCIC TACHYKININ RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,415
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gavlo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X8849B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-0756
TELEFAX: 317-276-3861
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-415-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOFGFM 11
DB 1 RPKQOFGFM 11

RESULT 18
US-08-463-874-2
Sequence 2, Application US/08463874
Patent No. 5684033
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Crowell, Thomas A.
APPLICANT: Gitter, Bruce D.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, Jeffery J.
APPLICANT: Krushinski, Joseph H.
APPLICANT: Lobb, Karen L.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: NON-PEPTIDE TACHYKININ RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN

COUNTRY: US
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,874
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gavlo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X8849C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-0756
TELEFAX: 317-276-3861
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-874-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOFGFM 11
DB 1 RPKQOFGFM 11

RESULT 19
US-08-464-247A-1
Sequence 1, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: NO. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 20
US-08-464-248A-1
; Sequence 1, Application US/08464248A
; Patent No. 5703209

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 21
US-08-444-135-2
; Sequence 2, Application US/08444135

Patent No. 5723575
GENERAL INFORMATION:
APPLICANT: Gilson, Chaim
APPLICANT: Zeligler, Zvi
APPLICANT: Byk, Gerardo
TITLE OF INVENTION: Backbone Cyclic Peptides, Processes For
TITLE OF INVENTION: Their Preparation and Pharmaceutical Compositions
TITLE OF INVENTION: Containing Them
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,135
FILING DATE:
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/955,380
FILING DATE: 01-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jarkovsky, Issac

REGISTRATION NUMBER: 22,713
REFERENCE/DOCKET NUMBER: 7754-003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-135-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 22
US-08-318-391-2
; Sequence 2, Application US/08318391
; Patent No. 5744482

GENERAL INFORMATION:
APPLICANT: Cohen, Marlene L.
APPLICANT: Johnson, Kirk W.

APPLICANT: Phebus, Lee A.
TITLE OF INVENTION: USE OF A SEROTONIN AGONIST IN
TITLE OF INVENTION: COMBINATION WITH A TACHYKININ RECEPTOR ANTAGONIST IN THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF MIGRAINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America

ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,391
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9664
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-391-2

Query Match 100.0%, Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 RPKPOQFFGLM 11

RESULT 23
US-08-796-598-11
Sequence 11, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Esq., Kerry A.
REGISTRATION NUMBER: 33,693
REFERENCE/DOCKET NUMBER: SYP-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-796-598-11

Query Match 100.0%, Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 RPKPOQFFGLM 11

RESULT 24
US-08-447-175A-11
Sequence 11, Application US/08447175A
Patent No. 5869240
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,175A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: RAUSCHENBACH, Kurt
REGISTRATION NUMBER: 40,137
REFERENCE/DOCKET NUMBER: SYP-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-447-175A-11

Query Match 100.0%, Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 RPKPOQFFGLM 11

RESULT 25

US-07-737-371E-77
; Sequence 77, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-77

Query Match 100.0%; Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 26
US-08-848-766A-1
; Sequence 1, Application US/08848766A
; Patent No. 5932551
; GENERAL INFORMATION:
; APPLICANT: Caldwell, Charles G.
; APPLICANT: Chapman, Kevin T.
; APPLICANT: Euretelle, Philippe L.
; APPLICANT: Esser, Craig K.
; APPLICANT: Hagmann, William K.
; APPLICANT: Hopka, Ihor E.
; APPLICANT: Iolo, Scott A.
; APPLICANT: Sahoo, Soumya P.
; TITLE OF INVENTION: SUBSTITUTED N-CARBOXYALKYLPEPTIDYL
; TITLE OF INVENTION: DERIVATIVES AS ANTIDEGENERATIVE ACTIVE AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway

STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,766A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/873,905
FILING DATE: 24-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Panzer, Curtis C
REGISTRATION NUMBER: 33,752
REFERENCE/DOCKET NUMBER: 183551A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3199
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-848-766A-1

Query Match 100.0%; Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 27
US-08-927-128-17
; Sequence 17, Application US/08927128
; Patent No. 6127150
; GENERAL INFORMATION:
; APPLICANT: Coolidge, Thomas
; APPLICANT: Wagner, Fred
; APPLICANT: ven Heeke, Gino
; APPLICANT: Schuster, Sheldon
; APPLICANT: Stout, Jay
; APPLICANT: Wylie, Dwane
; TITLE OF INVENTION: PURIFICATION DIRECTED CLOSING OF PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6127150west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,128
; FILING DATE: 05-SEP-1997
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; APPLICATION NUMBER: 08/680,004

```

1      FILING DATE: 15-JUL-1995
2
3      ATTORNEY/AGENT INFORMATION:
4      NAME: Carter, Charles G
5
6      REGISTRATION NUMBER: 35,093
7
8      REFERENCE/DOCKET NUMBER: 8648.20SD1
9
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 612/332-5300
12
13     TELEFAX: 612/332-9081
14
15     INFO:
16
17     INFORMATION FOR SEQ. ID NO.: 17:
18
19     SEQUENCE CHARACTERISTICS:
20
21     LENGTH: 11 amino acids
22
23     TYPE: amino acid
24
25     STRANDEDNESS: single
26
27     TOPOLOGY: linear
28
29     MOLECULE TYPE: peptide
30
31     HYPOTHETICAL: NO
32
33     ANTI-SENSE: NO
34
35     FRAGMENT TYPE: N-terminal
36
37     ORIGINAL SOURCE:
38
39     OS-08-927-128-17

```

Query Match	100.0%	Score 61	DB 3	Length 11
Best Local Similarity	100.0%	Pred. No.	7 2e-05	
Matches	11	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	1 RPKPQPFGLM	11		
Db	1 RPKPQPFGLM	11		

```

1      RESULT 28
2      US-08-257-966-2
3      Sequence 2, Application US/08257966
4      Patent No. 6175013
5      GENERAL INFORMATION:
6      APPLICANT: Hyskind, Philip A.
7      APPLICANT: Howbert, James J.
8      APPLICANT: Muehl, Brian S.
9      TITLE OF INVENTION: IMIDAZOLINYL TACHYKININ RECEPTOR
10     TITLE OF INVENTION: ANTAGONISTS
11     NUMBER OF SEQUENCES: 4
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Eli Lilly and Company
14     STREET: Lilly Corporate Center/1104
15     CITY: Indianapolis
16     STATE: Indiana
17     COUNTRY: United States of America
18     ZIP: 46285
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0. Version #1.25
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/257,966
26     FILING DATE:
27     CLASSIFICATION: 514
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Gaylo, Paul J.
30     REGISTRATION NUMBER: 36,808
31     REFERENCE/DOCKET NUMBER: X-9197
32     TELECOMMUNICATION INFORMATION:
33     TELEPHONE: (317) 276-0756
34     TELEFAX: (317) 276-3861
35     INFORMATION FOR SEQ ID NO: 2:
36     SEQUENCE CHARACTERISTICS:
37     LENGTH: 11 amino acids
38     TYPE: amino acid
39     STRANDEDNESS: single
40     TOPOLOGY: linear
41     MOLECULE TYPE: peptide

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US-08-257-966-2

Query Match      100.0%; Score 61; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RPKPOOFFGLM 11
        |||||
Db      1 RPKPOOFFGLM 11

```

RESULT 29
 PCT-US95-05600-23
 Sequence 23, Application PC/TUS9505600
 GENERAL INFORMATION:
 APPLICANT: GOLD, LARRY
 APPLICANT: NIEWLANDT, DAN
 APPLICANT: WECKER, MATTHEW
 APPLICANT: SCHNEIDER, DANIEL J.
 APPLICANT: FEIGON, JULI
 APPLICANT: ALLEN, PATRICK
 APPLICANT: SULLENGER, BRUCE A.
 APPLICANT: DOUDNA, JENNIFER, A.
 TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
 INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCES
 TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Swanson & Bratschun, L.L.C.
 STREET: 8400 E. Prentice Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
 MEDIUM TYPE: Storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05600
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/238, 863
 FILING DATE: 06-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/248, 632
 FILING DATE: 24-MAY-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/303, 362
 FILING DATE: 09-SEPTEMBER-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/361, 795
 FILING DATE: 21-DECEMBER-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/117, 991
 FILING DATE: 08-SEPTEMBER-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/931, 473
 FILING DATE: 17-AUGUST-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/964, 624
 FILING DATE: 21-OCTOBER-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/536, 428
 FILING DATE: 11-JUNE-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/714, 131
 FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05600-23

Query Match 100.0%; Score 61; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 30
5441935-1
PATENT NO. 5441935
APPLICANT: Rozenfurt, Enrique; Zachary, Ian; Moll, Penella
TITLE OF INVENTION: ROTH FACTOR RECEPTORS
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 29-NOV-1989
SEQ ID NO: 1:
LENGTH: 11
5441935-1

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 31
US-08-441-591-7
Sequence 7, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA

ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-7

Query Match 100.0%; Score 61; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 32
US-08-303-362A-7
Sequence 7, Application US/08303362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/06532
;; FILING DATE: 19920805
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyer, Scott J.
;; REGISTRATION NUMBER: 25,275
;; REFERENCE/DOCKET NUMBER: 07-24(776)A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (314)694-3117
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 12
;; OTHER INFORMATION: /label= amide
PCT-US92-06532-4

Query Match 100.0%; Score 61; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOFFGLM 11
Db 2 RPKQOFFGLM 12

RESULT 36
PCT-US95-05600-24
; Sequence 24, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEM
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLINGER, BRUCE A.
; APPLICANT: DOODNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P. HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/303,362
;; FILING DATE: 09-SEPTEMBER-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/361,795
;; FILING DATE: 21-DECEMBER-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/117,991
;; FILING DATE: 08-SEPTEMBER-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/931,473
;; FILING DATE: 17-AUGUST-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/964,624
;; FILING DATE: 21-OCTOBER-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/714,131
;; FILING DATE: 10-JUNE-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/714,131
;; FILING DATE: 10-JUNE-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX17/PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US95-05600-24

Query Match 100.0%; Score 61; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOFFGLM 11
Db 1 RPKQOFFGLM 11

RESULT 37
US-08-890-157A-2
; Sequence 2, Application US/08890157A
; Patent No. 6063758
; GENERAL INFORMATION:
; APPLICANT: Douglas A. Iapri and Ronald G. Wiley
; TITLE OF INVENTION: Substance P-saporin (SP-SAP) Conjugates And
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,157A
; FILING DATE: 09-JUL-1997
; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Phillips, Peter J.
REGISTRATION NUMBER: 29,691
REFERENCE/DOCKET NUMBER: 53984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-157A-2

Query Match 100.0%; Score 61; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
|||
Db 10 RPKPOQFFGLM 20

RESULT 38
US-08-505-250-50
Sequence 50, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-08-505-250-50

Query Match 100.0%; Score 61; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
|||
Db 2 RPKPOQFFGLM 12

RESULT 39
5268359-5
Patent No. 5268359
APPLICANT: HARMAR, ANTHONY J.;PASCALL, JOHN;MCKEOWN, ANN
TITLE OF INVENTION: HUMAN TACHYKININS AND THEIR PRECURSOR
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/285,964
FILING DATE: 03-JUN-1987
SEQ ID NO: 5
LENGTH: 126
5268359-5

Query Match 100.0%; Score 61; DB 6; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
|||
Db 58 RPKPOQFFGLM 68

RESULT 40
5268359-2
Patent No. 5268359
APPLICANT: HARMAR, ANTHONY J.;PASCALL, JOHN;MCKEOWN, ANN
TITLE OF INVENTION: HUMAN TACHYKININS AND THEIR PRECURSOR
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/285,964
FILING DATE: 03-JUN-1987
SEQ ID NO: 2
LENGTH: 130
5268359-2

Query Match 100.0%; Score 61; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
|||
Db 58 RPKPOQFFGLM 68

RESULT 41
US-08-462-859A-9
Sequence 9, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
DB 362 RPKQOQFFGLM 372

RESULT 42

US-08-123-659A-9
Sequence 9, Application US/08123659A
Patent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0611
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
DB 362 RPKQOQFFGLM 372

RESULT 43
US-08-464-247A-9
Sequence 9, Application US/08464247A

Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
DB 362 RPKQOQFFGLM 372

RESULT 44
US-08-464-248A-9
Sequence 9, Application US/08464248A
Patent No. 5703209

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
|||||
DB 362 RPKPOOFFGLM 372

RESULT 45
US-08-462-859A-7
Sequence 7, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPOOFFGLM 11
|||||
DB 362 RPKPOOFFGLM 372

RESULT 46
US-08-123-659A-7
Sequence 7, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
|||||
DB 362 RPKPOOFFGLM 372

RESULT 47
US-08-464-247A-7
Sequence 7, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive

CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 362 RPKPOQFFGLM 372

RESULT 48
US-08-464-248A-7
Sequence 7, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Valek, M. P.
TITLE OF INVENTION: NO. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3505
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 362 RPKPOQFFGLM 372

RESULT 49
US-07-899-205-1
Sequence 1, Application US/07899205
Patent No. 5288730
GENERAL INFORMATION:
APPLICANT: Baker, Raymond
APPLICANT: Teall, Martin R.
APPLICANT: Swain, Christopher J.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: AZABICYCLIC COMPOUNDS PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS CONTAINING THEM AND THEIR USE IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,205
FILING DATE: 19920616
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polk, Manfred
REGISTRATION NUMBER: 27,102
REFERENCE/DOCKET NUMBER: T-1106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4285
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-899-205-1

Query Match 95.1%; Score 58; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 50
US-08-496-118-1

Sequence 1, Application US/08496118
Patent No. 5830854
GENERAL INFORMATION:
APPLICANT: Hargreaves, Richard J.
TITLE OF INVENTION: THERAPEUTIC USE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robert J. No. 5830854th
STREET: 126 E. Lincoln Avenue - P. O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,118
FILING DATE: 27-JUNE-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5830854th, Robert J.
REGISTRATION NUMBER: T-1213CA
REFERENCE/DOCKET NUMBER:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-496-118-1

Query Match 95.1%; Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
DB 1 RRPQOQFFGLM 11

RESULT 51
US-07-737-371E-12
Sequence 12, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-12

Query Match 95.1%; Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
DB 1 RRPQOQFFGLM 11

RESULT 52
US-07-737-371E-25
Sequence 25, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-25

Query Match 95.1%, Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 53
PCT-US92-06532-1

Sequence 1, Application PC/TUS9206532
GENERAL INFORMATION:
APPLICANT: Krause, James E.
TITLE OF INVENTION: Human Substance P Receptor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., ASD
STREET: 800 N. Landbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06532
FILING DATE: 19920805
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24(776)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /Label- amide
PCT-US92-06532-1

Query Match 95.1%; Score 58; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 54
US-07-737-371E-9

Sequence 9, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-9

Query Match 91.8%; Score 56; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPOQFFGLM 11
|||||
Db 1 PKPOQFFGLM 10

RESULT 55
US-08-031-325A-26

Sequence 26, Application US/08031325A
Patent No. 5369094
GENERAL INFORMATION:
APPLICANT: Schally, Andrew V.
TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: OMRI M. BEHR, ESQ
STREET: 325 PIERSON AVENUE
CITY: EDISON
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 08837
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,325A
FILING DATE: 15-MAR-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,747
FILING DATE: 29-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: BEHR, OMRI M.


```
;
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHA13.0-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 494-5240
; TELEFAX: (908) 494-04281
; TELEFAX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 11
; OTHER INFORMATION: /note="Res 11 = Met-NH2"
; US-08-031-325A-26

Query Match
Best Local Similarity 91.8%; Score 56; DB 1; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOPFGL 10
Db 1 RPKPOPFGL 10

RESULT 56
US-07-737-371E-13
; Sequence 13, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11
```

```
;
; OTHER INFORMATION: where Xaa at position 11 is ethionine
; US-07-737-371E-13

Query Match
Best Local Similarity 91.8%; Score 56; DB 2; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOPFGL 10
Db 1 RPKPOPFGL 10

RESULT 57
US-07-737-371E-14
; Sequence 14, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11
; OTHER INFORMATION: where Xaa at position 11 is Nle
; US-07-737-371E-14

Query Match
Best Local Similarity 91.8%; Score 56; DB 2; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOPFGL 10
Db 1 RPKPOPFGL 10

RESULT 58
US-07-737-371E-16
; Sequence 16, Application US/07737371E
```

```
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 1...1
; OTHER INFORMATION: where xaa at position 1 is ethionine
;
; US-07-737-371E-16
;
; Query Match          91.8%; Score 56; DB 2; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.00053;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      2 PKPOQFFGLM 11
;         |||||
;         2 PKPOQFFGLM 11
;
; Db
;
; RESULT 59
; US-07-737-371E-18
; Sequence 18, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-07-737-371E-18
;
; Query Match          91.8%; Score 56; DB 2; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.00053;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      2 PKPOQFFGLM 11
;         |||||
;         2 PKPOQFFGLM 11
;
; Db
;
; RESULT 60
; US-07-737-371E-61
; Sequence 61, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
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; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-07-737-371E-18
;
; Query Match          91.8%; Score 56; DB 2; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.00053;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      2 PKPOQFFGLM 11
;         |||||
;         2 PKPOQFFGLM 11
;
; Db
;
; RESULT 60
; US-07-737-371E-61
; Sequence 61, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 10...10
OTHER INFORMATION: where Xaa at location 10 is Me-Leu
US-07-737-371E-61

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 11
|||||
Db 1 RPKPOOFFGL 11

RESULT 61
US-07-737-371E-63
Sequence 63, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 11...11
OTHER INFORMATION: where Xaa at position 11 is Me-Met
US-07-737-371E-63

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
|||||

Db 1 RPKPOOFFGL 10

RESULT 62
US-07-737-371E-64
Sequence 64, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-64

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
|||||
Db 1 RPKPOOFFGL 10

RESULT 63
US-07-737-371E-66
Sequence 66, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 10...10
OTHER INFORMATION: where Xaa at position 10 is Me-Leu
US-07-737-371E-66

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOQFFGLM 11
|||||
Db 1 RPKPQOQFFGXM 11

RESULT 64
US-08-747-137-34
Sequence 34, Application US/08747137
Patent No. 5945033
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /product= "Met-Amide"
US-08-747-137-34

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOQFFGL 10
|||||
Db 1 RPKPQOQFFGL 10

RESULT 65
US-08-505-250-34
Sequence 34, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 11
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-34

Query Match 91.8%; Score 56; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOQFFGL 10
|||||
Db 2 RPKPQOQFFGL 11

RESULT 66
US-08-428-488-15
; Sequence 15, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = H-Arg."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /note= "Position 5 = Glu-NH2."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Position 6 = Glu-NH2."
US-08-428-488-15

Query Match 90.2%; Score 55; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.00079;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPEEFGGLM 11

RESULT 67
US-07-737-371E-15
; Sequence 15, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-15

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 68
US-07-737-371E-17
; Sequence 17, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-17

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 69
US-07-737-371E-19
Sequence 19, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-19

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 70
US-07-737-371E-20
Sequence 20, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-20

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 71
US-07-737-371E-21
Sequence 21, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is D-Ala
US-07-737-371E-21

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
DB 1 RPKPOQFFXLM 11

RESULT 72
US-07-737-371E-22
Sequence 22, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Ser
US-07-737-371E-22

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
DB 1 RPKPOQFFXLM 11

RESULT 73
US-07-737-371E-24
Sequence 24, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is D-Pro

US-07-737-371E-24

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||111111
Db 1 RPKPOQFFFXLM 11

RESULT 74

US-07-737-371E-26

; Sequence 26, Application US/07737371E

; Patent No. 5876943

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; LOCATION: 8...8

; OTHER INFORMATION: where Xaa at position 8 is Me-Phe

; US-07-737-371E-26

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||111111
Db 1 RPKPOQFFFXLM 11

RESULT 75

US-07-737-371E-27

; Sequence 27, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; LOCATION: 9...9

; OTHER INFORMATION: where Xaa at position 9 is Me-Gly

; US-07-737-371E-27

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||111111
Db 1 RPKPOQFFFXLM 11

RESULT 76

US-07-737-371E-62

; Sequence 62, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95


```

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-62

Query Match      88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPKPOQFFGLM 11
Db      1 RPKPOQFFGPM 11

RESULT 77
US-07-737-371E-65
; Sequence 65, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is Me-Gly
; US-07-737-371E-65

Query Match      88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPKPOQFFGLM 11
Db      1 RPKPOQFFXLM 11

RESULT 78
US-07-737-371E-23
; Sequence 23, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-23

Query Match      86.9%; Score 53; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPKPOQFFGLM 11
Db      1 RPKPOQFFPLM 11

RESULT 79
```

5441935-3
; Patent No. 5441935
; APPLICANT: Rosegurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 3:
; LENGTH: 11
5441935-3

Query Match 86.9%; Score 53; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFGLM 11
| | | | | | | | | | | | | |
Db 1 RPKPOQFGLM 11

RESULT 80
5441935-8
; Patent No. 5441935
; APPLICANT: Rosegurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 8:
; LENGTH: 11
5441935-8

Query Match 86.9%; Score 53; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFGLM 11
| | | | | | | | | | | | | |
Db 1 RPKPOQFGLM 11

RESULT 81
US-07-737-371E-11
; Sequence 11, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Tankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/07/737,371E
APPLICATION NUMBER: 536
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-11

Query Match 85.2%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFG 9
| | | | | | | | | |
Db 1 RPKPOQFG 9

RESULT 82
US-08-462-413-2
; Sequence 2, Application US/08462413
; Patent No. 5530009
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Copp, James D.
; APPLICANT: Glnah, Francis O.
; APPLICANT: Hansen, Guy J.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Huff, Bret E.
; APPLICANT: Martineilli, Michael J.
; APPLICANT: Staszak, Michael A.
; TITLE OF INVENTION: PROCESS FOR PREPARING NON-PEPTIDYL
; TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,413
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,708
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36, 808
REFERENCE/DOCKET NUMBER: X-9475
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-413-2

Query Match 85.2%; Score 52; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
||| |||||
Db 1 RPKPOFFGLM 11

RESULT 83
US-07-737-371E-67
; Sequence 67, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11..11
; OTHER INFORMATION: where Xaa at position 11 is Me-Met
US-07-737-371E-67

Query Match 85.2%; Score 52; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOFFG 9
||| |||||
Db 1 RPKPOFFG 9

RESULT 84
US-07-737-371E-30
; Sequence 30, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5..5
; OTHER INFORMATION: where Xaa at position 5 is homocysteine
; LOCATION: 10..10
; OTHER INFORMATION: where Xaa at position 10 is homocysteine
US-07-737-371E-30

Query Match 82.0%; Score 50; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
||| |||||
Db 1 RPKPOFFGLM 11

RESULT 85
US-07-737-371E-32
; Sequence 32, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:

```

; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5...5
; OTHER INFORMATION: where Xaa at position 5 is homocysteine
; LOCATION: 11...11
; OTHER INFORMATION: where Xaa at position 11 is homocysteine
; US-07-737-371E-32

Query Match      82.0%: Score 50; DB 2; Length 11;
Best Local Similarity 90.0%: Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPODFGL 10
    |||||
Db 1 RPKPXFGL 10

RESULT 86
US-08-468-514-11
; Sequence 11, Application US/08468514
; Patent No. 5576296
; GENERAL INFORMATION:
; APPLICANT: Barfal, Tamas
; APPLICANT: Hekfel, Tomas
; APPLICANT: Langel, Uto
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesentfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```

; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,514
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,139
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/SE92/00316
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101472-0
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner Ph.D., Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-354-8113
; TELEFAX: 212-819-8783
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 22
; OTHER INFORMATION: /note="amide"
; US-08-468-514-11

Query Match      82.0%: Score 50; DB 1; Length 22;
Best Local Similarity 90.0%: Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPODFGLM 11
    ||||||
Db 13 PPQDFGLM 22

RESULT 87
US-07-737-371E-60
; Sequence 60, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
```

FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-60

Query Match 80.3%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFFGLM 11
DB 1 KPOQFFGLM 9

RESULT 88
US-07-737-371E-55
Sequence 55, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CURRENT APPLICATION DATA:
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Sar
LOCATION: 11...11
OTHER INFORMATION: where Xaa at position 11 is Met(O2)
US-07-737-371E-55

Query Match 80.3%; Score 49; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.0086;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGL 10
DB 1 RPKPOQFFGL 10

RESULT 89
US-07-712-828B-5
Sequence 5, Application US/07712828B
Patent No. 5235039
GENERAL INFORMATION:
APPLICANT: Heath et al.
TITLE OF INVENTION: Assay Method for Hydrolytic
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
FILING DATE: 19010610
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-712-828B-5

Query Match 80.3%; Score 49; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.01;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
DB 1 RRPPOQFFGLM 11

RESULT 90
US-07-737-371E-29
Sequence 29, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CURRENT APPLICATION DATA:
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 5...5
OTHER INFORMATION: where Xaa at position 5 is homocysteine
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is homocysteine
US-07-737-371E-29

Query Match 78.7%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
||| ||| ||| |||
DB 1 RPKPOOFFGLM 11

RESULT 91
US-07-737-371E-31
Sequence 31, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172

FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-31

Query Match 78.7%; Score 48; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
||| ||| ||| |||
DB 1 RPKPOOFFGL 10

RESULT 92
5441935-5
Patent No. 5441935
APPLICANT: Rozengurt, Enrique; Zachary, Ian; Moll, Penelope
TITLE OF INVENTION: GROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 29-NOV-1989
SEQ ID NO: 5;
LENGTH: 11
5441935-5

Query Match 78.7%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
||| ||| ||| |||
DB 1 RPKPOOFFGLM 11

RESULT 93
US-07-737-371E-33
Sequence 33, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 5...5
OTHER INFORMATION: where Xaa at position 5 is D-Cys
US-07-737-371E-33

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPOQFGLM 11
|||||
Db 1 RPKPXQFCGLM 11

RESULT 94
US-07-737-371E-34
Sequence 34, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 5...5
OTHER INFORMATION: where Xaa at position 5 is D-Cys
US-07-737-371E-34

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPOQFGLM 11
|||||
Db 1 RPKPXQFCGLM 11

RESULT 95
US-07-737-371E-35
Sequence 35, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 3...3
OTHER INFORMATION: where Xaa at position 3 is D-Cys
US-07-737-371E-35

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||| |||||
Db 1 RPKPCFFGLM 11

RESULT 96
US-07-737-371E-54
; Sequence 54, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 7...7
; OTHER INFORMATION: where Xaa at position 7 is p-Chloro-Phe
; LOCATION: 8...8
; OTHER INFORMATION: where Xaa at position 8 is p-Chloro-Phe
; US-07-737-371E-54

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||| |||||
Db 1 RPKPOQXXGLM 11

RESULT 97
US-08-890-157A-4
; Sequence 4, Application US/08890157A
; Patent No. 6063758
; GENERAL INFORMATION:
; APPLICANT: Douglas A. Lappi and Ronald G. Wiley
; TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,157A
FILING DATE: 09-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Phillips, Peter J.
REGISTRATION NUMBER: 29,691
REFERENCE/DOCKET NUMBER: 53984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-157A-4

Query Match 77.0%; Score 47; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||| |||||
Db 1 RPKRWFFGLM 11

RESULT 98
US-07-737-371E-57
; Sequence 57, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-57

Query Match 75.4%; Score 46; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
|||||
Db 1 RPKPOOFF 8

RESULT 99
US-08-890-157A-1

Sequence 1, Application US/08890157A
Patent No. 6063758

GENERAL INFORMATION:

APPLICANT: Douglas A. Lapl and Ronald G. Wiley
TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/890,157A

FILING DATE: 09-JUL-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Phillips, Peter J.

REGISTRATION NUMBER: 29,691

REFERENCE/DOCKET NUMBER: 53984

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)278-0400

TELEFAX: (212)391-0526

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-890-157A-1

Query Match 75.4%; Score 46; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
|||||
Db 10 RPKPOOFF 17

RESULT 100
US-09-168-548-2

Sequence 2, Application US/09168548

Patent No. 6265542

GENERAL INFORMATION:

APPLICANT: Fahner, Robert

TITLE OF INVENTION: PURIFICATION OF MOLECULES

FILE REFERENCE: P10281

CURRENT APPLICATION NUMBER: US/09/168,548

CURRENT FILING DATE: 1998-10-08

NUMBER OF SEQ ID NOS: 2

SEQ ID NO: 2

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: Artificial sequence

LOCATION: 1-10

OTHER INFORMATION: Sequence is synthesized

Patent No. 6265542

US-09-168-548-2

Query Match 74.6%; Score 45.5; DB 4; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKPOOFFGLM 11
|||||
Db 1 RPKP-QFFGLM 10

RESULT 101
5169865-11

Patent No. 5169865

APPLICANT: ANANTHANARAYANAN, V. S.

TITLE OF INVENTION: METHOD AND COMPOSITION FOR CALCIUM

BINDING TRANSLOCATION AND MEDIATING

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/323,421

FILING DATE: 14-MAR-1989

SEQ ID NO: 11

LENGTH: 10

5169865-11

Query Match 74.6%; Score 45.5; DB 6; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKPOOFFGLM 11
|||||
Db 1 RPKP-QFFGLM 10

RESULT 102
US-07-737-371E-36

Sequence 36, Application US/07737371E

Patent No. 5876948

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.

TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-36

Query Match 73.8%; Score 45; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||
Db 1 RPKPOQFFGLM 11

RESULT 103
5441935-2
PATENT NO. 5441935
APPLICANT: Rozenfurt, Enrique; Zachary, Ian; Woll, Penella
TITLE OF INVENTION: ROWNTH FACTOR RECEPTORS
NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 29-NOV-1989
SEQ ID NO: 2:
LENGTH: 11
5441935-2

Query Match 73.8%; Score 45; DB 6; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.042;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||
Db 1 RPKPOQFFGLM 11

RESULT 104
US-07-737-371E-10
Sequence 10, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.

TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
TITLE OF INVENTION: 77
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-10

Query Match 72.1%; Score 44; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||||
Db 1 PQOFFGLM 8

RESULT 105
US-08-505-250-29
Sequence 29, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokiichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-08-505-250-29

Query Match 72.1%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOQFFGL 10
|||||
Db 2 KPOQFFGL 9

RESULT 106
US-07-737-371E-28
; Sequence 28, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-28

Query Match 72.1%; Score 44; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFGGLM 11
|||||
Db 1 RPKQOFGGLM 11

RESULT 107
US-08-468-514-1
; Sequence 1, Application US/08468514
; Patent No. 5576296

GENERAL INFORMATION:
; APPLICANT: Bartfal, Tamas
; APPLICANT: HOKfelt, Tomas
; APPLICANT: Langel, Olo
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,514
; FILING DATE:
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,139
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/SE92/00316
; FILING DATE: 14-MAY-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: SE 9101472-0
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner Ph.D., Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8783
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYDROPHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 20
; OTHER INFORMATION: /note= "amide or free acid"
; US-08-468-514-1

Query Match 72.1%; Score 44; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQOQFFGLM 11
|||||
Db 13 PQOQFFGLM 20

RESULT 108
US-08-088-322-6
; Sequence 6, Application US/08088322
; Patent No. 5413914
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; TITLE OF INVENTION: YEAST ASSAY TO IDENTIFY INHIBITORS OF
; DIBASIC AMINO ACID PROCESSING ENDOPEPTIDASES

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,322
FILING DATE: 07-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
TELEX: 467377
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-088-322-6

Query Match
Best Local Similarity 71.3%; Score 43.5; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKQOQFFGLM 11
||| |||||
DB 1 RPK-QOQFFGLM 10

RESULT 109
US-08-437-820-6
Sequence 6, Application US/08437820
Patent No. 5627043
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: YEAST STRAINS USED TO IDENTIFY
TITLE OF INVENTION: INHIBITORS OF DIBASIC AMINO ACID PROCESSING ENDOPROTEASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,820
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2848-7-1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-437-820-6

Query Match
Best Local Similarity 71.3%; Score 43.5; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKQOQFFGLM 11
||| |||||
DB 1 RPK-QOQFFGLM 10

RESULT 110
US-07-737-371E-37
Sequence 37, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-37

Query Match
Best Local Similarity 68.9%; Score 42; DB 2; Length 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFFGLM 11
||| |||||
DB 1 RPKQOQFFGLM 11

RESULT 111
US-07-737-371E-4
Sequence 4, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-4

Query Match 65.6%; Score 40; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOF 7
DB 1 RPKPOOF 7

RESULT 112
US-08-505-250-37
Sequence 37, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kohichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27

EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-37

Query Match 65.6%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOF 7
DB 2 RPKPOOF 8

RESULT 113
US-07-737-371E-3
Sequence 3, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 1...1
OTHER INFORMATION: where xaa at position 1 is D-Arg
LOCATION: 7...7
OTHER INFORMATION: where xaa at position 7 is D-Trp
LOCATION: 9...9
OTHER INFORMATION: where xaa at position 9 is D-Trp
US-07-737-371E-3

Query Match 63.9%; Score 39; DB 2; Length 11;
Best Local Similarity 70.0%; Pred. No. 0.46;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQOFFGLM 11
| | | | |
Db 2 PKPQOFFGLM 11

RESULT 114

US-07-737-371E-2
; Sequence 2, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 2...2
; OTHER INFORMATION: where Xaa at position 2 is D-Pro
; LOCATION: 7...7
; OTHER INFORMATION: where Xaa at position 7 is D-Arg
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is D-Trp
US-07-737-371E-2

Query Match 62.3%; Score 38; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | |
Db 1 RPKPQOFFGLM 11

RESULT 115

US-07-737-371E-38
; Sequence 38, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-38

Query Match 62.3%; Score 38; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | |
Db 1 RPKPQOFFGLM 11

RESULT 116

US-08-468-514-4
; Sequence 4, Application US/08468514
; Patent No. 5576296
; GENERAL INFORMATION:
; APPLICANT: Bartfal, Tamás
; APPLICANT: Horkfel, Tomas
; APPLICANT: Langell, Ulo
; APPLICANT: Ahren, Bo
; APPLICANT: Lindsog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,514
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,139
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/SE92/00316
FILING DATE: 14-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101472-0
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8783
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21
OTHER INFORMATION: /note= "amide or free acid"
US-08-468-514-4

Query Match 62.3%; Score 38; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
11111111
DB 14 PQOFFGLM 21

RESULT 117
US-07-737-371E-8
Sequence 8, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-8

Query Match 60.7%; Score 37; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGLM 11
11111111
DB 1 QOFFGLM 7

RESULT 118
US-07-737-371E-56
Sequence 56, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

LOCATION: 1...1
OTHER INFORMATION: where Xaa at position 1 is D-Ala
US-07-737-371E-56

Query Match 60.7%; Score 37; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.0e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 OQFFGLM 11
111111
DB 2 OQFFGLM 8

RESULT 119
US-07-737-371E-39
Sequence 39, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737, 371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559, 172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29, 066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-39

Query Match 59.0%; Score 36; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQOFGML 11
111111
DB 1 RPKQOFGML 11

RESULT 120
US-08-428-488-18
Sequence 18, Application US/08428488
Patent No. 5624834
GENERAL INFORMATION:

APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428, 488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /note="Position 12 = Met-NH2."
US-08-428-488-18

Query Match 59.0%; Score 36; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKQOFGML 11
111111
DB 3 PKQOFGML 12

RESULT 121
US-08-796-598-10
Sequence 10, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
STREET: 7thbeault
CITY: High Street Tower, 125 High Street
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/796,598
;; FILING DATE: 07-FEB-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/446,055
;; FILING DATE: 19-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FLYNN Esq., Kerry A.
;; REGISTRATION NUMBER: 33,693
;; REFERENCE/DOCKET NUMBER: SYP-115
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-796-598-10

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGIM 11
11 11 11 11
DB 3 PKSDQFVGIM 12

RESULT 122
US-08-447-175A-10
; Sequence 10, Application US/08447175A
; Patent No. 5869240
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESS: Thibault, LLP
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,175A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: RAUSCHENBACH, Kurt
; REGISTRATION NUMBER: 40,137
; REFERENCE/DOCKET NUMBER: SYP-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE: peptide
;; US-08-447-175A-10

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGIM 11
11 11 11 11
DB 3 PKSDQFVGIM 12

RESULT 123
US-07-737-371E-76
; Sequence 76, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

;; INFORMATION FOR SEQ ID NO: 76:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-737-371E-76

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGIM 11
11 11 11 11
DB 3 PKSDQFVGIM 12

RESULT 124
US-08-505-250-40
; Sequence 40, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya

APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokihiro
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-40

Query Match 57.4%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RPKPOOF 7
111111
Db 2 RPKPOOF 7

RESULT 125
US-08-346-849-7
Sequence 7, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (517) 861-9540

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-7

Query Match 57.4%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
111111
Db 1 RPKPOOF 7

RESULT 126
US-08-293-284A-7
Sequence 7, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-7

Query Match 57.4%; Score 35; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
111111

Db 1 RPKPOQM 7

RESULT 127

US-07-753-909B-2

; Sequence 2, Application US/07753909B
; Patent No. 5304632

; GENERAL INFORMATION:

; APPLICANT: Vaudry, Hubert

; APPLICANT: Conlon, Michael J.

; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease

; STREET: 801 Grand, Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/753,909B

; FILING DATE: 19910903

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9106759

; FILING DATE: 04-JUN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Sease, Edmund J.

; REGISTRATION NUMBER: 24,741

; TELEPHONE: (515)-288-3667

; TELEFAX: (515)-288-1338

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Rana ridibunda

; DEVELOPMENTAL STAGE: adult

; TISSUE TYPE: brain

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 1 is a basic type amino

; OTHER INFORMATION: acid, for example Arg, Glu, or Lys."

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 3

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 3 is Lys, Asx, or Asn."

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 5

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 5 is Glu, Lys, or Arg."

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 6

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 6 of the sequence is Glu,

; OTHER INFORMATION: Lys, or Arg."

Query Match 57.4%; Score 35; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;Qy 2 RPKPOQFFGLM 11
| | | | |
Db 2 RPKPOQFFGLM 11

RESULT 128

US-07-737-371E-41

; Sequence 41, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 28-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-07-737-371E-41

; Query Match 57.4%; Score 35; DB 2; Length 11;

; Best Local Similarity 63.6%; Pred. No. 2.2;

; Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
| | | | |
Db 1 RPKPOQFFGLM 11

RESULT 129

US-08-833-876-4

; Sequence 4, Application US/08833876

; Patent No. 6270999

; GENERAL INFORMATION:

; APPLICANT: Lawlor, Elizabeth

; TITLE OF INVENTION: NO. 6270999e1 Compounds

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

STREET: 705 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833.876
FILING DATE: 10-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P11458-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-876-4

Query Match 57.4%; Score 35; DB 4; Length 130;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 10
|||:|
DB 45 RPLPEKFHGL 54

RESULT 130
US-09-483-054-4
Sequence 4, Application US/09483054
Patent No. 6303124
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6303124e1 Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/483.054
FILING DATE: 13-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833.876
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P11458-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-483-054-4

Query Match 57.4%; Score 35; DB 4; Length 130;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 10
|||:|
DB 45 RPLPEKFHGL 54

RESULT 131
US-08-978-741-8
Sequence 8, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinpatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978.741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9861
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-978-741-8

Query Match 57.4%; Score 35; DB 3; Length 474;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10

Db 457 PRPSAFPGI 465

RESULT 132

US-09-333-729A-12
Sequence 12, Application US/09333729A

Patent No. 6270987

GENERAL INFORMATION:

APPLICANT: Wang, Yang

APPLICANT: Spellman, Michael W.

TITLE OF INVENTION: O-Fucosyltransferase

FILE REFERENCE: P1041PDI1-Substitute

CURRENT APPLICATION NUMBER: US/09/333,729A

CURRENT FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: US 08/798,741

PRIOR FILING DATE: 1997-11-26

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 12

LENGTH: 474

TYPE: PRT

ORGANISM: Caenorhabditis Elegans

US-09-333-729A-12

Query Match 57.4%; Score 35; DB 4; Length 474;
Best Local Similarity 55.6%; Pred. NO. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPOFFGL 10

Db 457 PRPSAFPGI 465

RESULT 133

US-08-833-876-2

Sequence 2, Application US/08833876

Patent No. 6270999

GENERAL INFORMATION:

APPLICANT: Lawlor, Elizabeth

TITLE OF INVENTION: NO. 6270999el Compounds

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,876

FILING DATE: 10-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9607991.8

FILING DATE: 18-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimm, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P31458-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-876-2

Query Match 57.4%; Score 35; DB 4; Length 496;
Best Local Similarity 60.0%; Pred. NO. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGL 10

Db 145 RPLPEKPHGL 154

RESULT 134

US-09-483-054-2

Sequence 2, Application US/09483054

Patent No. 6303124

GENERAL INFORMATION:

APPLICANT: Lawlor, Elizabeth

TITLE OF INVENTION: NO. 6303124el Compounds

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/483,054

FILING DATE: 13-Jan-2000

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,876

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Gimm, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P31458-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 57.4%; Score 35; DB 4; Length 496;

Best Local Similarity 60.0%; Pred. NO. 1.1e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGL 10

Db 145 RPLPEKPHGL 154

RESULT 135

US-07-737-371E-58

Sequence 58, Application US/07737371E

Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-58

Query Match 55.7%; Score 34; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQ 6
Db 1 RPKPOQ 6

RESULT 136
US-07-737-371E-40
Sequence 40, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-40

Query Match 55.7%; Score 34; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 137
US-08-457-274A-24
Sequence 24, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
TITLE OF INVENTION: Tomilita, Takashi
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,274A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: papillio polyxnes
STRAIN:
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
US-08-457-274A-24

Query Match 55.7%; Score 34; DB 1; Length 498;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
DB 34 PKPVFFG 41

RESULT 138
PCT-US95-05758-24
Sequence 24, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: papillio polyxnes
STRAIN:
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
PCT-US95-05758-24

Query Match 55.7%; Score 34; DB 5; Length 498;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOFFG 9
DB 34 PKPVFFG 41

DB 34 PKPVFFG 41

RESULT 139
US-08-457-274A-25
Sequence 25, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,274A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
STRAIN:
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
US-08-457-274A-25

Query Match 55.7%; Score 34; DB 1; Length 504;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
DB 41 PKPLPFFG 48

RESULT 140
PCT-US95-05758-25
Sequence 25, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square

CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
STRAIN: Unknown
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Unknown
PCT-US95-05758-25

Query Match 55.7%; Score 34; DB 5; Length 504;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPODFG 9
Db 41 PKPLPFG 48

RESULT 141
US-08-481-190-19
Sequence 19, Application US/08481190
Patent No. 6160204
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphenol Oxidase cDNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481.190
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 203.533

FILING DATE: 02-24-1994
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: UA 816 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-190-19

Query Match 55.7%; Score 34; DB 4; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPODFG 9
Db 296 PCPSQFG 303

RESULT 142
PCT-US93-00869-19
Sequence 19, Application PC/TUS9300869
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphenol Oxidase cDNAs: Cloning
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00869
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-00869-19

Query Match 55.7%; Score 34; DB 5; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPODFG 9

Db 296 PCPSQFPG 303

```
RESULT 143
US-08-481-190-4
; Sequence 4, Application US/08481190
; Patent No. 6160204
; GENERAL INFORMATION:
; APPLICANT: John C. Steffens
; TITLE OF INVENTION: Polyphenol Oxidase CDNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,190
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 203,533
; FILING DATE: 02-24-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: UA 816 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 587 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-190-4

Query Match 55.7%; Score 34; DB 4; Length 587;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 PKPOFPG 9
Db 300 PCPSQFPG 307

```
RESULT 144
PCT-US93-00869-4
; Sequence 4, Application PC/TUS9300869
; GENERAL INFORMATION:
; APPLICANT: John C. Steffens
; TITLE OF INVENTION: Polyphenol Oxidase CDNAs: Cloning
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00869
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 587 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-00869-4
```

Query Match 55.7%; Score 34; DB 5; Length 587;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFPG 9
Db 300 PCPSQFPG 307

```
RESULT 145
US-08-481-190-16
; Sequence 16, Application US/08481190
; Patent No. 6160204
; GENERAL INFORMATION:
; APPLICANT: John C. Steffens
; TITLE OF INVENTION: Polyphenol Oxidase CDNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,190
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 203,533
; FILING DATE: 02-24-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: UA 816 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 588 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-190-16

Query Match 55.7%; Score 34; DB 4; Length 588;
Best Local Similarity 75.0%; Pred. NO. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFFG 9
| | | | |
Db 301 PCPSQFFG 308

RESULT 146
PCT-US93-00869-16
Sequence 16, Application PC/TUS9300869
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphehol Oxidase cDNAs: Cloning
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00869
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-00869-16

Query Match 55.7%; Score 34; DB 5; Length 588;
Best Local Similarity 75.0%; Pred. NO. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFFG 9
| | | | |
Db 301 PCPSQFFG 308

RESULT 147
US-08-346-849-6
Sequence 6, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd

TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-6

Query Match 54.1%; Score 33; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. NO. 1.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGLM 11
| | | | |
Db 1 RPKOFGLM 9

RESULT 148
US-08-293-284A-6
Sequence 6, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-6

Query Match 54.1%; Score 33; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PQOFFGLM 11
I:|:|:|:|:|
Db 1 RPKQFFGLM 9

RESULT 149
US-08-053-451B-159
Sequence 159, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dittow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-053-451B-159

Query Match 54.1%; Score 33; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 5;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
I:|:|:|:|:|
Db 4 PAQFFGIL 11

RESULT 150
US-08-480-434-63
Sequence 63, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Dittow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOETHERICAL: N
ANTI-SENSE: N
US-08-480-434-63

Query Match 54.1%; Score 33; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
I:|:|:|:|:|
Db 4 PAQFFGIL 11

RESULT 151
US-08-053-451B-63
Sequence 63, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:

APPLICANT: Cien, Francis W.
APPLICANT: Dittlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-63

Query Match 54.1%; Score 33; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPOFFGLM 11
DB 4 PPOFFGL 11

RESULT 152
US-09-129-030-56
Sequence 56, Application US/09129030A
Patent No. 6242221
GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
TITLE OF INVENTION: GENOMIC PPO CLONES
FILE REFERENCE: 57072-PCT-US
CURRENT APPLICATION NUMBER: US/09/129,030A
FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: AU PNT856
EARLIER FILING DATE: 1996-02-05
EARLIER APPLICATION NUMBER: AU P02361
EARLIER FILING DATE: 1996-09-16
EARLIER APPLICATION NUMBER: PCT/AU97/00041
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 171
TYPE: PPT
ORGANISM: POTATO

US-09-129-030-56

Query Match 54.1%; Score 33; DB 4; Length 171;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
DB 73 PKPOFFG 80

RESULT 153
US-08-793-410-30
Sequence 30, Application US/08793410
Patent No. 5955650
GENERAL INFORMATION:
APPLICANT: HITT, WILLIAM DEAN
TITLE OF INVENTION: NOBLEOTIDE SEQUENCES OF CANOLA
AND SOYBEAN PALMITOYL-ACP THIO-
ESTERASE GENES AND THEIR USE IN
THE REGULATION OF FATTY ACID
CONTENT OF THE OILS OF SOYBEAN
AND CANOLA PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,410
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10627
FILING DATE: AUGUST 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNN M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-9567-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-773-0164
TELEFAX: 302-992-5481
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-793-410-30

Query Match 54.1%; Score 33; DB 2; Length 324;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
DB 306 RPKPVNMGV 316

RESULT 154
US-08-793-410-7

; Sequence 7, Application US/08793410
; Patent No. 5955650
; GENERAL INFORMATION:
; APPLICANT: HITZ, WILLIAM DEAN
; TITLE OF INVENTION: NOCLEOTIDE SEQUENCES OF CANOLA
; TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-
; TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN
; TITLE OF INVENTION: THE REGULATION OF FATTY ACID
; TITLE OF INVENTION: CONTENT OF THE OILS OF SOYBEAN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,410
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10627
; FILING DATE: AUGUST 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: CR-9567-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; US-08-793-410-7

Query Match 54.1%; Score 33; DB 2; Length 328;
Best Local Similarity 54.5%; Pred No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
||| ||:
DB 310 RPKPVNFGV 320

RESULT 155
US-08-666-367B-7
; Sequence 7, Application US/08666367B
; Patent No. 5854042
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
; TITLE OF INVENTION: PRODUCING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,367B
; FILING DATE: August 19, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: G. gallus (chicken)
; US-08-666-367B-7

Query Match 54.1%; Score 33; DB 2; Length 404;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOQFGL 10
||: |||
DB 288 EPQKVFGL 295

RESULT 156
US-09-143-438-7
; Sequence 7, Application US/09143438
; Patent No. 6218161
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
; TITLE OF INVENTION: PRODUCING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,438
; FILING DATE: August 28, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/666,367
; FILING DATE: August 19, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: G. gallus (chicken)
US-09-143-438-7

Query Match 54.1%; Score 33; DB 4; Length 404;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 PQQFFGL 10
:111:111
Db 288 EPQKYFGL 295

RESULT 157
US-08-222-616-20
Sequence 20, Application US/08222616
Patent No. 5635177
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
NUMBER OF SEQUENCES: 42
TITLE OF INVENTION: ANTIBODIES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-616-20

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQQFFGLM 11
1111:1
Db 459 PQQFYNNM 466

RESULT 158
PCT-US95-04228-20
Sequence 20, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-04228-20

Query Match 54.1%; Score 33; DB 5; Length 505;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQQFFGLM 11
1111:1
Db 459 PQQFYNNM 466

RESULT 159
PCT-US95-05008-6
Sequence 6, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.

APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: München 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-6

Query Match 54.1%; Score 33; DB 5; Length 511;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFFGLM 11
||||: :|
DB 465 PQQFYNIM 472

RESULT 160
US-08-949-588-2
Sequence 2, Application US/08949588
Patent No. 6025156
GENERAL INFORMATION:
APPLICANT: Gwynn, Michael
APPLICANT: Kallender, Howard
APPLICANT: Palmer, Leslie
TITLE OF INVENTION: No. 6025156el Topoisomerase III
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,588
FILING DATE: 14-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,417
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50567
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-588-2

Query Match 54.1%; Score 33; DB 3; Length 711;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGL 10
||||: |
DB 209 KPOQFFTL 216

RESULT 161
US-09-108-020-49
Sequence 49, Application US/09108020A
Patent No. 6143561
GENERAL INFORMATION:
APPLICANT: Randall, Douglas D.
APPLICANT: Johnston, Mark L.
APPLICANT: Miernyk, Jan A.
APPLICANT: Luethy, Michael H.
APPLICANT: Mooney, Brian P.
TITLE OF INVENTION: USE OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND
TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO
TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS
FILE REFERENCE: UMO 1482
CURRENT APPLICATION NUMBER: US/09/108,020A
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: 60/051,291
EARLIER FILING DATE: 1997-06-30
EARLIER APPLICATION NUMBER: 60/055,255
EARLIER FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/076,544
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 49
LENGTH: 325
TYPE: PRT
ORGANISM: B. subtilis
US-09-108-020-49

Query Match 53.3%; Score 32.5; DB 4; Length 325;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 1 RPKPO-OFGGLM 11
11111111
Db 76 RPVEIOFGFV 87

RESULT 162
US-08-430-238-15
Sequence 15, Application US/08430238
Patent No. 5693612
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: HOLZEMANN, GUNTHER
APPLICANT: GOODMAN, SIMON
APPLICANT: KESSLER, HORST
APPLICANT: HAUBNER, ROLAND
APPLICANT: WERMUTH, JOCHEN
TITLE OF INVENTION: Cyclopeptides of the Formula I
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,238
FILING DATE: 28-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4415310.4
FILING DATE: 30-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lehovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1692
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-430-238-15
Query Match 52.5%; Score 32; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 OFGGLM 11
111111
Db 1 OFGGLM 6
RESULT 163
US-07-737-371E-5
Sequence 5, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-5

Query Match 52.5%; Score 32; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 OFGGLM 11
111111
Db 1 OFGGLM 6
RESULT 164
US-08-428-488-16
Sequence 16, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = p-Glu."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Position 11 = Met-NH2."
US-08-428-488-16

Query Match 52.5%; Score 32; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
| : : : :
DB 4 PNKFYGLM 11

RESULT 165
US-08-796-598-7
; Sequence 7, Application US/08796598
; Patent No. 5827659
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESS: Thibault
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,598
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,055
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FLYNN Esq., Kerry A.
; REGISTRATION NUMBER: 33,693
; REFERENCE/DOCKET NUMBER: SY-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-796-598-7

Query Match 52.5%; Score 32; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
| : : : :
DB 4 PNKFYGLM 11

RESULT 166
US-08-447-175A-7
; Sequence 7, Application US/08447175A
; Patent No. 5869240
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESS: Thibault, LLP
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,175A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: RAUSCHENBACH, Kurt
; REGISTRATION NUMBER: 40,137
; REFERENCE/DOCKET NUMBER: SY-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-447-175A-7

Query Match 52.5%; Score 32; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
| : : : :
DB 4 PNKFYGLM 11

RESULT 167
US-09-214-614-1
; Sequence 1, Application US/09214614
; Patent No. 6225100
; GENERAL INFORMATION:
; APPLICANT: Grund, Alan D.
; APPLICANT: Maurina-Brunker, Julie
; TITLE OF INVENTION: NOVEL ARYLSULFOTRANSFERASE
; NUMBER OF SEQUENCES: 10

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sheridan Ross P.C.
;; STREET: 1700 Lincoln Street, Suite 3500
;; CITY: Denver
;; STATE: Colorado
;; COUNTRY: U.S.A
;; ZIP: 80203
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/214,614
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Connell, Gary J.
;; REGISTRATION NUMBER: 32,020
;; REFERENCE/DOCKET NUMBER: 3161-15-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 303/863-9700
;; TELEFAX: 303/863-0223
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-214-614-1

Query Match 52.5%; Score 32; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQQFFGLM 11
|:1:111|
Db 4 PNKFFGLM 11

RESULT 168
US-08-967-867-4
; Sequence 4, Application US/08967867
; Patent No. 6001604
; GENERAL INFORMATION:
; APPLICANT: HARTMAN, JACOB R.
; APPLICANT: KENDELOVITZ, SIMONA
; APPLICANT: GORECKI, MARIAN
; TITLE OF INVENTION: GENERATION OF HUMAN INSULIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,867
; FILING DATE: 12-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,454
; FILING DATE: 29-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P.
; REGISTRATION NUMBER: 28,678

;; REFERENCE/DOCKET NUMBER: 41425-A/JPM/GUG
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0525
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 54 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; US-08-967-867-4

Query Match 52.5%; Score 32; DB 3; Length 54;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQFFFG 9
|111111|
Db 22 RPKPYFFFG 30

RESULT 169
US-09-129-030-8
; Sequence 8, Application US/09129030A
; Patent No. 6242221
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
; TITLE OF INVENTION: GENOMIC PPO CLONES
; FILE REFERENCE: 57072-PCT-US
; CURRENT APPLICATION NUMBER: US/09/129,030A
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: AU PN7856
; EARLIER FILING DATE: 1996-02-05
; EARLIER APPLICATION NUMBER: AU P02361
; EARLIER FILING DATE: 1996-09-16
; EARLIER APPLICATION NUMBER: PCT/AU97/00041
; EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 181
; TYPE: PRT
; ORGANISM: TOBACCO
; US-09-129-030-8

Query Match 52.5%; Score 32; DB 4; Length 181;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPQFFFG 9
|111111|
Db 80 PCPQLFFFG 87

RESULT 170
US-09-025-578-2
; Sequence 2, Application US/09025578
; Patent No. 6194167
; GENERAL INFORMATION:
; APPLICANT: John A. Browse and James P. Spychalla
; TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan E. Dow, Ph.D.
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600

CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,578
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,409
FILING DATE: February 18, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Alan E. Dow, Ph.D.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-49462/AED
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid residues
TYPE: amino acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-09-025-578-2

Query Match 52.5%; Score 32; DB 4; Length 402;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOEFGLM 11
Db 266 PLSEFGLM 273

RESULT 171
US-08-068-392-3
Sequence 3, Application US/08068392
Patent No. 6150152
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloprotease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,392
FILING DATE: 19930528
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: 07-24(12406)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-068-392-3

Query Match 52.5%; Score 32; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOEFGL 10
Db 61 QOEFGL 66

RESULT 172
US-08-396-988-3
Sequence 3, Application US/08396988
Patent No. 6204043
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloprotease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,988
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,392
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: 07-24(12406)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-396-988-3

Query Match 52.5%; Score 32; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOEFGL 10
Db 61 QOEFGL 66

RESULT 173
US-09-017-706-9
Sequence 9, Application US/09017706A

; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-9

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOEFFGL 10
: 1:1111
DB 252 QPSQYFGL 259

RESULT 174
US-09-017-706-10
; Sequence 10, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-10

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOEFFGL 10
: 1:1111
DB 252 QPSQYFGL 259

RESULT 175
US-09-017-706-11
; Sequence 11, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05

; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-11

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOEFFGL 10
: 1:1111
DB 252 QPSQYFGL 259

RESULT 176
US-09-017-706-12
; Sequence 12, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-12

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOEFFGL 10
: 1:1111
DB 252 QPSQYFGL 259

RESULT 177
US-09-017-706-13
; Sequence 13, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-13

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGL 10
:1:1:1:1
DB 252 QPSQYFGL 259

RESULT 178
US-09-017-706-14
; Sequence 14, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOSE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-14

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGL 10
:1:1:1:1
DB 252 QPSQYFGL 259

RESULT 179
5441935-10
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Moll, Penella
; TITLE OF INVENTION: ROWNTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO:10:
; LENGTH: 8
5441935-10

Query Match 50.8%; Score 31; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGL 11
:1:1:1:1
DB 1 POOMFWLM 8

RESULT 180
US-09-024-975-3

; Sequence 3, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-3

Query Match 50.8%; Score 31; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPPPOFF 8
:1:1:1:1
DB 1 RRPPEFF 8

RESULT 181
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: John W. Collins, Hovey, Williams, Timmons &
; ADDRESS: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 50.8%; Score 31; DB 2; Length 26;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
11:111
DB 11 RRPPEFF 18

RESULT 182
US-09-024-975-2
Sequence 2, Application US/09024975
Patent No. 613323
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: SHI, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23585-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9057
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-2

Query Match 50.8%; Score 31; DB 4; Length 26;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
11:111
DB 11 RRPPEFF 18

RESULT 183
US-08-162-052-1
Sequence 1, Application US/08162052
Patent No. 5489575
GENERAL INFORMATION:
APPLICANT: LEE, Jong-Youn
APPLICANT: BOMAN, Hans G
APPLICANT: MUTT, Viktor
APPLICANT: JORNVAL, Hans

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 02-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92-22578
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-299
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-162-052-1

Query Match 50.8%; Score 31; DB 1; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
11:111
DB 11 RRPPEFF 18

RESULT 184
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Murt, Viktor
; AUTHORS: Joinwall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1
Query Match 50.8%; Score 31; DB 1; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RPRPOOF 8
Db 11 RPRPPPF 18
RESULT 185
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &

ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-1

Query Match 50.8%; Score 31; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RPRPOOF 8
Db 11 RPRPPPF 18

RESULT 186
US-08-728-333-1
; Sequence 1, Application US/08728333
; Patent No. 5863897
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,333
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,722
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jorntvall, Hans
TITLE: No. 5863897e1 Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-728-333-1

Query Match 50.8%; Score 31; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFF 8
11:11
Db 11 RRPDPFF 18

RESULT 187
US-09-024-975-1
Sequence 1, Application US/09024975
Patent No. 6133233
GENERAL INFORMATION:
APPLICANT: HOSS, CHRISTOPHER R.
APPLICANT: HLECHA, FRANK
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-09-024-975-1

Query Match 50.8%; Score 31; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFF 8
11:11
Db 11 RRPDPFF 18

RESULT 189

LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-1

Query Match 50.8%; Score 31; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFF 8
11:11
Db 11 RRPDPFF 18

RESULT 188
PCT-US95-12080-1
Sequence 1, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
JOURNAL: PCT/US95/12080
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
PCT-US95-12080-1

Query Match 50.8%; Score 31; DB 5; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFF 8
11:11
Db 11 RRPDPFF 18

RESULT 189

US-08-553-619B-7
; Sequence 7, Application US/08553619B
; Patent No. 5919705
; GENERAL INFORMATION:
; APPLICANT: Dehaan, Petrus T.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5919705artis Crop Protection
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,619B
; FILING DATE: December 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Marcus-Wyner, Lynn
; REGISTRATION NUMBER: 34,869
; REFERENCE/DOCKET NUMBER: 137-1082/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/354-3588
; TELEFAX: 415/857-1125
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-619B-7

Query Match 50.8%; Score 31; DB 2; Length 264;
Best local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOF 7
11111
Db 233 RPKPKSF 239

RESULT 190
US-08-414-926A-22
; Sequence 22, Application US/08414926A
; Patent No. 5721354
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,926A
; FILING DATE: March 31, 1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-011/OOUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.16
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..316
; OTHER INFORMATION: /label= UL148
; US-08-414-926A-22

Query Match 50.8%; Score 31; DB 1; Length 316;
Best local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOOFF 8
11111
Db 136 RPKPOFF 141

RESULT 191
US-08-926-922-22
; Sequence 22, Application US/08926922
; Patent No. 5925751
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cserr Attorney at Law
; STREET: 750 Arlino Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.16
; FEATURE:
; NAME/KEY: Protein

LOCATION: 1..316
OTHER INFORMATION: /label= U1148
US-08-926-922-22

Query Match 50.8%; Score 31; DB 2; Length 316;
Best Local Similarity 83.3%; Pred. NO. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOF 3
:|||||
DB 136 RPOOF 141

RESULT 192
US-09-253-682-22
Sequence 22, Application US/09253682
Patent No. 6040170
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cseerr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253.682
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926.922
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.16
FEATURE:
NAME/KEY: Protein
LOCATION: 1..316
OTHER INFORMATION: /label= U1148
US-09-253-682-22

Query Match 50.8%; Score 31; DB 3; Length 316;
Best Local Similarity 83.3%; Pred. NO. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOF 8
:|||||
DB 136 RPOOF 141

RESULT 193
US-09-527-657-22
Sequence 22, Application US/09527657
Patent No. 6291236
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cseerr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527.657
FILING DATE: 17-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/926.922
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.16
FEATURE:
NAME/KEY: Protein
LOCATION: 1..316
OTHER INFORMATION: /label= U1148
US-09-527-657-22

Query Match 50.8%; Score 31; DB 4; Length 316;
Best Local Similarity 83.3%; Pred. NO. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOF 8
:|||||
DB 136 RPOOF 141

RESULT 194
US-09-527-657-22
Sequence 22, Application US/09527657
Patent No. 5212296
GENERAL INFORMATION:
APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LENO, KENNETH
J.; O'KEEFE, DANIEL P.; OWER, CHARLES A.; ROMESSER, JAMES A.
TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
CYTOCHROMES
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569.781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
SEQ ID NO: 6
LENGTH: 406
5212296-6

Query Match 50.8%; Score 31; DB 6; Length 406;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
DB 89 RSPQAFGL 98

RESULT 195
US-08-533-669A-8
Sequence 8, Application US/08533669A
Patent No. 5834592
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-669A-8

Query Match 50.8%; Score 31; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
DB 355 RPLRPFIFGM 364

RESULT 196
US-08-511-872-2
Sequence 2, Application US/08511872
Patent No. 5965142
GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.
APPLICANT: Reed, Steven G.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: POLYPEPTIDES AND METHODS FOR THE
TITLE OF INVENTION: DETECTION OF L. tropica INFECTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,872
FILING DATE: 04-AUG-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5965142tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 210121.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-511-872-2

Query Match 50.8%; Score 31; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
DB 355 RPLRPFIFGM 364

RESULT 197
US-08-448-489-17
Sequence 17, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489.
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 17
LENGTH: 631
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Known Member of
US-08-448-489-17

Query Match 50.8%; Score 31; DB 4; Length 631;

Best Local Similarity 75.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFFGL 10
11111111
Db 47 KMOKFFGL 54

RESULT 198

US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: KINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; US-08-704-711A-18

Query Match 50.8%; Score 31; DB 3; Length 660;
Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFFGL 10
11111111
Db 76 KMOKFFGL 83

RESULT 199
US-08-222-617A-13
; Sequence 13, Application US/08222617A
; Patent No. 5882879

GENERAL INFORMATION:

; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Sanliago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet
; APPLICANT: Van Liempt, Henk
; APPLICANT: Montenegro, Eduardo P.
; TITLE OF INVENTION: A Method for Influencing Beta-Lactam
; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,617A
; FILING DATE: 04-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 97,157
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3665 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Acremonium chrysogenum
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..3665
; OTHER INFORMATION: /label= ACVS
; OTHER INFORMATION: /note= "ACV Synthetase from Acremonium
; US-08-222-617A-13
; chrysogenum; aa 1-3665"

Query Match 50.8%; Score 31; DB 2; Length 3665;
Best Local Similarity 71.4%; Pred. No. 4.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
11111111
Db 2189 RPKPOQF 2195

RESULT 200

US-08-222-617A-4
; Sequence 4, Application US/08222617A
; Patent No. 5882879
; GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Sanliago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet

APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of Acv Synthetase
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3712 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2555
OTHER INFORMATION:
US-08-222-617A-4

Query Match 50.8%; Score 31; DB 2; Length 3712;
Best Local Similarity 71.4%; Pred. No. 4.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOQF 7
11:1111
DB 2189 RRPRAQF 2195

Search completed: April 1, 2002, 16:18:44
Job time: 75 sec


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!!AA_SEQUENCE 1.0
ID AAP30142 standard; Protein: 11 AA.
AC AAP30142;
XX
XX 14-JUN-1992 (first entry)
XX
XX Sequence of peptides with substance P inhibiting activity.
XX
XX Substance P antagonist; pain therapy; hypertension.
XX
XX Key
XX Location/Qualifiers
XX 2
XX Modified-site
XX /label= D-P
XX 7
XX Modified-site
XX /label= D-W
XX 8
XX Misc-difference
XX /label= F,I
XX 9
XX Modified-site
XX /label= D-W
XX 11
XX Modified-site
XX /label= M,I
XX /note= "bonded to NH2"
XX
XX WO8301251-A.
XX
XX 14-APR-1983.
XX
XX 09-OCT-1981; 81WO-DE00171.
XX
XX 09-OCT-1981; 81WO-DE00171.
XX
XX 09-OCT-1981; 81EP-0902802.
XX
XX (FERR) FERRING ARZNEIMITTE.
XX (HORI/) HORIG J.
XX
XX Horig J;
XX
XX WPI; 1983-39155K/16 (39155K).
XX
XX Undeca-peptide derivs. with substance P inhibiting activity -
XX useful for treating pain and hypertension
XX
XX Claim 2; Page 18; 25pp; German.
XX
XX The peptides of the invention are powerful antagonists of Substance
XX P and so are useful in human and veterinary medicine, for treating
XX pain and hypertension (esp.) chronic conditions. A 10 microm concn.
XX of the peptide produced about 50% inhibition at a Substance P concn. of
XX 7.5-20 nanom.
XX
XX Sequence 11 AA;
XX
AAP30142 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO WFWLM
!!AA_SEQUENCE 1.0
ID AAP40479 standard; peptide: 11 AA.
XX
XX AAP40479;
XX
XX 27-NOV-1991 (first entry)
XX
XX Substance P analogue.
XX
XX Substance P; analogue; antiinflammatory agent; analgesic.
XX
XX US4481139-A.
XX
XX 06-NOV-1984.
XX
XX 13-APR-1983; 83US-0484646.
XX
XX

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XX
XX 13-APR-1983; 83US-0484646.
XX
XX (UYTE-) UNIVERSITY OF TEXAS SYSTEM.
XX
XX PI Folkers K, Ji-cheng X;
XX
XX WPI; 1984-294258/47.
XX
XX Peptide analogues of substance P - useful as antagonists, e.g. as
XX antiinflammatory agents and analgesics.
XX
XX Claim 1; page 5; 5pp; English.
XX
XX The peptide is a D-Arg1, D-Trp7, D-Trp9, Leu11 analogue of substance
XX P. The peptide is a substance P antagonist with higher activity than
XX known substance P analogues. It may be used as a biological
XX research tool, ophthalmological antiinflammatory agent and analgesic.
XX
XX Sequence 11 AA;
XX
AAP40479 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO WFWL
!!AA_SEQUENCE 1.0
ID AAP40481 standard; Protein: 11 AA.
XX
XX AAP40481;
XX
XX 27-NOV-1991 (first entry)
XX
XX Substance P analogue.
XX
XX Substance P; analogue; antiinflammatory agent; analgesic.
XX
XX US4481139-A.
XX
XX 06-NOV-1984.
XX
XX 13-APR-1983; 83US-0484646.
XX
XX 13-APR-1983; 83US-0484646.
XX
XX (UYTE-) UNIVERSITY OF TEXAS SYSTEM.
XX
XX PI Folkers K, Ji-cheng X;
XX
XX WPI; 1984-294258/47.
XX
XX Peptide analogues of substance P - useful as antagonists, e.g. as
XX antiinflammatory agents and analgesics.
XX
XX Claim 4; page 5; 5pp; English.
XX
XX The peptide is a D-Arg1, D-Pro2, D-Phe 5, D-Trp7, D-Trp9, Leu11
XX analogue of substance P. The peptide is a substance P antagonist
XX with higher activity than known substance P analogues. It may be
XX used as a biological research tool, ophthalmological antiinflammatory
XX agent and analgesic.
XX
XX Sequence 11 AA;
XX
AAP40481 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO WFWL
!!AA_SEQUENCE 1.0
ID AAP61480 standard; peptide: 11 AA.
XX
XX AAP61480;
XX
XX 22-AUG-1991 (first entry)
XX

```

XX DE Sequence of undeca peptide substance P1.
 XX KM Hypertension therapy; sleep disorder; anti-stress agent.
 XX FH Key Location/Qualifiers
 FT MISC-difference 11
 FT /label= Met-NH2
 XX PN DD29593-A.
 XX PD 13-NOV-1985.
 XX PF 28-NOV-1984; 84DD-0269954.
 XX PR 28-NOV-1984; 84DD-0269954.
 XX PA (DEAK) AKAD WISSENSCHAFT DDR.
 XX PI Oehme P, Hecht K, Wachtel E, Roske I, Kolometsewa IA;
 PI Alirapetjanz M, Blenert M, Vogt WE, Hlase H, Gores E, Poppel M;
 PI Nieber K, Bergmann J;
 XX DR WPI; 1986-069387/11.
 XX PS Cpds. having N-terminal sequences of undeca:peptide substance P -
 PT are medicinal agents with anti-stress activity
 XX CC Claim 1; Page 1; 15pp; German.
 XX CC The inventors claim an antistress compound which contains the N-
 CC terminal SQ of AAP61480, pref. Arg-Pro-Lys-Pro-X (X= COOH or NH2).
 CC Compared with the full undecapeptide they have much reduced
 CC side effects (acute hypotension, spastic effects on the ileum and
 CC histamine release from peritoneal mast cells).
 XX SQ Sequence 11 AA;
 AAP61480 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBCQE ZGHSQILKMF PSTWVSGOT HERSRPRPQ FPGLM
 11AA_SEQUENCE 1.0
 ID AAP70431 standard; protein; 129 AA.
 XX AC AAP70431;
 XX DT 17-JAN-1991 (first entry)
 XX DE Human beta-preprotachykinin.
 XX KW Preprotachykinin; substance P; neurokinin A; tachykinin;
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 20..56
 FT /label=claimed polypeptide
 FT Region 1..126
 FT /label=claimed polypeptide
 FT Region 111..126
 FT /label=claimed polypeptide
 XX PN WO8707643-A.
 XX PD 17-DEC-1987.
 XX PF 03-JUN-1987; 87WO-GB00382.
 XX PR 03-JUN-1986; 86GB-0013431.
 XX PA (RESE) RESEARCH CORPORATION LTD.
 XX CC

PI Harnar AJ, Pascall J, Mckeown A;
 XX DR WPI: 1987-362730/51.
 DR N-PSDB; AAN70688.
 XX XX
 PT New DNA sequence coding for the new polypeptide preprotachykinin -
 PT a precursor for substance P, etc., useful as neurotransmitters,
 PT diagnostic reagents, etc.
 XX PS
 PS Claim 1; page 15; 25pp; English.
 XX CC Beta-preprotachykinin includes sequences identical to tachykinins, eg
 CC substance P, neurokinin A, or other biologically active peptides, eg
 CC neuropeptide K. These peptides are, eg neurotransmitters, hormones,
 CC analgesics and anti-inflammatory. The polypeptides can be used
 CC as reagents in RIA, eg to monitor or diagnose carcinoid syndrome.
 XX SQ Sequence 129 AA;
 AAP70431 Length: 163 April 1, 2002 16:31 Type: P Check: 5532 ..
 1 SQARNDBCQE ZGHSQILKMF PSTWVSGOT HERSMKILVA LAVFLVSTO
 51 LEAEIGAND DINWSDWDYD SDQIKELPE PEPHLQRIA RRPKQOEFQ
 101 LMGKRDADSS IEQVALLKA LYGHQISHK RHRTDSFVGL MGKRALNSVA
 151 YERSAMQNYE RRR
 11AA_SEQUENCE 1.0
 ID AAP80312 standard; protein; 11 AA.
 XX AC AAP80312;
 XX DT 14-SEP-1990 (first entry)
 XX DE Sequence of neuropeptide substance P which binds with polypeptide
 DE receptor for bombesin type polypeptides.
 XX KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
 KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
 KW substance P.
 XX OS Swiss 3T3 cells.
 XX FH Key Location/Qualifiers
 FT MISC-difference 11
 FT /label=OTHER
 FT /note="Met-NH2"
 XX PN WO8807551-A.
 XX PD 06-OCT-1988.
 XX PF 31-MAR-1988; 88WO-GB00255.
 XX PR 25-NOV-1987; 87GB-0027638.
 XX PA (IMCR) IMPERIAL CANCER RES.
 XX PI Rosengurt E, Zachary I, Woll P;
 XX DR WPI; 1988-292842/41.
 XX PT New polypeptide receptor for bombesin type polypeptide(s) -
 PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 PT antagonists are useful for treating uncontrolled cell proliferation
 XX PS Disclosure; Table 2; 42pp; English.
 XX CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a

CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe3] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX

Sequence 11 AA:

AAP80312 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO FEGLM

!!AA_SEQUENCE 1.0

ID AAP80313 standard; protein; 11 AA.

AC AAP80313;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist A which binds with polypeptide
DE receptor for bombesin type polypeptides.

DE Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist A.

XX Swiss 3T3 cells.

OS Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

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XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe3] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX

Sequence 11 AA:

AAP80313 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO WFLL

!!AA_SEQUENCE 1.0

ID AAP80314 standard; protein; 11 AA.

AC AAP80314;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist B which binds with polypeptide
DE receptor for bombesin type polypeptides.

DE Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist B.

XX Swiss 3T3 cells.

OS Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

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XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe3] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX

Sequence 11 AA:

AAP80313 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO WFLL

!!AA_SEQUENCE 1.0

ID AAP80314 standard; protein; 11 AA.

AC AAP80314;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist B which binds with polypeptide
DE receptor for bombesin type polypeptides.

DE Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist B.

XX Swiss 3T3 cells.

OS Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

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XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

XX Swiss 3T3 cells.

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC (D-Arg1, D-Pro2, D-Trp7/9, Leu11) substance P. It is also known as
CC (D-Pro2) spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as (D-Phe5) spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

AAP80314 Length: 45 Apr11 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FFWML

!!AA_SEQUENCE 1.0

ID AAP80315 standard; protein; 11 AA.

XX AC AAP80315;

XX DT 14-SEP-1990 (first entry)

XX DE Sequence of neuropeptide antagonist C which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX KW Spantide: neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX antagonist C.

XX OS Swiss 3T3 cells.

XX FH Key Location/Qualifiers

FT MISC-difference 2 /label=OTHER

FT FT /note="DPro"

FT MISC-difference 7 /label=OTHER

FT FT /note="DPhe"

FT MISC-difference 1 /label=OTHER

FT FT /note="DTrp"

FT MISC-difference 11 /label=OTHER

FT FT /note="Met-NH2"

XX PN WO8807551-A.

XX PD 06-OCT-1988.

XX PF 31-MAR-1988; 88WO-GB00255.

XX PR 25-NOV-1987; 87GB-0027638.

XX PA (IMCR) IMPERIAL CANCER RES.

XX PI Rosengurt E, Zachary I, Woll P;

XX DR WPI; 1988-292842/41.

XX PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation
XX PS Disclosure; Table 2; 42pp; English.

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC (D-Arg1, D-Pro2, D-Trp7/9, Leu11) substance P. It is also known as
CC (D-Pro2) spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as (D-Phe5) spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

AAP80315 Length: 45 Apr11 1, 2002 16:31 Type: P Check: 1410 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FFWLM

!!AA_SEQUENCE 1.0

ID AAP80316 standard; protein; 11 AA.

XX AC AAP80316;

XX DT 14-SEP-1990 (first entry)

XX DE Sequence of neuropeptide antagonist D which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX KW Spantide: neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides.

XX OS Swiss 3T3 cells.

XX FH Key Location/Qualifiers

FT MISC-difference 1 /label=OTHER

FT FT /note="DArg"

FT MISC-difference 5 /label=OTHER

FT FT /note="DPhe"

FT MISC-difference 7 /label=OTHER

FT FT /note="DTrp"

FT MISC-difference 9 /label=OTHER

FT FT /note="DTrp"

FT MISC-difference 11 /label=OTHER

FT FT /note="Leu-NH2"

XX PN WO8807551-A.

XX PD 06-OCT-1988.

XX PF 31-MAR-1988; 88WO-GB00255.

XX PR 25-NOV-1987; 87GB-0027638.

XX PA (IMCR) IMPERIAL CANCER RES.

XX PI Rosengurt E, Zachary I, Woll P;
XX DR WPI; 1988-292842/41.
XX PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation

PS Disclosure; Table 2; 42pp; English.
XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA;

AAP80316 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRKPFPQ WFWLL

!!AA_SEQUENCE 1.0
ID AAP80317 standard; protein: 11 AA.

AC AAP80317;
XX

DT 14-SEP-1990 (first entry)
XX

DE Sequence of neuropeptide antagonist E which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist E.
XX

OS Swiss 3T3 cells.
XX

FH Key Location/Qualifiers
FT Misc-difference 2 /label=OTHER

FT /note="DPro"
FT Misc-difference 7 /label=OTHER

FT /note="DTrp"
FT Misc-difference 9 /label=OTHER

FT /note="DTrp"
FT Misc-difference 11 /label=OTHER

FT /note="Met-NH2"
FT
FT

W08807551-A.
XX

PD 06-OCT-1988.
XX

PF 31-MAR-1988; 88WO-GB00255.
XX

PR 25-NOV-1987; 87GB-0027638.
XX

PA (IMCR) IMPERIAL CANCER RES.
XX

PI Rosengurt E, Zachary I, Woll P;
XX

DR WPI, 1988-292842/41.
XX

PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX

PS Disclosure; Table 2; 42pp; English.
XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA;

AAP80317 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRKPFPQ WFWLL

!!AA_SEQUENCE 1.0
ID AAP80320 standard; protein: 11 AA.

AC AAP80320;
XX

DT 14-SEP-1990 (first entry)
XX

DE Sequence of neuropeptide antagonist H which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist H.
XX

OS Swiss 3T3 cells.
XX

FH Key Location/Qualifiers
FT Misc-difference 1 /label=OTHER

FT /note="DArg"
FT Misc-difference 2 /label=OTHER

FT /note="DPro"
FT Misc-difference 7 /label=OTHER

FT /note="DPhe"
FT Misc-difference 9 /label=OTHER

FT /note="DHIS"
FT Misc-difference 11 /label=OTHER

FT /note="Met-NH2"
FT
FT

W08807551-A.
XX

PD 06-OCT-1988.
XX

PF 31-MAR-1988; 88WO-GB00255.
XX

PR 25-NOV-1987; 87GB-0027638.
XX

PA (IMCR) IMPERIAL CANCER RES.
XX

PI Rosengurt E, Zachary I, Woll P;
XX

DR WPI, 1988-292842/41.
XX

PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX

CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

AAR21966 Length: 45 April 1, 2002 16:31 Type: P Check: 704 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPCQ FFCXM

11AA_SEQUENCE 1.0
ID AAR21965 standard; Peptide; 11 AA.

XX
AC AAR21965;

XX
DT 25-JUN-1992 (first entry)

XX
DE Cyclic substance P [Cys 5,9].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.

OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 5..9

XX
PN WO9202248-A.

XX
PD 20-FEB-1992.

XX
PE 29-JUL-1991; 91WO-US05323.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MED CENT.

XX
PI Yankner BA;

XX
DR WPI; 1992-079804/10.

XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX
PS Claim 11; Page 22; 35pp; English.

XX
CC The peptide is the tachykinin agonist substance P with Cys
CC residues substituted at positions 5 and 9, with a disulphide bond
CC formed between them, making the peptide cyclic. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal accumu-
CC lation of beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21932-75.

XX
SQ Sequence 11 AA;

AAR21965 Length: 45 April 1, 2002 16:31 Type: P Check: 4 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPCQ FFCXM

11AA_SEQUENCE 1.0

ID AAR21967 standard; Peptide; 11 AA.

XX
AC AAR21967;

XX
DT 25-JUN-1992 (first entry)

XX
DE Cyclic substance P [Cys 5,11].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

KW syndrome; hereditary cerebral haemorrhage.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 5..11

XX
PN WO9202248-A.

XX
PD 20-FEB-1992.

XX
PE 29-JUL-1991; 91WO-US05323.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MED CENT.

XX
PI Yankner BA;

XX
DR WPI; 1992-079804/10.

XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX
PS Claim 11; Page 22; 35pp; English.

XX
CC The peptide is the tachykinin agonist substance P with Cys
CC residues substituted at positions 5 and 11, with a disulphide bond
CC formed between them, making the peptide cyclic. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal accumu-
CC lation of beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21932-75.

XX
SQ Sequence 11 AA;

AAR21967 Length: 45 April 1, 2002 16:31 Type: P Check: 9726 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPCQ FFCXM

11AA_SEQUENCE 1.0

ID AAR21960 standard; Peptide; 11 AA.

XX
AC AAR21960;

XX
DT 25-JUN-1992 (first entry)

XX
DE Cyclic substance P [hcys 5,9].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT MISC-difference 5

XX
FT MISC-difference 5 /label= OTHER

XX
FT MISC-difference 9 /note= "OTHER = homocysteine"

XX
FT MISC-difference 9 /label= OTHER /note= "OTHER = homocysteine"

XX
PN WO9202248-A.

XX
PD 20-FEB-1992.

XX
PE 29-JUL-1991; 91WO-US05323.

```

PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX PS Claim 11; Page 22; 35pp; English.
XX
XX The peptide is the tachykinin agonist, substance P with
XX homocysteine substituted at positions 5 and 9, with a disulphide
XX bond formed between them making the peptide cyclic. The
XX peptide was synthesised by standard solid phase synthesis.
XX Neuronal accumulation of beta-amyloid may be treated by administ-
XX ration of tachykinin agonists. The peptide can reduce the neuro-
XX toxic effects of a beta-amyloid related polypeptide on cultured
XX neurons. The peptide and its analogues are useful for controlling
XX diseases characterised by beta amyloid accumulation in the brain
XX such as Alzheimer's disease and Down's syndrome.
XX
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21960 Length: 45 April 1, 2002 16:31 Type: P Check: 1726 ..
XX
XX 1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRKPXQ FFXLM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21961 standard; peptide; 11 AA.
XX
XX AAR21961;
XX
XX 25-JUN-1992 (first entry)
XX
XX DE Cyclic substance P [Hcys 5,11].
XX
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 5 //label= OTHER
XX FT //note= "OTHER = homocysteine"
XX FT Misc-difference 11 //label= OTHER
XX FT //note= "OTHER = homocysteine"
XX
XX XN WO9202248-A.
XX
XX PN 20-FEB-1992.
XX
XX PD 29-JUL-1991; 91WO-US05323.
XX
XX PE 27-JUL-1990; 90US-0559173.
XX
XX PR (CHIL-) CHILDRENS MED CENT.
XX
XX PA Yankner BA;
XX
XX PI WPI; 1992-079804/10.
XX
XX DR Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX PS Claim 11; Page 22; 35pp; English.

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XX
XX The peptide is the tachykinin agonist, substance P with
XX homocysteine substituted at positions 5 and 11, with a disulphide
XX bond formed between them making the peptide cyclic. The
XX peptide was synthesised by standard solid phase synthesis.
XX Neuronal accumulation of beta-amyloid may be treated by administ-
XX ration of tachykinin agonists. The peptide can reduce the neuro-
XX toxic effects of a beta-amyloid related polypeptide on cultured
XX neurons. The peptide and its analogues are useful for controlling
XX diseases characterised by beta amyloid accumulation in the brain
XX such as Alzheimer's disease and Down's syndrome.
XX
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21961 Length: 45 April 1, 2002 16:31 Type: P Check: 1490 ..
XX
XX 1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRKPXQ FFXLM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21932 standard; peptide; 9 AA.
XX
XX AAR21932;
XX
XX 25-JUN-1992 (first entry)
XX
XX DE Substance P (1-9) fragment.
XX
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX OS Synthetic.
XX
XX PN WO9202248-A.
XX
XX PD 20-FEB-1992.
XX
XX PE 29-JUL-1991; 91WO-US05323.
XX
XX PR 27-JUL-1990; 90US-0559173.
XX
XX PA (CHIL-) CHILDRENS MED CENT.
XX
XX PI Yankner BA;
XX
XX DR WPI; 1992-079804/10.
XX
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX PS Claim 9; Page 21; 35pp; English.
XX
XX The peptide is a tachykinin agonist consisting of residues 1-9 of
XX substance P. The peptide was synthesised by standard solid phase
XX synthesis. Analogues of the peptide, with C-terminal deletions down
XX to substance P (1-4) were also synthesised. Neuronal accumulation of
XX beta-amyloid may be treated by administration of these tachykinin
XX agonists. The peptides reduce the neurotoxic effects of a beta-
XX amyloid related polypeptide on cultured neurons. The peptide and
XX its analogues are useful for controlling diseases characterised by
XX beta amyloid accumulation in the brain such as Alzheimer's disease
XX and Down's syndrome.
XX
XX See also AAR21933-75.
XX
XX Sequence 9 AA;
XX
XX AAR21932 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
XX
XX 1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRKPXQ FFXLM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21934 standard; Protein; 11 AA.

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```

XX AC AAR21934:
XX DT 25-JUN-1992 (first entry)
XX DE Substance P [Tyr7] and fragment (7-11) [Tyr 7].
XX DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX DE syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.
XX PR 27-JUL-1990: 90US-0559173.
XX PA (CHIL-) CHILDERNS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with a Tyr
XX CC residue substituted at position 7. The peptide was synthesised
XX CC by standard solid phase synthesis. A N-terminal deleted peptide
XX CC (7-11) with the Tyr substitution was also synthesised. Neuronal
XX CC accumulation of beta-amyloid may be treated by administration
XX CC of tachykinin agonists. The peptides can reduce the neurotoxic
XX CC effects of a beta-amyloid related polypeptide on cultured neurons.
XX CC The peptide and its analogues are useful for controlling diseases
XX CC characterised by beta amyloid accumulation in the brain such as
XX CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;
AAR21934 Length: 45 April 1, 2002 16:31 Type: P Check: 1501 ..
1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPPQO YFGLM
11AA_SEQUENCE 1.0
ID AAR21935 standard; protein; 11 AA.
XX AC AAR21935;
XX DT 25-JUN-1992 (first entry)
XX DE Substance P [Pro 9] or [D-Pro 9].
XX DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX DE syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.
XX FT Modified-site 9 Location/Qualifiers
XX FT /note= "either L or D form"
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.

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XX PR 27-JUL-1990: 90US-0559173.
XX PA (CHIL-) CHILDERNS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with a Pro (D/L)
XX CC residue substituted at position 9. The peptide was synthesised
XX CC by standard solid phase synthesis. Neuronal accumulation of
XX CC beta-amyloid may be treated by administration of tachykinin
XX CC agonists. The peptide can reduce the neurotoxic effects of a beta-
XX CC amyloid related polypeptide on cultured neurons. The peptide and
XX CC its analogues are useful for controlling diseases characterised by
XX CC beta amyloid accumulation in the brain such as Alzheimer's disease
XX CC and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;
AAR21935 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..
1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FPLLM
11AA_SEQUENCE 1.0
ID AAR21936 standard; protein; 11 AA.
XX AC AAR21936;
XX DT 25-JUN-1992 (first entry)
XX DE Substance P or (7-11) [Ethionine 11].
XX DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX DE syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.
XX PR 27-JUL-1990: 90US-0559173.
XX PA (CHIL-) CHILDERNS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with an Ethionine
XX CC residue substituted at position 11. The peptide was synthesised

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CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XQ Sequence 11 AA;

AAAR21936 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..

1 S0ARNBCQE ZGHSQILKMF PSTWVSQOT HERSRPPQQ FFG LX

ID	11AA_SEQUENCE 1.0
XX	AA:21937 standard; Protein; 11 AA.
XX	AA:21937;
XX	25-JUN-1992 (first entry)
XX	Substance P or (7-11) [Norelucine 11].
DE	Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX	syndrome; hereditary cerebral haemorrhage.
KW	Synthetic.
OS	
XX	
XX	Key Location/Qualifiers
XX	Misc-difference 11
XX	/label= OTHER
XX	/note= "OTHER = Nle"
XX	
XX	MO9202248-A.
XX	
XX	20-FEB-1992.
XX	
XX	29-JUL-1991; 91WO-US05323.
XX	
XX	27-JUL-1990; 90US-0559173.
XX	
XX	(CHIL-) CHILDRENS MED CENT.
XX	
XX	Yankner BA;
XX	
XX	WPI; 1992-079804/10.
XX	
XX	Treatment of neuronal accumulation of beta-amyloid - using
XX	tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX	B, for treating Alzheimer's disease, Downs syndrome, etc.
XX	
XX	Claim 10; Page 21; 35pp; English.
XX	
XX	The peptide is the tachykinin agonist substance P with a Norelucine
XX	residue substituted at position 11. The peptide was synthesised
XX	by standard solid phase synthesis. An N-terminal deleted peptide
XX	(7-11) with the same substitution was also synthesised. Neuronal
XX	accumulation of beta-amyloid may be treated by administration of
XX	tachykinin agonists. The peptides can reduce the neurotoxic effects
XX	of a beta-amyloid related polypeptide on cultured neurons. The
XX	peptide and its analogues are useful for controlling diseases
XX	characterised by beta amyloid accumulation in the brain such as
XX	Alzheimer's disease and Down's syndrome.
XX	See also AA:21932-75.
XX	
XX	Sequence 11 AA;

AAR21937 Length: 45 April 1, 2002 16:31 Type: P Check: 677 ..

1 SQRNDBCQE ZGHSQILKMF PSTWYSQOT HERSRPKPQD FFGLL

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!!AA_SEQUENCE 1.0
ID AAR21938 standard; protein; 11 AA.
AC AAR21938;
XX
XX
XX 25-JUN-1992 (first entry)
DT
XX
XX Substance P [Me-Leu 10].
DE
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
RM
XX
XX Synthetic.
OS
XX
XX
XX key Location/Qualifiers
FH 10
FT Modified-site /label= OTHER
FT /note= "OTHER = Me-Leu"
FT

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AAR21938 Length: 45 April 1, 2002 16:31 Type: P Check: 722 . .

1 SÖARNDBCQE ZGHSÖILKMF PSTWVVSÖOT HERSRPKPÖÖ FFGGLM

11AA_SEQUENCE 1.0	
ID	AAR21940 standard; Protein; 11 AA.
XX	
AC	AAR21940;
XX	
DT	25-JUN-1992 (first entry)
XX	
DE	Substance P [Pro 10].
KW	Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KM	syndrome; hereditary cerebral haemorrhage.
XX	
OS	Synthetic.
XX	
PN	W09202248-A.
XX	
PD	20-FEB-1992.

XX 29-JUL-1991: 91WO-US05323.
XX
XX 27-JUL-1990: 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX
XX Claim 10: Page 21: 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Proline
XX residue substituted at position 10. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21940 Length: 45 April 1, 2002 16:31 Type: P Check: 898 ..
XX
XX 1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGPM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21942 standard; Protein; 11 AA.
XX
XX AAR21942;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Memet 11].
XX
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX
XX Location/Qualifiers
XX FT Misc-difference 11
XX FT /Label= OTHER
XX FT /note= "OTHER = Methyl Methionine"
XX
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991: 91WO-US05323.
XX
XX 27-JUL-1990: 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10: Page 21: 35pp; English.
XX

CC The peptide is the tachykinin agonist substance P with a methyl
CC methionine residue substituted at position 11. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21942 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
XX
XX 1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21944 standard; Protein; 11 AA.
XX
XX AAR21944;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Pro 11].
XX
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991: 91WO-US05323.
XX
XX 27-JUL-1990: 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10: Page 21: 35pp; English.
XX
XX
XX The peptide is the tachykinin agonist substance P with a Proline
XX residue substituted at position 11. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21944 Length: 45 April 1, 2002 16:31 Type: P Check: 857 ..
XX
XX 1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLP
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21946 standard; Protein; 11 AA.
XX
XX AAR21946;
XX

DT 25-JUN-1992 (first entry)
 XX
 DE Substance P [Me-Phe 8].
 XX
 KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 XX syndrome; hereditary cerebral haemorrhage.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /label= OTHER
 FT /note= "OTHER = Methyl phenylalanine"
 XX
 PN W09202248-A.
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHTL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI, 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 21; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a methyl
 CC phenylalanine residue substituted at position 8. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 CC
 XX Sequence 11 AA;
 SQ
 AAR21946 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFGLM
 !!AA_SEQUENCE 1.0
 ID AAR21951 standard; Peptide; 11 AA.
 XX
 AC AAR21951;
 XX
 DF 25-JUN-1992 (first entry)
 XX
 DE Substance P [Glu 3].
 XX
 XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN W09202248-A.
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX

PA (CHTL-) CHILDRENS MED CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI, 1992-079804/10.
 XX
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 21; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a glutamic
 CC acid residue substituted at position 5. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 CC
 XX Sequence 11 AA;
 SQ
 AAR21951 Length: 45 April 1, 2002 16:31 Type: P Check: 254 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFGLM
 !!AA_SEQUENCE 1.0
 ID AAR21954 standard; Protein; 11 AA.
 XX
 AC AAR21954;
 XX
 DF 25-JUN-1992 (first entry)
 XX
 DE Substance P [Me-Gly 9].
 XX
 KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 9 /label= OTHER
 FT /note= "OTHER = Methyl glycine"
 XX
 PN W09202248-A.
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHTL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI, 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 22; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a methyl
 CC glycine residue substituted at position 9. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects

CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 CC XX

SQ Sequence 11 AA;

AAR21954 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM

!!AA_SEQUENCE 1.0

ID AAR21958 standard; Peptide: 11 AA.

XX AAR21958;

XX 25-JUN-1992 (first entry)

XX Substance P [Ala 9] or [D-Ala 9].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.
 OS
 XX

FH Key Location/Qualifiers

FT Modified-site 9 /note="either L or D form"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Down's syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

PS The peptide is the tachykinin agonist substance P with an Ala (D/L)

CC residue substituted at position 9. The peptide was synthesised
 CC by standard solid phase synthesis. Neuronal accumulation of
 CC beta-amyloid may be treated by administration of tachykinin
 CC agonists. The peptide can reduce the neurotoxic effects of a beta-
 CC amyloid related polypeptide on cultured neurons. The peptide and
 CC its analogues are useful for controlling diseases characterised by
 CC beta amyloid accumulation in the brain such as Alzheimer's disease
 CC and Down's syndrome.
 CC See also AAR21932-75.
 CC XX

SQ Sequence 11 AA;

AAR21958 Length: 45 April 1, 2002 16:31 Type: P Check: 464 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM

!!AA_SEQUENCE 1.0

ID AAR21962 standard; Peptide: 11 AA.

XX AAR21962;

XX 25-JUN-1992 (first entry)

XX Substance P [p-Chloro-Phe 7,8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.
 OS
 XX

FH Key Location/Qualifiers

FT Modified-site 7 /label="OTHER

FT Modified-site 8 /note="OTHER - p-Chloro-phenylalanine"

XX Substance P [Me Gly 6, Met (O2) 11].

DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 XX syndrome; hereditary cerebral haemorrhage.

XX Synthetic.
 OS
 XX

FH Key Location/Qualifiers

FT Misc-difference 6 /label="OTHER

FT Misc-difference 11 /note="OTHER - Methyl glycine"

FT /label="OTHER

FT /note="OTHER - Met (O2)"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Down's syndrome, etc.

XX Claim 10; Page 22; 35pp; English.

PS The peptide is the tachykinin agonist, substance P with methyl
 CC glycine substituted at position 9 and Met (O2) at position 11.
 CC The peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 CC XX

SQ Sequence 11 AA;

AAR21962 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM

!!AA_SEQUENCE 1.0

ID AAR21963 standard; Peptide: 11 AA.

XX AAR21963;

XX 25-JUN-1992 (first entry)

XX Substance P [p-Chloro-Phe 7,8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.
 OS
 XX

FH Key Location/Qualifiers

FT Modified-site 7 /label="OTHER

FT Modified-site 8 /note="OTHER - p-Chloro-phenylalanine"

FT /note= "OTHER = p-Chloro-phenylalanine"
XX WO9202248-A.
XX 20-FEB-1992.
PD
XX 29-JUL-1991; 91WO-US05323.
PF
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MED CENT.
PA
XX Yankner BA;
PI
XX WPI: 1992-079804/10.
DR
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 22; 35pp: English.
PS
XX The peptide is the tachykinin agonist, substance P fragment
CC with p-Chloro-phenylalanine residues substituted at positions 7 and
CC 8. The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ
AAR21963 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPKPOQ FFGLM
!!AA_SEQUENCE 1.0
ID AAR28442 standard; peptide: 11 AA.
XX
XX AAR28442;
AC
XX 22-MAR-1993 (first entry)
DT
XX Substance P.
DE
XX NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 11
FT /note= "amdated"
FT
XX WO9218536-A.
PM
XX 29-OCT-1992.
PD
XX 22-APR-1992; 92MO-US03307.
PF
XX 22-APR-1991; 91EP-0200955.
PR
XX (MLCW) MALLINCKRODT MEDICAL INC.
PA
XX Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
PI
XX WPI: 1992-382047/46.
DR
XX Detection and localisation of tissues with neurokinine-1 receptors
PT

PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX
XX Disclosure: Page 4; 22pp; English.
PS
XX Substance P or its Tyr0 deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See also AAR28443-R28446.
XX
XX Sequence 11 AA;
SQ

AAR28442 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPKPOQ FFGLM
!!AA_SEQUENCE 1.0
ID AAR28443 standard; peptide: 11 AA.
XX
XX AAR28443;
AC
XX 22-MAR-1993 (first entry)
DT
XX Neurokinine 1 ligand #1.
DE
XX NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 9 /label= MeGly
FT Modified-site 11
FT /label= OTHER
FT /note= "Met(O)2-NH2"
FT
XX WO9218536-A.
PM
XX 29-OCT-1992.
PD
XX 22-APR-1992; 92MO-US03307.
PF
XX 22-APR-1991; 91EP-0200955.
PR
XX (MLCW) MALLINCKRODT MEDICAL INC.
PA
XX Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
PI
XX WPI: 1992-382047/46.
DR
XX Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX
XX Disclosure: Page 4; 22pp; English.
PS
XX This peptide or its Tyr0 deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See AAR28442-R28446.
XX
XX Sequence 11 AA;
SQ
AAR28443 Length: 45 April 1, 2002 16:31 Type: P Check: 980 ..

PT /note= "D-form residue"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /label= Nle
 PN WO9217201-A.
 PD 15-OCT-1992.
 XX
 PF 30-MAR-1992; 92MO-US02431.
 XX
 PR 01-APR-1991; 91US-0677391.
 PR 27-MAR-1992; 92US-0859582.
 XX
 PA (CORT-) CORTECH INC.
 XX
 PI Allen IG, Blodgett JK, Cheronis JC, Eubanks SR, Nguyen KT,
 PI Whalley ET;
 XX
 DR WPI: 1992-365995/44.
 XX
 PT Bradykinin antagonists comprising linked bradykinin antagonist
 PT chains - are for treatment of post-operative pain, asthma and
 PT aseptic shock
 XX
 PS Disclosure: Page 76; 109pp; English.
 XX
 CC The sequence given is a bradykinin receptor antagonist which can form
 CC homo- or heterodimers or higher oligomers. It demonstrates greater
 CC potency and/or duration of action than the parent peptide itself.
 CC Bradykinin receptors antagonists such as this can be used in the
 CC treatment of burns, perioperative pain, migraine and other forms of
 CC pain, shock CNS injury, asthma, rhinitis, premature labour,
 CC inflammatory arthritis, inflammatory bowel disease etc.
 CC
 SQ Sequence 11 AA;
 AAR28392 Length: 45 April 1, 2002 16:31 Type: P Check: 1785 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPRKPN FFWLX
 !!AA-SEQUENCE 1.0
 ID AAR45229 standard; Protein; 492 AA.
 XX
 AC AAR45229;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE APP-REP 751 amyloid precursor protein/reporter protein.
 XX
 KW Amyloid precursor protein; APP; beta amyloid protein; BAP;
 KW detection; Alzheimer's disease; Down's syndrome.
 XX
 OS Homo sapiens.
 OS
 PN AU9338358-A.
 PN
 PD 04-NOV-1993.
 XX
 PF 03-MAY-1993; 93AU-0038358.
 XX
 PR 01-MAY-1992; 92US-0877675.
 XX
 PA (AMCT) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 PI
 DR WPI: 1993-406194/51.
 DR N-PSDB; AAO54257.
 XX
 PT New mutant forms of amyloid precursor protein - for detecting
 PT cpds. that modify activity of enzymes involved in precursor

PT cleavage, also new nucleic acid encoding them
 XX
 PS Claim 5; Figure 7; 66pp; English.
 XX
 CC This mutant form of amyloid precursor protein comprises from the 5'
 CC to the 3' end a sequence encoding a marker and either (1) a
 CC sequence encoding the N-terminus of an amyloid precursor protein
 CC (APP) up to, but not including, the nucleotides encoding the beta
 CC amyloid protein (BAP) domain or (2) the BAP domain. Recombinant
 CC polypeptides generated from this proteins coding sequence can be
 CC used to detect drugs or compounds that inhibit/augment the
 CC activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments (deposition of which occurs in patients with Alzheimers
 CC disease and Down's syndrome).
 XX
 SQ Sequence 492 AA;
 AAR45229 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAWTAR
 51 ALEVPITDGN GLAEPOIAM FCGRLNMHMN VQNGKWDSDP SGTKTCTIDK
 101 EGILOYCOEV YPELOITNVV EANOPTION WCKRGRKCK TDPHFVTPYR
 151 CLVGEFVSDA LLVPDKCKFL HQERNDVCEI HLHHTYAKE TCSEKSTNLH
 201 DYGMLLPCGI DKFRGVEYVC CPLAESDNV DSADAEEDSD DVMWGCADTD
 251 YADGSEDKV EVAEEBEVAE VEEBEADDE DDEGDGEVEE EAEPEYEAT
 301 ERTTSIATTT TTTESVVEV VREVCSEQA TGPCRAMISR WYEDVTEGKC
 351 APFFYGGCGG NNNNDTEY CMAVCGSAIP TTAASITDAV DYLEPKRQ
 401 QPFGLMGSLT NIKTEISEV KMDAEFRHS GYEVHOKIV PRAEDVGSNK
 451 GAILGLMWG VVIATYIVIT LVMLKKROYT SIHNGVEVD AAVTPERHL
 501 SKMQQNGYEN PTYKPEQMO NYGFFM
 !!AA-SEQUENCE 1.0
 ID AAR32798 standard; peptide; 12 AA.
 XX
 AC AAR32798;
 XX
 DT 17-JUN-1993 (first entry)
 XX
 DE Tyr-1 substance P used for binding assay.
 XX
 KW human substance P receptor protein; SP; neurotransmitter;
 KW neuromodulator; central nervous system; peripheral nervous system;
 KW gastrointestinal disorders; Inflammation; Immune disease.
 XX
 OS Homo sapiens.
 OS
 PN WO9303137-A.
 PN
 PD 18-FEB-1993.
 XX
 PF 05-AUG-1992; 92MO-US06532.
 XX
 PR 07-AUG-1991; 91US-0741200.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Krause JE;
 PI
 DR WPI: 1993-076495/09.
 DR
 XX New human substance P receptor protein and DNA encoding it - used
 PT e.g. for screening substance P antagonists
 XX

PS Example; Page 8; 40pp; English.

CC This sequence represents Tyr-1 substance P and was used in its
CC 125-Iodinated form in a ligand binding assay of COS-7 cells
CC transfected with substance P receptor coding plasmids (see AA037210).

XX Sequence 12 AA;

AA037298 Length: 46 April 1, 2002 16:31 Type: P Check: 4680 ..

1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO QRFGLM

!!AA_SEQUENCE 1.0

ID AAR42646 standard; peptide; 11 AA.

XX AAR42646;

DT 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide (Substance P).

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KM hormone; intra-operativ; tumour; low energy gamma photon;

XX radionuclide.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "the C-terminal is amidated"

XX W09318797-A.

PD 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI; 1993-320461/40.

PT Intra-operatively detecting and locating tumour tissues - using

XX specific peptide(s) labelled with low energy gamma photon

PT emitting radionuclide

XX Disclosure; Page 4; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral

CC tissues makes use of peptides having selective neurokinin 1

CC receptor affinity (AAR42644; generic formula: AAR42646-R42650;

CC specific examples), peptides having selective somatostatin

CC receptor affinity (AAR42645; generic formula: AAR42651-R42660;

CC specific examples), and peptides selected from cytokines,

CC growth factors and hormones.

XX Sequence 11 AA;

AA042646 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO FFLGLM

!!AA_SEQUENCE 1.0

ID AAR42647 standard; peptide; 11 AA.

XX AAR42647;

DT 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide.

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KM hormone; intra-operativ; tumour; low energy gamma photon;

XX radionuclide.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 9 /label= Megly

FT Modified-site 11 /note= "Met is Met(O2); the C-terminal is amidated"

XX W09318797-A.

PD 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI; 1993-320461/40.

PT Intra-operatively detecting and locating tumour tissues - using

XX specific peptide(s) labelled with low energy gamma photon

PT emitting radionuclide

XX Disclosure; Page 5; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral

CC tissues makes use of peptides having selective neurokinin 1

CC receptor affinity (AAR42644; generic formula: AAR42646-R42650;

CC specific examples), peptides having selective somatostatin

CC receptor affinity (AAR42645; generic formula: AAR42651-R42660;

CC specific examples), and peptides selected from cytokines,

CC growth factors and hormones.

XX Sequence 11 AA;

AA042647 Length: 45 April 1, 2002 16:31 Type: P Check: 1453 ..

1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO FFLGLM

!!AA_SEQUENCE 1.0

ID AAR42649 standard; peptide; 11 AA.

XX AAR42649;

DT 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide.

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KM hormone; intra-operativ; tumour; low energy gamma photon;

XX radionuclide.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "the C-terminal is amidated"

XX W09318797-A.

PD 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.
 XX Doedens BJ, Ensing GJ, Panek KT;
 XX WPI: 1993-320461/40.
 XX Intra-operatively detecting and locating tumour tissues - using
 PT specific peptides) labelled with low energy gamma photon
 PT emitting radionuclide
 XX
 PS Disclosure: Page 5; 31pp; English.
 XX
 CC The method of intraoperatively detecting and locating tumoral
 CC tissues makes use of peptides having selective neurokinin 1
 CC receptor affinity (AAR42644: generic formula: AAR42646-R42650:
 CC specific examples), peptides having selective somatostatin
 CC receptor affinity (AAR42645: generic formula: AAR42651-R42660:
 CC specific examples), and peptides selected from cytokines,
 CC growth factors and hormones.
 XX
 SQ Sequence 11 AA;

AAR42649 Length: 45 April 1, 2002 16:31 Type: P Check: 1520 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRKPQO FYGLM

!!AA_SEQUENCE 1.0
 ID AAR85243 standard; peptide; 11 AA.

AC AAR85243;

DT 18-AUG-1997 (first entry)

DE Substance P peptide.

XX Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
 KW Systematic Evolution of Ligands by Exponential enrichment; primer;
 KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
 KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
 KW diabetic retinopathy.

XX Synthetic.

OS Synthetic.

XX Key

FT Modified-site 11 Location/Qualifiers

FT Modified-site /note="contains C-terminal NH2 group"

PN W09530775-A1.

PD 16-NOV-1995.

PF 03-MAY-1995; 95WO-US05600.

XX 21-DEC-1994; 94US-0361795.

PR 06-MAY-1994; 94US-0238863.

PR 24-MAY-1994; 94US-0248632.

PR 09-SEP-1994; 94US-0303362.

PR 11-JUN-1990; 90US-0536428.

PR 10-JUN-1991; 91US-0714131.

PR 21-OCT-1992; 92US-0964624.

XX (UYRE-) UNIV RES CORP.

PA Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
 PI Schneider DJ, Sullenger BA, Wecker M;
 DR WPI: 1995-404132/51.

XX Systematic evolution of ligands by exponential enrichment - for
 PT identifying nucleic acid ligands used in the treatment of, e.g. type
 PT B insulin resistance and HIV
 XX

PS Example 10: Fig 8; 209pp; English.

XX The invention relates to a novel method of isolating ligands that bind
 CC to target proteins e.g. antibodies or receptors, which bind other
 CC proteins or ligands. The method, designated Systematic Evolution of
 CC Ligands by Exponential enrichment (SELEX), comprises generating a library
 CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
 CC and binding these sequences to the target proteins. After removal of
 CC unbound material, the remaining bound nucleotides sequences are amplified
 CC e.g. by PCR, and the newly amplified material is bound again with the
 CC target protein. This cycle continues until a sufficiently pure
 CC oligonucleotide sequence is isolated. The method allows the isolation of
 CC ligand. Ligands AAT06098-130 are examples of nucleic acid ligands which
 CC bind the tachykinin-family neuropeptide Substance P (this sequence). The
 CC new ligands were split into 2 groups based on their affinities for
 CC Substance P. Class 1 ligands had binding affinities up to 2 micromolar
 CC whereas class 2 ligands bound at above 2 micromolar. This sequence
 CC represents the consensus of the class 1 ligands. The ligands can be
 CC used to block the activity of Substance P and is useful in the treatment
 CC of e.g. rheumatoid arthritis, atherosclerosis, diabetic retinopathy or
 CC cancer.
 XX
 SQ Sequence 11 AA;

AAR85243 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRKPQO FYGLM

!!AA_SEQUENCE 1.0
 ID AAR85244 standard; peptide; 12 AA.

AC AAR85244;

DT 18-AUG-1997 (first entry)

DE Substance P analogue peptide Cys-SP.

XX Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
 KW Systematic Evolution of Ligands by Exponential enrichment; primer;
 KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
 KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
 KW diabetic retinopathy.

XX Synthetic.

OS Synthetic.

XX Key

FT Modified-site 1 Location/Qualifiers

FT Modified-site /note="Ac-Arg"

PN W09530775-A1.

PD 16-NOV-1995.

PF 03-MAY-1995; 95WO-US05600.

XX 21-DEC-1994; 94US-0361795.

PR 06-MAY-1994; 94US-0238863.

PR 24-MAY-1994; 94US-0248632.

PR 09-SEP-1994; 94US-0303362.

PR 11-JUN-1990; 90US-0536428.

PR 10-JUN-1991; 91US-0714131.

PR 21-OCT-1992; 92US-0964624.

XX (UYRE-) UNIV RES CORP.

PA Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
 PI Schneider DJ, Sullenger BA, Wecker M;
 DR WPI: 1995-404132/51.
 XX Systematic evolution of ligands by exponential enrichment - for
 PT identifying nucleic acid ligands used in the treatment of, e.g. type
 PT

PT B Insulin resistance and HIV
XX
PS Example 11; Fig 8; 209pp; English.
XX
CC The invention relates to a novel method of isolating ligands that bind
CC to target proteins e.g. antibodies or receptors, which bind other
CC proteins or ligands. The method, designated Systematic Evolution of
CC Ligands by Exponential enrichment (SELEX), comprises generating a library
CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
CC and binding these sequences to the target proteins. After removal of
CC unbound material, the remaining bound nucleotides sequences are amplified
CC e.g. by PCR, and the newly amplified material is bound again with the
CC target protein. This cycle continues until a sufficiently pure
CC oligonucleotide sequence is isolated. The method allows the isolation of
CC oligonucleotide sequences which structurally mimic the target protein's
CC ligand. This peptide represents an analogue of Substance P (AAR85243) in
CC which the N-terminal amine has been acylated in order to determine
CC whether this functional group interacts with nucleic acid ligands binding
CC substance P (see AAR06098-130). The ligands can be used to block the
CC activity of substance P and is useful in the treatment of e.g. rheumatoid
CC arthritis, atherosclerosis, diabetic retinopathy or cancer.
XX
SQ Sequence 12 AA;
AAR85244 Length: 46 April 1, 2002 16:31 Type: P Check: 3804 ..
1 SOARNDBCOE ZGHSQILKMF PSTWYVSGOT HERSRPRPQQ FGLMCG
!!AA_SEQUENCE 1.0
ID AAW09003 standard; peptide; 11 AA.
XX
AC AAW09003;
XX
DT 03-MAR-1997 (first entry)
XX
DE Substance P analogue, acts as substance P antagonist.
XX
XX
KM Analogue; substance P; spantide; non-peptide bond;
KM competitive inhibitor; receptor; neurogenic inflammation;
KM rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
KM anti-proliferative agent; small cell lung carcinoma; fibroblast.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 6..7
FT /label= Gln-psi[CH2-NH]-Phe
FT /note= "Opt. non-peptide linkage"
FT 7..8
FT /label= Phe-psi[CH2-NH]-Phe
FT /note= "Opt. non-peptide linkage"
FT 8..9
FT /label= Phe-psi[CH2-NH]-Gly
FT /note= "Opt. non-peptide linkage"
FT 9..10
FT /label= Gly-psi[CH2-NH]-Leu
FT /note= "Opt. non-peptide linkage"
FT 10..11
FT /label= Leu-psi[CH2-NH]-Leu
FT /note= "Position of claimed non-peptide linkage"
FT 11
FT /note= "Amidated C-terminal"
XX
XX
PN US5410019-A.
XX
PD 25-APR-1995.
XX
XX
PF 24-SEP-1987; 87US-0100571.
XX
XX 30-MAR-1992; 92US-0860675.
XX 24-SEP-1987; 87US-0100571.
PR 25-MAR-1988; 88US-0173311.
PR 08-JUN-1988; 88US-0204171.

PR 16-JUN-1988; 88US-0207759.
PR 23-SEP-1988; 88US-0248771.
PR 14-OCT-1988; 88US-0257998.
PR 09-DEC-1988; 88US-0282328.
PR 02-MAR-1989; 89US-0317941.
PR 16-AUG-1989; 89US-0394727.
PA (TULANE) TULANE EDUCATIONAL FUND.
XX
XX
PI Coy DH, Moreau J;
XX
XX WPI; 1995-169633/22.
DR
XX
XX Novel linear peptide substance P analogues - useful as substance P
PT antagonists, for treating neurogenic inflammation
XX
XX
PS Claim 3; Column 19, 16pp; English.
XX
XX The sequences given in AAW09003-04 represent analogues of substance P
CC and spantide, respectively. These analogues comprise a non-peptide
CC bond between an amino acid residue of the active site, which occurs
CC in the C-terminal half of the peptide, and an adjacent amino acid
CC residue. They act as competitive inhibitors of the naturally
CC occurring peptide by binding to its receptor. These peptides may be
CC used in the treatment of diseases involving neurogenic inflammation,
CC e.g. rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
CC disease. They are also useful as anti-proliferative agents, in
CC the treatment of small cell lung carcinoma or disorders involving the
CC proliferation of fibroblasts.
XX
SQ Sequence 11 AA;
AAW09003 Length: 45 April 1, 2002 16:31 Type: P Check: 677 ..
1 SOARNDBCOE ZGHSQILKMF PSTWYVSGOT HERSRPRPQQ FGLL
!!AA_SEQUENCE 1.0
ID AAW09004 standard; peptide; 11 AA.
XX
AC AAW09004;
XX
DT 03-MAR-1997 (first entry)
XX
XX
DE Spantide analogue, acts as substance P antagonist.
XX
XX
KM Analogue; substance P; spantide; non-peptide bond;
KM competitive inhibitor; receptor; neurogenic inflammation;
KM rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
KM anti-proliferative agent; small cell lung carcinoma; fibroblast.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 6..7
FT /label= Gln-psi[CH2-NH]-Trp
FT /note= "Opt. non-peptide bond, Claim 7"
FT 7..8
FT /note= "D-form residue"
FT 7..8
FT /label= Trp-psi[CH2-NH]-Phe
FT /note= "Opt. non-peptide bond, Claim 6"
FT 8..9
FT /label= Phe-psi[CH2-NH]-Trp
FT /note= "Opt. non-peptide bond"
FT 9
FT /note= "D-form residue"
FT Modified-site 9..10
FT /label= Trp-psi[CH2-NH]-Leu
FT /note= "Opt. non-peptide bond, Claim 4"
FT 10..11
FT /label= Leu-psi[CH2-NH]-Nle

FT	/note= "Opt. non-peptide bond, Claim 5"
FT	Modified-site 11
FT	/label= Nle
FT	/note= "amidated C-terminal"
XX	
PN	US5410019-A.
XX	
PD	25-APR-1995.
XX	
PF	24-SEP-1987; 87US-0100571.
XX	
PR	30-MAR-1992; 92US-0860675.
PR	24-SEP-1987; 87US-0100571.
PR	25-MAR-1988; 88US-017311.
PR	08-JUN-1988; 88US-0204171.
PR	16-JUN-1988; 88US-0207759.
PR	23-SEP-1988; 88US-0248771.
PR	14-OCT-1988; 88US-0257988.
PR	09-DEC-1988; 88US-0282328.
PR	02-MAR-1989; 89US-0317941.
PR	16-AUG-1989; 89US-0394727.
XX	
PA	(TULA) TULANE EDUCATIONL FUND.
XX	
PI	Coy DH, Moreau J;
XX	
DR	WPI: 1995-169633/22.
XX	
PT	Novel linear peptide substance P analogues - useful as substance P
PT	antagonists, for treating neurogenic inflammation
XX	
PS	Claim 4-7; Column 20; 16pp; English.
XX	
CC	The sequences given in AAM09003-04 represent analogues of substance P
CC	and spantide, respectively. These analogues comprise a non-peptide
CC	bond between an amino acid residue of the active site, which occurs
CC	in the C-terminal half of the peptide, and an adjacent amino acid
CC	residue. They act as competitive inhibitors of the naturally
CC	occurring peptide by binding to its receptor. These peptides may be
CC	used in the treatment of diseases involving neurogenic inflammation,
CC	e.g. rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
CC	disease. They are also useful as anti-proliferative agents, in
CC	the treatment of small cell lung carcinoma or disorders involving the
CC	proliferation of fibroblasts.
XX	
SQ	Sequence 11 AA;
AAM09004	Length: 45 April 1, 2002 16:31 Type: P Check: 2602 ..
1	SQARNDBQCE ZGHSQILKMF PSTWYVSOOT HERSRPKPOQ WFLX
11AA_SEQUENCE 1.0	
ID	AAR77310 standard; peptide; 11 AA.
XX	
AC	AAR77310;
XX	
DT	08-MAR-1996 (first entry)
XX	
DE	Substance P.
XX	
KM	Substance P; neurokinin; neurokinin receptor antagonist;
KM	sensory perception; tachykinin receptor; therapy;
KM	neurodegenerative disorder; Alzheimer's disease; demyelinating disease
KM	multiple sclerosis; respiratory disease; ophthalmic disease;
KM	addiction disorder; adverse immune reaction; gastrointestinal disorder
KM	bladder function disorder; fibrosing disease; collagen disease;
diagnosis.	
XX	
OS	Synthetic.
XX	
PH	Key Location/Qualifiers
FT	11
FT	Modified-site
FT	/note= "amidated"

XX	US5434158-A.
PN	
XX	18-JUL-1995.
PD	
XX	26-APR-1994; 94US-0233487.
PF	
XX	26-APR-1994; 94US-0233487.
PR	
XX	(MERI) MERCK & CO INC.
PA	
XX	Shah SK;
PI	
XX	WPI; 1995-268290/35.
DR	
XX	New 1'-subst.d. spiro-indoline-3,4'-piperidine derivs. - useful as
PT	selective neurokinin-3 antagonists, e.g. for treating CNS disorders,
PT	migraine or esp. asthma.
XX	
PS	Disclosure; Column 1; 16pp; English.
XX	
XX	This sequence represents Substance P. This sequence, and those shown in
CC	AA77311 and AA77312 are tachykinins. These three sequences are
CC	pharmacologically active neuropeptides, and are neurokinin receptor
CC	agonists. Neurokinin receptors are widely distributed throughout the
CC	mammalian nervous system, circulatory system and peripheral tissues.
CC	Neurokinin receptors are involved in sensory perception. These
CC	sequences were used in the design and testing of neurokinin antagonists.
CC	These antagonists could be used in the treatment of conditions
CC	characterised by overstimulation of tachykinin receptors. The
CC	antagonists can also be used, for the treatment of neurodegenerative
CC	disorders (e.g. Alzheimer's disease), demyinating diseases (e.g.
CC	multiple sclerosis), respiratory diseases, ophthalmic diseases, addiction
CC	disorders, adverse immune reactions, gastrointestinal disorders, bladder
CC	function disorders, fibrosis and collagen diseases. The antagonists can
CC	also be used as diagnostic agents.
XX	
XX	Sequence 11 AA;
SQ	
AA77310	Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1	SOANDECOE ZGHSQILKMF PSTWYVSQOT HENSRKPKQD PFGLM
11AA-SEQUENCE 1.0	
ID	AA74982 standard; peptide; 11 AA.
XX	
AC	AA74982;
XX	
DT	19-JAN-1996 (first entry)
XX	
XX	[D-Arg1, D-Phe5, D-Trp7,9, Leu11]-Substance P.
DE	
XX	
KW	Vasoactive intestinal peptide; VIP; conjunctiva; goblet cell;
KW	mucous secretion; keratoconjunctivitis; Sjogren's syndrome;
KW	vitamin A deficiency; anaesthetic cornea; Stevens-Johnson syndrome; eye;
KW	inactive trichoma; thermal burn; chemical burn; superior limb keratitis;
XX	drug induced pseudopemphigoid; atopic disease.
OS	
XX	Synthetic.
XX	
XX	Key Location/Qualifiers
FT	Misc-difference 1
FT	/note- "D-form residue"
FT	Misc-difference 5
FT	/note- "D-form residue"
FT	Misc-difference 7
FT	/note- "D-form residue"
FT	Misc-difference 9
FT	/note- "D-form residue"
XX	
PN	W09513087-A1.
XX	
PD	18-MAY-1995.

XX 10-NOV-1994; 94WO-US13084.
 PE
 XX
 PR 12-NOV-1993; 93US-0152175.
 XX
 PA (SCHE-) SCHEPENS EYE RES INST INC.
 XX
 PI Darlt DA, Kessler TL;
 XX
 DR WPI: 1995-193902/25.
 XX
 PT Treatment of aberrant conjunctival goblet cell mucous secretion - by
 PT topical or subcutaneous admin of, eg. dopamine, serotonin, Substance
 PR P or vasoactive intestinal peptide
 XX
 PS Claim 6; : 67pp; English.
 XX
 CC This sequence represents an analogue of substance P and is used in
 CC the method of the invention for the treatment of patients suffering
 CC from aberrant conjunctival goblet cell mucous secretion. This is
 CC associated with a disorder of, or injury to, the eye. The treatment
 CC is especially useful for treating keratoconjunctivitis, Sjogren's
 CC syndrome, vitamin A deficiency, anaesthetic cornea, Stevens-Johnson
 CC syndrome, inactive trachoma, thermal and chemical burns, drug induced
 CC pseudophthalmoid, atopic diseases and superior limb keratitis. This
 CC VIP analogue acts to stimulate the neural system.
 XX
 SQ Sequence 11 AA;

AA074982 Length: 45 April 1, 2002 16:31 Type: P Check: 1342 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPRY FFYL

!!AA_SEQUENCE 1.0
 ID AAW32620 standard; Protein; 220 AA.
 XX
 AC AAW32620;
 XX
 DT 28-JAN-1998 (first entry)
 XX
 DE Bacillus smithii nitrile hydratase subunit alpha.
 XX
 KW Nitrile hydratase subunit alpha; nitrile hydratase subunit beta;
 KW acrylonitrile; acryloamide; biological catalysis; amide;
 KW thermally stable protein.
 XX
 OS Bacillus smithii.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT Region 2..18
 FT /Label= N-terminal_sequence
 XX
 PN JP09248188-A.
 XX
 PD 22-SEP-1997.
 XX
 PF 18-MAR-1996; 96GP-0060732.
 XX
 PR 18-MAR-1996; 96GP-0060732.
 XX
 PA (SUMO) SUMITOMO CHEM CO LTD.
 XX
 DR WPI: 1997-520742/48.
 XX
 DR N-PSDB; AAT92381.
 XX
 PT Gene encoding nitrile hydratase - for producing amide from nitrile
 PT by biological catalysis
 XX
 PS Claim 1; Page 9; 16pp; Japanese.
 XX
 CC The present sequence represents nitrile hydratase subunit alpha, a

CC novel protein isolated from Bacillus smithii. The protein has hydration
 CC activity for converting acrylonitrile into acryloamide. It is useful
 CC for producing amide from nitrile by biological catalysis.
 XX
 SQ Sequence 220 AA;

AAW32620 Length: 254 April 1, 2002 16:31 Type: P Check: 4569 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSMAIECK LMDHHEVD
 51 REPNNHPPQ SFWEARAKAL ESLIEKRL SSDAIEVRK HYEELGPMN
 101 GAKVYAKAT DPEKQRLLE DPETVLELG YEGLOEHIR VVENTDTVHN
 151 VVVCITLCSY PMPILGLPPS WKKEPAVRSR VVKEPRKVLQ EFGDLDPDSV
 201 EIRWDSSE VRFMYLPORP EGTEGMTEEE LMQIVTRDSM IGVAKVOPPK
 251 VTQE
 !!AA_SEQUENCE 1.0
 ID AAW33181 standard; peptide; 11 AA.
 XX
 AC AAW33181;
 XX
 DT 29-JAN-1998 (first entry)
 XX
 DE Mono-DTPA-Lys1 Substance P.
 XX
 KW Substance P; radiolabel; diagnostic imaging; therapy;
 KW mono-DTPA-Lys1.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 11
 FT /note= "amidated"
 XX
 PN W09640292-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09706.
 XX
 PR 07-JUN-1995; 95US-0480372.
 XX
 PA (MLCW) MALLINCKRODT MEDICAL INC.
 XX
 PI Sriivasan A;
 XX
 DR WPI: 1997-087027/08.
 XX
 PT Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -
 PT by combining protected poly(amino:carboxylate) ligand with peptide
 PT and forming complex with radionuclide
 XX
 PS Example 4; Page 12; 20pp; English.
 XX
 CC Preparing a radiolabelled peptide composition, comprises combining
 CC a triamine or diamine chelating agent with a peptide, e.g. the
 CC present peptide, in a solid phase peptide synthesiser, and
 CC complexing a radionuclide with the chelate-peptide conjugate.
 CC Radiolabelled peptides or peptidomimetics can be used as diagnostic
 CC imaging agents, or in therapeutic applications, e.g. iodine(111)
 CC labelled pentetreotide can be used for somatostatin receptor
 CC imaging of neuroendocrine tumours. The radiolabelled products are
 CC obtained efficiently and inexpensively in high purity. The
 CC protected poly(amino:carboxylate) ligands can be added to the peptide
 CC by standard solution or solid phase peptide synthesis and
 CC deprotected with conventional reagents to give only the
 CC mono-addition product, free of di-addition product impurities. The

CC deprotected product can be labelled with medically useful
 CC radionuclides, e.g. lanthanides or actinides, at any desired
 CC location. Pre-derivatisation of individual amino acids is not
 CC required.

XX Sequence 11 AA;

AAW3181 Length: 45 April 1, 2002 16:31 Type: P Check: 477 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSKPRQO FFGIM

!!AA_SEQUENCE 1.0

ID AAW3180 standard; peptide; 11 AA.

AC AAW3180;

XX 29-JAN-1998 (first entry)

DE Mono-DTPA-Arg1 Substance P.

KW Substance P; radiolabel; diagnostic imaging; therapy;
 KW mono-DTPA-Arg1.

XX Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "DTPA-Arg"

FT Modified-site 11 /note= "amidated"

XX WO9640292-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09706.

XX 07-JUN-1995; 95US-0480372.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Srinivasan A;

XX WPI; 1997-087027/08.

PT Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging
 PT by combining protected poly(amino:carboxylate) ligand with peptide
 PT and forming complex with radionuclide

PS Example 3; Page 12; 20pp; English.

CC Preparing a radiolabelled peptide composition, comprises combining
 CC a triamine or diamine chelating agent with a peptide, e.g. the
 CC present peptide, in a solid phase peptide synthesiser, and

CC completing a radionuclide with the chelate-peptide conjugate.

CC Radiolabelled peptides or peptidomimetics can be used as diagnostic
 CC imaging agents, or in therapeutic applications, e.g. iodine(111)

CC labelling of neuroendocrine tumours. The radiolabelled products are
 CC obtained efficiently and inexpensively in high purity. The

CC protected polyaninocarboxylate ligands can be added to the peptide
 CC by standard solution or solid phase peptide synthesis and

CC deprotected with conventional reagents to give only the
 CC mono-addition product, free of di-addition product impurities. The

CC deprotected product can be labelled with medically useful
 CC radionuclides, e.g. lanthanides or actinides, at any desired

CC location. Pre-derivatisation of individual amino acids is not
 CC required.

XX Sequence 11 AA;

AAW3180 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSKPRQO FFGIM

!!AA_SEQUENCE 1.0

ID AAW26509 standard; Protein; 492 AA.

AC AAW26509;

XX 06-JAN-1998 (first entry)

DE Amyloid precursor protein substrate APP-REP 751.

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;

KW substrate; mutain; secretase; Alzheimer's disease; human;

KW APP-REP 751; PCLL602.

XX Chimeric Homo sapiens.

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Peptide 362..372

FT /label= SP

FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP

FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

FT /note= "secretase cleavage site"

FT Domain 417..440

FT /label= Transmembrane

FT Peptide 488..492

FT /label= ME

FT /note= "Met-enkephalin reporter epitope"

XX US5656477-A.

XX 12-AUG-1997.

XX 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobson JS, Vittek MP;

XX WPI; 1997-414594/38.

XX P-PSDB; AAT87083.

XX Nucleic acid encoding amyloid precursor muten(s) - comprising

XX reporter gene and coding sequence, for identifying compounds which

XX modify the activity of proteolytic enzymes which cleave APP

XX Disclosure; Fig 7; 84pp; English.

XX This polypeptide, designated APP-REP 761, comprises an amyloid

XX precursor protein (APP) that has a 276-amino acid deletion of the

XX native APP and which carries Substance P and Met-enkephalin epitope

XX markers placed, respectively, on the N-terminal and C-terminal

XX sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can

XX be used in a claimed method for screening for a compound which

XX reduces the formation of beta-amyloid protein, determined by

XX measuring the amount of marker in a medium containing transfected

XX cells. The method is used to detect compounds which inhibit the

XX activity of proteolytic enzymes which cleave APP to generate BAP

XX fragments. Such compounds can be used in the treatment of e.g.

XX Alzheimer's disease. The deletion of a 276 amino acid portion of

XX APP distinguishes the construct from endogenously expressed APP,

XX and beneficially increases the resolution of APP-REP fragments

XX resulting from the proteolytic cleavage by secretase or other

XX amyloidogenic, BAP-generating cleavage events.

XX Sequence 492 AA;

AAW26509 Length: 526 April 1, 2002 16:31 Type: P Check: 2172

```
1 SQARNDBCE ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAMTAR
51 ALEVPDNGA GLAEPQIAM FCGRLNMNM VONGKWDSP SGTKTCIDTK
101 EGILOYCOEV YPELQITNVV EANOPTIYN WCKRGKQCK THPHFVIPYR
151 CLVGEFVSIA LLVPDKCKFL HOERMDYCEI HLHMTVAKE TCSEKSTNLH
201 DYGMLLPGCI DKFRGVEFVC CPLAESDNV DSADAEEDS DVMWGADTD
251 YADGSEDKV EVAREEVEAE VEEBEADDE DDEGDDEVEE EAEPYEERAT
301 ERTTSIATTT TTTESVSEV VREVCSEQAE TGPCRAMISR WYFDYTEGKC
351 APFFYGGCGG NRRNFDTEBY CMAVCGSAIP TTAASTPDAY DKYLERPKQ
401 QFFGLMGSJT NIKTEEISEV KMDAEFRHDS GYEVHHQKLV FFAEDVGSNK
451 GAIIGLMWG VVIATVIYIT LVMLKKQYT SIHNGVEVD AAVTPEERHL
501 SKMQNGYEN PTYKFEQMO NYGSEF
```

```
!!AA_SEQUENCE 1.0
ID AAW26510 standard; Protein; 487 AA.
```

AC AAW26510;

DT 06-JAN-1998 (first entry)

DE Amyloid precursor protein substrate APP-REP 751.

KM Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutelin; secretase; Alzheimer's disease; human;
KM APP-REP 751; PCLL621.

OS Chimeric Homo sapiens.
OS Chimeric synthetic.

FH Key Location/Qualifiers

FT Peptide 362..372

FT /label= SP

FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP

FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

FT /note= "secretase cleavage site"

FT Domain 417..440

FT /label= Transmembrane

PM US5656477-A.

XX 12-AUG-1997.

PD 01-MAY-1992; 92US-0877675.

XX

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

PA

PI Jacobsen JS, Vitek MP;

XX WPI: 1997-414594/38.

DR P-PSDB: AAT87083.

XX Nucleic acid encoding amyloid precursor mutelin(s) - comprising
PT reporter gene and coding sequence; for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP
XX

PS Disclosure: Fig 8; 84pp; English.

XX This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries a substance P epitope markers placed
CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751
CC can be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.

CC Sequence 487 AA;

SQ AAW26510 Length: 521 April 1, 2002 16:31 Type: P Check: 8039

```
1 SQARNDBCE ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAMTAR
51 ALEVPDNGA GLAEPQIAM FCGRLNMNM VONGKWDSP SGTKTCIDTK
101 EGILOYCOEV YPELQITNVV EANOPTIYN WCKRGKQCK THPHFVIPYR
151 CLVGEFVSIA LLVPDKCKFL HOERMDYCEI HLHMTVAKE TCSEKSTNLH
201 DYGMLLPGCI DKFRGVEFVC CPLAESDNV DSADAEEDS DVMWGADTD
251 YADGSEDKV EVAREEVEAE VEEBEADDE DDEGDDEVEE EAEPYEERAT
301 ERTTSIATTT TTTESVSEV VREVCSEQAE TGPCRAMISR WYFDYTEGKC
351 APFFYGGCGG NRRNFDTEBY CMAVCGSAIP TTAASTPDAY DKYLERPKQ
401 QFFGLMGSJT NIKTEEISEV KMDAEFRHDS GYEVHHQKLV FFAEDVGSNK
451 GAIIGLMWG VVIATVIYIT LVMLKKQYT SIHNGVEVD AAVTPEERHL
501 SKMQNGYEN PTYKFEQMO N
```

```
!!AA_SEQUENCE 1.0
ID AAW26393 standard; Protein; 492 AA.
```

AC AAW26393;

DT 15-DEC-1997 (first entry)

DE Amyloid precursor protein substrate APP-REP 751.

KM Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutelin; secretase; Alzheimer's disease; human;
KM APP-REP 751; PCLL602.

OS Chimeric Homo sapiens;
OS Chimeric synthetic.

FH Key Location/Qualifiers

FT Peptide 362..372

FT /label= SP

FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP

FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

FT /note= "secretase cleavage site"

FT Domain 417..440

FT /label= Transmembrane

FT Peptide 488..492

FT /label= ME

FT /note= "Met-enkephalin reporter epitope"
XX
XX US5652092-A.
PN 29-JUL-1997.
PD 01-MAY-1992; 92US-0877675.
PF 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
PR 05-JUN-1995; 95US-0462859.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
PI WPI: 1997-392937/36.
DR N-PSDB; AAT84561.
XX
XX Screening for compounds which reduce beta-amyloid protein formation
PT - using cells which express a construct encoding a marker and an
PT amyloid precursor muten derived from APP isoforms
XX
XX Disclosure; Fig 7; 84pp; English.
XX
XX This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries Substance P and Met-enkephalin epitope
CC markers placed, respectively, on the N-terminal and C-terminal
CC sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can
CC be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.
XX
XX Sequence 492 AA:
SQ
AAM26393 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..
1 SQARNDBCQ ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAMTAR
51 ALEVPIDGNA GLAEPQIAM FCGRLNMNMN VQNGKNDSP SGTKTCTDTR
101 EGILOYCOEV YPELOITNVV EANOPIYIION WCKRGKRQCK TIRPHVIPIR
151 CLVGEFVSDA LLVPDKCKFL HOERMDVCET HLHWHVAKK TCSEKSTNLH
201 DYGMILPCGI DKFRGVEFVC CPLAESDNV DSADAEEDS DVMWGADTD
251 YADGSEDKV EVAREEVAA VEEEDADDE DDEDSGEVEE EAREPYEAT
301 ERTTSATTT TTTTSEVEE VREYCSQAE TQPCRAMISR WFDVTEGKC
351 ABFFYGGCGG NRNMPTDEEY CMAVCGSAIP TTAASTPDAY DYLERPKPO
401 OFEGLMGSLT NIKTEISEV KMDAEFRHDS GYEVNHOKLV FPAEDGSKK
451 GALTGLMVG VVIATVIVIT LVMLKKOYT SIHNGVEVD AAVTPEERHL
501 SKMQONGYEN PTYKFEQMQ NYGGFM
!!AA SEQUENCE 1.0
ID AAM26394 standard; Protein: 487 AA.
XX
XX AAM26394;
XX

DI 15-DEC-1997 (first entry)
XX
XX Amyloid precursor protein substrate APP-REP 751.
DE
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease; human;
KW APP-REP 751; PCL621.
XX
XX Chimeric Homo sapiens;
OS Chimeric synthetic.
XX
XX Key location/Qualifiers
FH 362..372
FT /label= SP
FT /note= "substance P reporter epitope"
FT 389..430
FT Domain /label= BAP
FT /note= "beta-amyloid protein"
FT Cleavage-site 404..405
FT /note= "secretase cleavage site"
FT Domain 417..440
FT /label= Transmembrane
XX
XX US5652092-A.
PN 29-JUL-1997.
PD 01-MAY-1992; 92US-0877675.
PF 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
PR 05-JUN-1995; 95US-0462859.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
PI WPI: 1997-392937/36.
DR N-PSDB; AAT84562.
XX
XX Screening for compounds which reduce beta-amyloid protein formation
PT - using cells which express a construct encoding a marker and an
PT amyloid precursor muten derived from APP isoforms
XX
XX Disclosure; Fig 8; 84pp; English.
XX
XX This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries a Substance P epitope markers placed
CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751
CC can be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.
XX
XX Sequence 487 AA:
SQ
AAM26394 Length: 521 April 1, 2002 16:31 Type: P Check: 8039 ..
1 SQARNDBCQ ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAMTAR
51 ALEVPIDGNA GLAEPQIAM FCGRLNMNMN VQNGKNDSP SGTKTCTDTR
101 EGILOYCOEV YPELOITNVV EANOPIYIION WCKRGKRQCK TIRPHVIPIR
151 CLVGEFVSDA LLVPDKCKFL HOERMDVCET HLHWHVAKK TCSEKSTNLH

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201 DYGMLLPCCI DKFRGEFVC CPLAESDNV DSADAEEDDS DVMGSGADTD
251 YAQSGEDKIV EVAEEBEVAE VEEBEADDE DDEGDDEVEE EAEPEFEAT
301 ERTTSIAFTT TTTTESVEEV VREVCSEAE TGPCRAMISR WFDVTEGKC
351 APEFYGGJGG NNNNPDTEEV CMAVCGSAIP TTAASTPDAY DKYLERPKPQ
401 QPFGLMGSLT NIKTEISEV KMDAEFRHDS GYEVHQKLV FFAEDVGSNK
451 GAIIGLMVGG VVIATYIVIT LVMLKKOYT SIHHGVEVD AAVTPEERHL
501 SKMQONGTEN PTKPFEDMOQ N

!!AA_SEQUENCE 1.0
ID AAM16339 standard; protein; 401 AA.
XX
AC AAM16339;
XX
DT 05-SEP-1997 (first entry)
XX
DE DAB389-SP-Gly fusion toxin.
XX
KM DAB389-SP-Gly; amidated polypeptide binding ligand; drug delivery;
XX diptheria toxin; substance P; cancer; therapy.
XX
OS Synthetic.
XX
PN WO9713410-A1.
XX
PD 17-APR-1997.
XX
PF 11-OCT-1996; 96WO-US16237.
XX
PR 13-OCT-1995; 95US-0005431.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Fisher CE, Leeman SE, Murphy JR, Vanderspek JC;
XX WPI, 1997-235583/21.
XX DR N-PSDB; AAT63359.
XX
XX
XX Hybrid molecule for targeting compound, especially a toxin, into
XX cells - includes polypeptide able to transport the compound across
XX cytoplasmic membranes and amidated ligand, useful for treatment of
XX cancer
XX
XX Example 1; Page 22-23; 51pp; English.
XX
XX DAB389-SP-Gly (AAM16339) is a hybrid toxin comprising DAB389 (i.e.
XX amino acids 1-386 plus His-484 and Ala-485 of mature diptheria
XX toxin) fused to C-terminal glycine-extended substance P. It was
XX expressed in E. coli HMS174(DE3) transformants using a vector
XX that carried DAB389-SP-Gly DNA (see also AAT63359). The fusion
XX protein was then amidated using peptidylglycino-alpha-amidating
XX monooxygenase. The amidated fusion protein used to target DAB389
XX toxin to specific cells contg. substance P receptors, esp. cancer
XX cells. For human IM9 (chronic myelogenous leukaemia) cells contg.
XX approx. 4000 substance P receptors per cell, the IC50 for amidated
XX DAB389-SP-Gly was 18 pM.
XX
SQ Sequence 401 AA;

```

AAM16339 Length: 435 April 1, 2002 16:31 Type: P Check: 9887 ..

```

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSMGADVY VDSKSEFVME
51 NFSSTHGTRP GYVDSIQKGI QPKSGTQGN YDDDMKGFYS TONKXDAAY
101 SVNENFELSG KAGGVYKVTY PGLTKVLALK VDNAETIKKE LGISTLEPLM

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151 EQVTEEFIRK RFQDGASRYV LSLPFAEGSS SVEYINNMEQ AKALSYELEI
201 NFETRCKRGQ DAMYEMAQA CAGNRVRSY GSSLSCINLD MWYIRKXTIT
251 KISLKEHCP IKNMSESPN KTVSEERAKQ YLEEFHOTAL EHPEISELKT
301 VTGTPVYFAG ANYAAMVNV AQVIDSETAD NLEKTPAALS ILPGISVNG
351 IADGAVHHNT EEIVASIAL SLMVAQAIP LVGELVDIGF AAVNFVESII
401 NLFQYVHNSY NRPATSPGKH THARPKPOOF FGLMG

!!AA_SEQUENCE 1.0
ID AAM04616 standard; peptide; 11 AA.
XX
AC AAM04616;
XX
DT 13-AUG-1997 (first entry)
XX
DE Substance P peptide for mass spectrometry analysis.
XX
KM Mass spectrometry; polymer analysis; biopolymer analysis.
XX
OS Synthetic.
XX
PN WO9636986-A1.
XX
PD 21-NOV-1996.
XX
PF 17-MAY-1996; 96WO-US071146.
XX
PR 19-MAY-1995; 95US-0447175.
XX PR 19-MAY-1995; 95US-0446055.
XX
PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.
XX
PI Patterson DH, Tarr GE;
XX WPI, 1997-012308/01.
XX
XX
XX Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
XX etc. - by obtaining mass to charge ratios of polymer fragments,
XX pref. using mass spectrometer, and performing statistical analysis
XX
XX Example 2; Page 32; 86pp; English.
XX
XX A method of obtaining sequence information about a polymer (e.g. DNA,
XX RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
XX comprising monomers of known mass has been claimed. The present
XX sequence represents a substance P peptide, and was used as
XX an example as a digestion before analysis by mass spectrometry,
XX using this novel on-plate strategy. Total sequence information
XX from a nine well digestion can be represented in a single digestion or
XX it is often derived from two or more wells. The methods, apparatus and
XX kit (claimed) can be used for the analysis of polymers, particularly
XX biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
XX and carbohydrates. It provides a rapid, automated and cost effective
XX sequencing of polymers, with a statistical certainty.
XX
SQ Sequence 11 AA;

```

AAM04616 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSRPRKPOQ FGLM

```

!!AA_SEQUENCE 1.0
ID AAM79775 standard; peptide; 11 AA.
XX
AC AAM79775;
XX
DT 07-JAN-1999 (first entry)
XX
DE Substance P.

```


DR WPI: 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX Disclosure: Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFDWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue, spantide I.
CC
SQ Sequence 11 AA;
AAW50966 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO WFWLL

!!AA_SEQUENCE 1.0
ID AAW50968 standard; peptide; 11 AA.
AC AAW50968;

DT 31-JUL-1998 (first entry)

DE Substance P analogue, [D-Pro2,D-Phe7,D-Trp9].

XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KM spantide.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NATM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

XX WPI: 1998-208959/19.

PT Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)

XX Disclosure: Page 13; 49pp; English.
PS
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFDWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
CC
SQ Sequence 11 AA;
AAW50966 Length: 45 April 1, 2002 16:31 Type: P Check: 1410 ..

1 SQARNDCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO WFWLL

!!AA_SEQUENCE 1.0
ID AAW50969 standard; peptide; 11 AA.
AC AAW50969;

DT 31-JUL-1998 (first entry)

DE Substance P analogue, [D-Pro2,D-Trp7,9].

XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KM spantide.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NATM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

XX WPI: 1998-208959/19.

PS Disclosure: Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFDWKPTSDC (3-14 disulphide bridge),
CC and for inhibiting over-expression of these peptide(s)

CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA:

AAW50969 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO WFWLM

!!AA_SEQUENCE 1.0
ID AAW50972 standard; peptide: 11 AA.

AC AAW50972:

DT 31-JUL-1998 (first entry)

XX Substance P analogue, [D-Arg1,D-Phe5,D-Trp7,9,Leu11].

KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KM Substance P; cancer; inhibition; growth hormone releasing factor;
XX spantide.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

XX WPI: 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

XX Disclosure: Page 13; 49pp; English.

CC The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFRDKRTPSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin

CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA:

AAW50972 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO WFWLL

!!AA_SEQUENCE 1.0
ID AAW50958 standard; peptide: 11 AA.

AC AAW50958:

DT 31-JUL-1998 (first entry)

XX Substance P analogue, [D-Arg1,D-Pro2,D-Trp7,9,Leu11]-substance P.

KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KM Substance P; cancer; inhibition; growth hormone releasing factor.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

XX WPI: 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

XX Disclosure: Page 12; 49pp; English.

CC The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFRDKRTPSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour

CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

XX
XX Sequence 11 AA;

AAW50958 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSRPPQQ WFWLL

!!AA_SEQUENCE 1.0

ID AAW50942 standard; peptide; 11 AA.

AC AAW50942;

XX 31-JUL-1998 (first entry)

XX Substance P antagonist (SP1).

XX Vasactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX Substance P; cancer; inhibition.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-size 13 /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

XX WPI: 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

XX Claim 1: Page 4; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
XX somatostatin analogue SOM2 AGCARNFDMKPTSDC (3-14 disulphide bridge),
XX and (ii) at least 4 of the peptides: antagonist of vasoactive
XX intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX more general compositions containing peptide analogues of somatostatin,
XX VIP, bombesin and substance P. The compositions are used in human or
XX veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
XX or cancer cells, particularly for treatment of leukaemia, lymphoma,
XX adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
XX breast, kidney or particularly rectum and colon, and (b) to prevent,
XX inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer

CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents substance P antagonist (SP1).

XX
XX Sequence 11 AA;

AAW50942 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSRPPQQ WFWLL

!!AA_SEQUENCE 1.0

ID AAW44744 standard; Protein; 492 AA.

AC AAW44744;

XX 01-JUN-1998 (first entry)

XX APP-REP 751 protein from PCLL602.

XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX Alzheimer's disease; cleavage.

XX Homo sapiens.

XX Synthetic.

XX US5693478-A.

XX 02-DEC-1997.

XX 05-JUN-1995; 95US-0464247.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX 05-JUN-1995; 95US-0464247.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vittek MP;

XX WPI: 1998-031744/03.

XX N-PSDB; AAW05849.

XX Amyloid precursor muten reporter molecule assay containing antibody
XX recognised marker - used to study pathways associated with
XX Alzheimer's disease

XX Disclosure; Fig 7; 84pp; English.

XX This is the amino acid sequence of a novel amyloid precursor protein
XX (APP) designated APP-REP 751, contained in construct PCLL602. The
XX sequence comprises a mutant version of the APP 751 isoform of human APP
XX which contains a deletion of 276 amino acids from the central region.
XX The deleted region is replaced by a substrate P reporter epitope sequence
XX (RPPQDFGLM) and a Met-enkephalin reporter epitope (YGGK) is fused at
XX the C-terminus. The shorter protein is generated for ease of detection
XX based on size difference with the wild type APP protein and also by
XX detection of the reporter epitopes. The mutant protein can be used in
XX a method to study secretase and beta-amyloid protein (BAP)-generating
XX pathways associated with Alzheimer's disease by studying proteolytic
XX cleavage of the reporter polypeptides.

XX Sequence 492 AA;

AAW44744 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSMLPGIA LLLAAMTAR

51 ALEVPDNGNA GLAEPQIAM FCGRLNMNM VQNGKMDSDP SGTKTCTIDTK

101 EGLYQCGEV YPELQITNVV EANOPTIYN WCKRGKQCK TPNHVIPIYR

151 CLVGEFVSDA LLYPDCKFL HQERMVCEY HLHWHTVAKE TCSEKSTNLH

201 DYGMLLPGCI DKFRGVEFVC CPLAEESDNV DSADAEEDDS DVMWGADTD
 251 YADGSEDKV EVAREEVAE VEEEDADDE DDEGDEVEE EAERPEEAT
 301 ERTSIATTT TTTSVEEV VREVCSEQAE TGPCRAMISR WYFDTEGKC
 351 APFYGGCGG NNNNFDTEY CMAVCSAIP TTAASTPDV DKYLERPRQ
 401 QFFGLMGLT NIKTEISEV KMDAEPHDS GYEVHOKLV FFAEDVGSNK
 451 GAIGLWGG VVIATVIYIT LVMLKKQYT SIHGVVEVD AAVTPEERHL
 501 SKMQNGYEN PTYKFEQMO NYGGM

!!AA_SEQUENCE 1.0
 ID AAM44745 standard; Protein: 487 AA.
 AC AAM44745;
 DT 01-JUN-1998 (first entry)
 DE APP-REP 751 protein from pCLL621.
 XX
 KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US5693478-A.
 PD 02-DEC-1997.
 XX
 PF 05-JUN-1995; 95US-0464247.
 XX
 PR 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 PR 05-JUN-1995; 95US-0464247.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 DR N-PSDB; AAV05850.
 XX
 PT Amyloid precursor muten reporter molecule containing antibody
 PT recognised marker - used to study pathways associated with
 PT Alzheimer's disease
 XX
 PS Disclosure: Fig 8; 84pp; English.
 XX
 CC This is the amino acid sequence of a novel amyloid precursor protein
 CC (APP) designated APP-REP 751, contained in construct pCLL621. The
 CC sequence comprises a mutant version of the APP 751 isoform of human APP
 CC which contains a deletion of 276 amino acids from the central region.
 CC The deleted region is replaced by a substrate P reporter epitope
 CC sequence (RRPRQDFGLM). In contrast to the APP-REP 751 encoded by the
 CC construct pCLL602 (AAM44744), this sequence does not contain a
 CC Met-enkephalin reporter epitope (YGGFM) fused at the C-terminus of the
 CC coding sequence. The shorter protein is generated for ease of detection
 CC based on size difference with the wild type APP protein and also by
 CC detection of the reporter epitopes. The mutant protein can be used in a
 CC method to study secretase and beta-amyloid protein (BAP)-generating
 CC pathways associated with Alzheimer's disease by studying proteolytic
 CC cleavage of the reporter polypeptides.
 XX
 SQ Sequence 487 AA;

AAM44745 Length: 521 April 1, 2002 16:31 Type: P Check: 8039

1 SOARNDBOE ZGHSQILKMF PSTWVSQOT HERSMLPGIA LLLLAWTAR

51 ALEVPDNGA GLLABQIAM FCGRLNMHN YONGKWDSDP SGTKCIDTK
 101 BGLIOQCEV YPELOITNV EANOPTION WCKRGKQCK THPHVITYR
 151 CLVGEFVSDA LLVPDKCKFL HOERMDVCEY HLHMTVAKE TCSEKSTLH
 201 DYGMLLPGCI DKFRGVEFVC CPLAEESDNV DSADAEEDDS DVMWGADTD
 251 YADGSEDKV EVAREEVAE VEEEDADDE DDEGDEVEE EAERPEEAT
 301 ERTSIATTT TTTSVEEV VREVCSEQAE TGPCRAMISR WYFDTEGKC
 351 APFYGGCGG NNNNFDTEY CMAVCSAIP TTAASTPDV DKYLERPRQ
 401 QFFGLMGLT NIKTEISEV KMDAEPHDS GYEVHOKLV FFAEDVGSNK
 451 GAIGLWGG VVIATVIYIT LVMLKKQYT SIHGVVEVD AAVTPEERHL
 501 SKMQNGYEN PTYKFEQMO N

!!AA_SEQUENCE 1.0
 ID AAM42978 standard; Protein: 492 AA.
 AC AAM42978;
 DT 01-MAY-1998 (first entry)
 DE Amyloid precursor protein mutant APP-APP 751.
 XX
 KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5703209-A.
 PD 30-DEC-1997.
 XX
 PF 05-JUN-1995; 95US-0464248.
 XX
 PR 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 DR N-PSDB; AAV04865.
 XX
 PT Amyloid precursor protein fusion polypeptides - comprising APP
 PT fragment and marker, useful for research and drug screening
 XX
 PS Disclosure: Fig 7A-Q; 84pp; English.
 XX
 CC The present sequence represents an amyloid precursor protein (APP),
 CC which has a deletion of 276 amino acids to within 15 amino acids of the
 CC beta-amyloid peptide (BAP) domain. The protein also contains the
 CC Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimers
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).

CC APP is expressed as an integral membrane protein, and is cleaved by
CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
CC amyloidogenesis and results in the release of the amino-terminal APP
CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
CC APP-770. These isoforms are derived by alternative splicing. APP-RPP 751
CC is constructed by ligating restriction fragments representing N- and
CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
CC APP can be used as a substrate for studying abnormal proteolytic cleavage
CC which results in the release of BAP, and also to screen for drugs that
CC will inhibit such cleavage.

XX Sequence 492 AA:

AA042978 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..

1 SQARNBCE ZGHSQILKMF PSTWVSQOT HERSMLPGLA LLLAAMTAR
51 ALEVPTDGNM GLAEPQIAM FCGRLNMNM VQNGKWDSP SGTKTCIDTK
101 EGILOYCEY YPELOITNV EANOPTIOM WCKRGKOCK THPHVIYR
151 CLVGEFVSDA LLYPDCKFL HQERMDYCEI HLHMTVAKE TCSEKSTNLH
201 DYGMILPCGI DKRGVEFVC CPLAESDNV DSADAEEDS DVMGAGADTD
251 YADGSEDKVY EVAEEEVAAE VEEEDADDE DDEGDVEEE EAEPEYEAT
301 ERTTSIATTT TTTESVEEV VREYCSQAE TGPCRAMISR WYFDTEGKC
351 APPEYGGCGG NRNFDTBEY CMAVCGSAIP TTAASPPDAV DYLBRRPKQ
401 QPEGLMGSLT NIKTEISEV KMDAEFRHDS GYEVHOKLY FFAEDVGSNK
451 GAIIGLMVGG VVIATVIVIT LVMLKKQYT SIHNGVEVD AAVTBERHL
501 SKMQNGYEN PTYKFEQMO NYGCFM

IIAA_SEQUENCE 1.0

ID AAM42979 standard; Protein; 487 AA.

XX AAM42979;

XX 01-MAY-1998 (first entry)

XX Amyloid precursor protein mutant APP-APP 751.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KM cerebrovascular deposit; Alzheimers disease; Downs syndrome;

KW amyloid precursor protein; APP; secretase; BAP aggregation;

KW abnormal proteolytic cleavage.

XX OS Synthetic.

OS Homo sapiens.

XX US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-0464248.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1998-076482/07.

XX N-PSDB; AAV04866.

XX Amyloid precursor protein fusion polypeptides - comprising APP

XX fragment and marker, useful for research and drug screening

PS Disclosure; Fig 8A-Q; 84pp; English.

XX The present sequence represents an amyloid precursor protein (APP),
CC which has a deletion of 276 amino acids to within 15 amino acids of the
CC beta-amyloid peptide (BAP) domain. The protein also contains the abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
CC is characteristic in brains of individuals suffering from Alzheimers
CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
CC protein which is derived from a larger amyloid precursor protein (APP).
CC APP is expressed as an integral membrane protein, and is cleaved by
CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
CC amyloidogenesis and results in the release of the amino-terminal APP
CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
CC APP-770. These isoforms are derived by alternative splicing. APP-RPP 751
CC is constructed by ligating restriction fragments representing N- and
CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
CC APP can be used as a substrate for studying abnormal proteolytic cleavage
CC which results in the release of BAP, and also to screen for drugs that
CC will inhibit such cleavage.

XX Sequence 487 AA:

AA042979 Length: 521 April 1, 2002 16:31 Type: P Check: 8039 ..

1 SQARNBCE ZGHSQILKMF PSTWVSQOT HERSMLPGLA LLLAAMTAR
51 ALEVPTDGNM GLAEPQIAM FCGRLNMNM VQNGKWDSP SGTKTCIDTK
101 EGILOYCEY YPELOITNV EANOPTIOM WCKRGKOCK THPHVIYR
151 CLVGEFVSDA LLYPDCKFL HQERMDYCEI HLHMTVAKE TCSEKSTNLH
201 DYGMILPCGI DKRGVEFVC CPLAESDNV DSADAEEDS DVMGAGADTD
251 YADGSEDKVY EVAEEEVAAE VEEEDADDE DDEGDVEEE EAEPEYEAT
301 ERTTSIATTT TTTESVEEV VREYCSQAE TGPCRAMISR WYFDTEGKC
351 APPEYGGCGG NRNFDTBEY CMAVCGSAIP TTAASPPDAV DYLBRRPKQ
401 QPEGLMGSLT NIKTEISEV KMDAEFRHDS GYEVHOKLY FFAEDVGSNK
451 GAIIGLMVGG VVIATVIVIT LVMLKKQYT SIHNGVEVD AAVTBERHL
501 SKMQNGYEN PTYKFEQMO N

IIAA_SEQUENCE 1.0

ID AAM42979 standard; Protein; 11 AA.

XX AAM42973;

XX 01-MAY-1998 (first entry)

XX Substrate P reporter epitope.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KM cerebrovascular deposit; Alzheimers disease; Downs syndrome;

KW amyloid precursor protein; APP; secretase; BAP aggregation;

KW abnormal proteolytic cleavage; substrate P reporter epitope.

XX OS Synthetic.

XX US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-0464248.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;
XX WPI; 1998-076482/07.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP
PT fragment and marker, useful for research and drug screening
XX
PS Disclosure; Column 3; 84pp; English.
XX
CC Peptid sequence AAM42978 represents an amyloid precursor protein (APP),
CC which has a deletion of 276 amino acids to within 15 amino acids of the
CC beta-amyloid peptide (BAP) domain. The protein also contains the
CC Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular
CC deposits is characteristic in brains of individuals suffering from
CC Alzheimer's disease and Downs syndrome. BAP is a poorly soluble,
CC self-aggregating protein which is derived from a larger amyloid precursor
CC protein (APP). APP is expressed as an integral membrane protein, and is
CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
CC precludes amyloidogenesis and results in the release of the
CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
CC APP-751 and APP-770. These isoforms are derived by alternative splicing.
CC APP-RFP 751 is constructed by ligating restriction fragments representing
CC N- and C-terminal APP-751 cDNA and substrate P reporter epitope
CC sequences (present sequence) APP can be used as a substrate for studying
CC abnormal proteolytic cleavage which results in the release of BAP, and
CC also to screen for drugs that will inhibit such cleavage.
XX
SQ Sequence 11 AA;
AAM42973 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRKQO FFGML
!!AA_SEQUENCE 1.0
ID AAY30985 standard; peptide; 11 AA.
XX
AC AAY30985;
XX
DT 21-OCT-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 34.
XX
KM Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
XX albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
XX /note="C-terminal amide"
XX
PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PE 12-NOV-1996; 96US-0747137.
XX
PR 14-MAR-1994; 94US-0212546.
PR 15-JAN-1991; 91US-0641720.
PR 13-OCT-1992; 92US-0959560.
PR 01-JUN-1993; 93US-0069831.
PR 12-NOV-1996; 96US-0747137.
XX
PA (HMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI; 1999-508153/42.
XX
XX Non-crosslinked protein particles for therapeutic and diagnostic use
XX
XX Example 22; Column 63-64; 65pp; English.

XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
XX
SQ Sequence 11 AA;
AAY30985 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRKQO FFGML
!!AA_SEQUENCE 1.0
ID AAY34864 standard; Protein; 218 AA.
XX
AC AAY34864;
XX
DT 13-SEP-1999 (first entry)
XX
DE Chlamydia pneumoniae transmembrane protein sequence.
XX
KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KM vaccine; neutralising epitope.
XX
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PE 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffiths R;
XX
DR WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae
XX
PS Page 809-810; Disclosure; 1912pp; English.
XX
CC AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX
SQ Sequence 218 AA;
AAY34864 Length: 252 April 1, 2002 16:31 Type: P Check: 8364 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRKQO GYPSYPAKK

51 LAQLEPGALT LVKHNDRF PKETLAFRIV DHSVAREIVD HCGTLIGTSA
101 NLSEPPSALT AQEIFADPAD HDLCIFDGPC SHGLESTYVA SDPLYTYREG
151 LISRSVIEI AGTEAKIFHR TSHAFSKHK IYTVKNQEOI VSFLSGLDF
201 KGVCSEHPPR KNEYTRLREA LKRRTPSIYF IYDINTSDYP ELFPFLSPY
251 IE

!!AA_SEQUENCE 1.0
ID AAY13564 standard; Protein: 1381 AA.

AC AAY13564;
XX 30-JUL-1999 (first entry)
DT Drosophila Robo 2 polypeptide.
XX
XX Comm polypeptide; Robo polypeptide; commissureless; roundabout;
KW modulation; nerve cell function.
XX
XX Drosophila sp.
XX WO9925833-A1.
XX 27-MAY-1999.
XX 13-NOV-1998; 98WO-US24327.
XX 14-NOV-1997; 97US-0065543.
PR (REGC) UNIV CALIFORNIA.
XX
XX Goodman C, Kidd T, Mitchell KJ, Russell C, Tear G;
DR N-PSDB: AAX55768.
XX
PT Modulation of Robo-Comm polypeptide interactions
PS Disclosure: Page 34-38; 56pp; English.
XX

The invention relates to a method for modulating the amount of Comm (commissureless) polypeptide in contact with a cell expressing active Robo (roundabout) on its surface. The method comprises modulating the effective amount of Comm polypeptide in contact with the cell, where the amount of expressed active Robo is specifically modulated inversely with the modulation of the effective amount of Comm in contact with the cell. The method is used to modulate the amount of active Robo expressed on a cell. The method can be used to screen for agents that modulate Robo:Comm interactions. This is particularly useful for modulating nerve cell function.

XX Sequence 1381 AA;

AAY13564 Length: 1415 April 1, 2002 16:31 Type: P Check: 940 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVYSQOT HERSGENPRI IEHMDTIVP
51 KNDPTEFKQ AEQNPTPTIQ WFKDGRLEKT DTGSHRIMLP AGGLEFLKVI
101 HSRRESDAGT YMCAKNEFG VARSNATLQ VAVLRDEFRL EPANTRVAOG
151 EVALMEGAP RGSPEQISW RKNQOTLNV GKKRIRIVDG GNLAIOEHRQ
201 SDDGTYQV VV KNYVGTRESA TAPLKVHVR FLIRPQNOT AVVGSSVVEQ
251 CRIGGDPAPD VLMRRTASG NMLRKFSWL HSASGRVHL EDRSLKLDYV
301 TLEDGGETTC EADNAVGIT ATGILTIVHAP PKFVIRPKNO LVEIGDEVLF

351 ECQANGHPPR TLIWVSREGNS SLLLPGRDG RMEVTLTPEG RSVLSIARFA
401 REDSGKVYTC NALNAVGSVS SRTVVSVDIQ FELPPRIHQ GPVNOQLPVK
451 STIVLPCRTL GTPVPQVSWY LDIPIPIVOE HERRNISDAG ALITSDLORH
501 EDEGLYTCVA SNRNGKSSWS GYLRLDPTN PIKFEFRAD LSTYGPBGK
551 PQWKEGENS VTLSTRSNK VGGSSLYGY IMFGEKNET GWVAVGTRVQ
601 NTTFTOTGLL PGVNYFFLIR AENSHGISLP SPMSERTYTG TRYNSGLDL
651 SEARASLSG DVELSNASV VDSTSMKLW QIINGKYEG FYVYAROLPN
701 PIVNPPAPVT SNTNPLDGT STSASASASA SALISTKPI AAAGKROGET
751 NOSGGAPTP LNTKYRMITI LINGGASSCT ITGLVOYITLY EFFIVPTKS
801 VEGKPSNSRI ARTLEDVPE APYGMALLL NSSAVFLKWK APELDRHGV
851 LLNYHIVRG IDTAHNSRI LTNVTIDAAS PTLVLANLTE GMYTVGVAA
901 GNNAGVPGYC VPATRLRDPIT TKRLDEPIHQ RQHVNDVLTO PWFITLLGAI
951 LAVLMLSEGA MVEYKRRHM MKQSAINTMR GHTSDVILKM PSLARNNG
1001 YWLDSTGGM VMRPSGDS LEMQKDIAD YAPVCGAPGS PAGGTSISGG
1051 SGGAGSGASG GDDIHGHS ERNQORYGE YSNIPDYAE VSSGKAPSE
1101 YGRHGNASPA PYATSSILSP HQOQOQOQPR YQORVPYGY LQRPMPHYQ
1151 QOOHQOQOAO QTHQOHALQ OHQQLPPSNI YQOMSTSEI YPTNTPRSR
1201 YSEQYIYYPK DKQRIHTE NKLNSCHTE AAPGAKQSSP ISSQFASVRR
1251 QQLPNCSTG RESARFVYN TDQKNOQNL LDLDSSMCY NGLDSCGG
1301 SPSPMAMLMS HEDERALYHT ADGDLDMMER LYVKYDEQOP PQOQOQLIPL
1351 VPQHAEGHL QSMRNOSTRS SRKNGOECIK EPELIIYAPG SVASERSILS
1401 NSGCTSSOP AGHNV

!!AA_SEQUENCE 1.0
ID AAY08402 standard; Protein: 1380 AA.

AC AAY08402;
XX 24-JUL-1999 (first entry)
DT Drosophila sp. ROBO2 extracellular domain protein.
XX
XX
KW ROBO1, ROBO2; roundabout; nerve guidance; human; murine; cell function;
KW cell morphology; screening assay.
XX

XX Drosophila sp.

XX WO9920764-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-US22164.

XX 14-NOV-1997; 97US-0971172.

XX 20-OCT-1997; 97US-0062921.

PA (REGC) UNIV CALIFORNIA.

XX Goodman CS, Kidd T, Mitchell KJ, Tear G;

XX WPI: 1999-312615/26.

DR N-PSDB: AAX57251.

XX Robo polypeptides, a new immunoglobulin superfamily member
PT
XX
PS Claim 1: Page 52-56; 80pp; English.
XX
CC This invention describes novel Robo (roundabout) polypeptides, involved
CC in nerve guidance which have been isolated from *Drosophila* sp.,
CC *C. elegans*, human and murine samples. The products of the invention can
CC be used to raise anti-Robo antibodies, which can be used to modulate cell
CC function or morphology. The Robo polynucleotides and fragments are useful
CC as probes and primers and for production of the Robo polypeptides. The
CC probes and primers are also useful in screening assays.
XX
SQ Sequence 1380 AA;

AAV08402 Length: 1414 April 1, 2002 16:31 Type: P Check: 7245 ..

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSGENPRI IEHPMDTVP
51 KNDPTFNCQ AEGNPTPTIQ WFKDGRRLKT DTGSHRIMLP AGGLFELKVI
101 HSRRESDAQT YWCEAKNEFG VARSRNATLQ VAVLRDEFRL EPANTRVAG
151 EVALMECGAP RGSPEPOISW RKNQOTLNLV GNNRIRIVDG GNIAIQEARQ
201 SDDGRYOCVY KNVGCTRESA TAFLLKVHVR FLIRGPONQT AVGSSVVFQ
251 CRIGGDPDLP VLWRTTASGG NMPLRKFSWL HSASGRVHVL EDRSLKLDDV
301 TLEDMEGYTC EADNAVGCIT ATGILTVHAP PKFVIRPKNO LVEIGDEVLP
351 ECOANGHPRP TLYWSEEGNS SILLPGRDG RMEVTLTPEG RSVLSIARPA
401 REDSGKVYVC NALNAVGSVS SRTVVSVDIQ FELPPIIEG GVNQTLPIK
451 STVILPCRTL GTPVPOVSWY LDGIPIDVQE HERRNLSDAG ALTIIDLORH
501 EDEGLTYCVA SNRNGKSSMS GYLRLDPTPN PNKFFRAPE LSTYGPPEK
551 PQWKEGENS VTLSTRTSKN VGSLSLVGY IEMFGNEND GWAVAGTRVQ
601 MTTFTOTGIL PGVNYFELLIR AENSHGLSLP SPSEPTIYWG TYRNSGLDL
651 SEARASILSG DVELSNASV VDSSTMKLTW QIINGRYVEG FYVYARQLPN
701 PIYNNAPAPT SNTNPLDGT STSASASASA SALISRKPN IAAAGRDGET
751 NMSGGAPTP LNTKYRMLTI LNSGGASCT ITGLVOYTYL EEFIYPEYKS
801 VEGKPSNSRI ARTLEDVPS E APYGMEALLL NSSAVFLKWK APELDRHGV
851 LNTYHYIVG IDTAINFSRI LTNVTIDAAS PTLVIANLTE GMYTYGVAA
901 GNNAGVGYC VPATLRLOPI TKRLDPTINQ RDHVNDVLTO PMFTILLGAI
951 LAVLMLSPGA WVFYKRKHMM MKGALNTMR GNHTSDVLKM PLSARNGNG
1001 YMLDSSTGGM VWRSPSGDS LEMOKDHIAD YAPVCCAPGS PAGGATSSCG
1051 SGGAGSGASG GDDIHGHGS ERNOORYVE YSNIPTDYAE VSSFGKAPSE
1101 YGRHGNASPA PYATSSILSP HQOQOQOOPR YQORPVGYG LQRPMPHYQ
1151 QOQHQQOQAO QTHQHQAQO QHQAQLPSNI YQOMSTTSEI YPTNCPSPS
1201 VYSEQYYRK DKORHIHEN KLSNCHTEA APGAKOSSPI SSQFASVRQ
1251 QLEPNCISGR ESARFKVLNT DQGNQOQML DLDGSSMCYN GLADSGCGS
1301 PSPMAMLMGH EDEHALYHTA DGDLDMDERL YKVVDEQPP QQQOQLIPLY
1351 PQHPABGHQ SWRNOSTRNS RKNQOEIKE PSELIYAPGS VASERSLSN
XX

1401 SCSGTSSQPA GHNV

11AA_SEQUENCE 1.0
ID AAV03156 standard; peptide; 11 AA.

AAV03156;

10-JUN-1999 (first entry)

Substance P.

Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
substance P.

Synthetic.

US5891842-A.

06-APR-1999.

12-APR-1996; 96US-0631434.

09-APR-1993; 93US-0044954.

12-APR-1996; 96US-0631434.

(TUFT) TUFTS COLLEGE.

Kream RM;

WPI; 1999-253906/21.

Synergistic method for enhancing opioid analgesia and anaesthesia
within a human

Disclosure; Column 14; 20pp; English.

This sequence represents substance P used in the method of the
invention. The method is for enhancing opioid analgesia within a human
subject for a duration of 15 minutes comprises concurrent administration
of substance P, or one of its precursors. The method is used to elicit
opioid analgesia and anaesthesia, either prior to or after the occurrence
of a nociceptive event. The components have a synergistic effect. The
method allows use of low doses of opioid that produce little or no
physiological effect reducing conventional risks of toxicity and
addiction, and allows the use of low doses of substance P and its related
analogs that limit their in vivo physiological consequences. The
analgesia is naloxone reversible allowing diminishment or complete
elimination of opioid analgesia if desired and on demand. The treatment
provides a durable analgesic effect, but only minimally disturbs and
interrupts the normal metabolic processes of the body.

Sequence 11 AA;

AAV03156 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSRPRQQ FFGIM

11AA_SEQUENCE 1.0
ID AAV03157 standard; peptide; 12 AA.

AAV03157;

10-JUN-1999 (first entry)

Substance P-Glycine.

Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
substance P.

Synthetic.

US5891842-A.

XX

PD 06-APR-1999.
XX
PF 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Kream RM:
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 12 AA;
AA03157 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FPLGMG
11AA_SEQUENCE 1.0
ID AAY03158 standard; peptide; 13 AA.
XX
AC AAY03158;
XX
DT 10-JUN-1999 (first entry)
XX
DE Substance P-Glycine-Lysine.
XX
KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
PF 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Kream RM:
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.

CC This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 13 AA;
AA03158 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FPLGMG
11AA_SEQUENCE 1.0
ID AAY03159 standard; peptide; 14 AA.
XX
AC AAY03159;
XX
DT 10-JUN-1999 (first entry)
XX
DE Substance P-Glycine-Lysine-Arginine.
XX
KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
PF 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Kream RM:
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 14 AA;
AA03159 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBOCE ZGHSQILKMF PSTWVYSQOT HERSRPRKPOQ FFGLMGKR
11AA_SEQUENCE 1.0
ID AAY03162 standard; peptide: 9 AA.
XX
AC AAY03162;
XX
DT 10-JUN-1999 (first entry)
XX
DE Substance P fragment P/1-9#.
XX
DE Substance P fragment P/1-9#.
XX
KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
PE 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
FI Kream RM:
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence is a fragment of substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 9 AA:
AAY03162 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
1 SQARNDBOCE ZGHSQILKMF PSTWVYSQOT HERSRPRKPOQ FFG
11AA_SEQUENCE 1.0
ID AAW99689 standard; peptide: 11 AA.
XX
AC AAW99689;
XX
DT 03-JUN-1999 (first entry)
XX
DE Substance P analogue #6.
XX
KW Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Modified-site 10. 11
FT FT /note= "Leu-psi(CH2-NH)-Leu"
FT Modified-site 11
FT FT /note= "amidated"
XX
PN W09907413-A1.
XX
PD 18-FEB-1999.
XX
PE 26-MAY-1998; 98WO-US10707.
XX
PR 11-AUG-1997; 97US-0055233.
XX
PA (ALGO-) ALGOS PHARM CORP.
XX
PI Caruso FS;
XX
DR WPI; 1999-167216/14.
XX
PT New analgesic composition comprises - a substance P receptor
PT antagonist with a substance P receptor antagonist potentiator, used
PT for the treatment of pain
XX
PS Claim 3; Page 29; 54pp; English.
XX
CC A method has been developed for treating pain with: (a) a substance P
CC receptor antagonist; and (b) a substance P receptor antagonist
CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
CC substance that blocks at least 1 major intracellular consequence of
CC NMDA receptor activation. The method can be used for treating muscular,
CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
CC sequence represents a substance P analogue for use in the method.
XX
SQ Sequence 11 AA:
AAW99689 Length: 45 April 1, 2002 16:31 Type: P Check: 677 ..
1 SQARNDBOCE ZGHSQILKMF PSTWVYSQOT HERSRPRKPOQ FFGLL
11AA_SEQUENCE 1.0
ID AAW99690 standard; peptide: 11 AA.
XX
AC AAW99690;
XX
DT 03-JUN-1999 (first entry)
XX
DE Substance P analogue #7.
XX
KW Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT FT /note= "D-form residue"
FT Misc-difference 7
FT FT /note= "D-form residue"
FT Misc-difference 9
FT FT /note= "D-form residue"
FT Modified-site 9. 10
FT FT /note= "Trip-psi(CH2-NH)-Leu"
FT Modified-site 11
FT FT /label= Nle
FT FT /note= "Norleucine, amidated"
XX
PN W09907413-A1.
XX
PD 18-FEB-1999.
XX
PE 26-MAY-1998; 98WO-US10707.
XX

XX 11-AUG-1997; 97US-0055233.
 PR (ALGO-) ALGOS PHARM CORP.
 PA Caruso FS;
 PI WPI; 1999-167216/14.
 DR
 XX New analgesic composition comprises - a substance P receptor
 PT antagonist with a substance P receptor antagonist potentiator, used
 PT for the treatment of pain
 PS Claim 3; Page 29; 54pp; English.
 CC A method has been developed for treating pain with: (a) a substance P
 CC receptor antagonist; and (b) a substance P receptor antagonist or
 CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
 CC substance that blocks at least 1 major intracellular consequence of
 CC NMDA receptor activation. The method can be used for treating muscular,
 CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
 CC sequence represents a substance P analogue for use in the method.
 SQ Sequence 11 AA;
 AAM99690 Length: 45 April 1, 2002 16:31 Type: P Check: 2602 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWYSQOR HERSRKPQO WFWLX
 IIAA_SEQUENCE 1.0
 ID AAM99691 standard; peptide; 11 AA.
 AC AAM99691;
 XX
 DT 03-JUN-1999 (first entry)
 XX
 DE Substance P analogue #8.
 XX
 XX Substance P :receptor antagonist; analgesic; inhibitor; NMDA blocker;
 KM nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
 KM musculoskeletal pain; chronic pain; neuropathic pain; migraine.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-sits 7.8 /note= "Trp-psl(CH2-NH)-Phe"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /label= Nle
 FT /note= "Norleucine, amidated"
 FT
 XX WO9907413-A1.
 PN 18-FEB-1999.
 XX
 PD 26-MAY-1998; 98WO-US10707;
 XX
 PF 11-AUG-1997; 97US-0055233.
 PR
 XX (ALGO-) ALGOS PHARM CORP.
 PA Caruso FS;
 PI WPI; 1999-167216/14.
 DR
 XX New analgesic composition comprises - a substance P receptor
 PT antagonist with a substance P receptor antagonist potentiator, used

PT for the treatment of pain
 XX
 PS Claim 3; Page 29; 54pp; English.
 CC A method has been developed for treating pain with: (a) a substance P
 CC receptor antagonist; and (b) a substance P receptor antagonist or
 CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
 CC substance that blocks at least 1 major intracellular consequence of
 CC NMDA receptor activation. The method can be used for treating muscular,
 CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
 CC sequence represents a substance P analogue for use in the method.
 SQ Sequence 11 AA;
 AAM99691 Length: 45 April 1, 2002 16:31 Type: P Check: 2602 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWYSQOR HERSRKPQO WFWLX
 IIAA_SEQUENCE 1.0
 ID AAM74445 standard; Protein; 1184 AA.
 XX
 AC AAM74445;
 XX
 DT 12-MAY-1999 (first entry)
 XX
 DE Human nucleotide pyrophosphohydrolase, NTPPH-1.
 XX
 KM NTPPH-1; human: nucleotide pyrophosphohydrolase; arthropathy; therapy;
 KM immunological disorders; cancer; haemodialysis; infection;
 KM extracorporeal circulation.
 XX
 OS Homo sapiens.
 XX
 PN US5876963-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-AUG-1997; 97US-0918914.
 XX
 PR 27-AUG-1997; 97US-0918914.
 XX
 PA (HUTC/) HUTCHINSON N.
 PA (LANT/) LANTON M.
 PA (MAGN/) MAGNA H.
 PA (MITC/) MITCHELL P.
 PA (MURR/) MURRY L E.
 PA (YOCU/) YOCUM S.
 XX
 PI Hutchinson N, Lanton M, Magna H, Mitchell P, Murry LE;
 PI Yocum S;
 DR WPI; 1999-189634/16.
 XX
 DR N-PSDB; AAX18449.
 XX
 PT New human nucleotide pyrophosphohydrolase - useful for providing
 PT methods for identifying and treating arthropies, immunological
 PT disorders, and cancer
 PS Claim 1; Fig 1; 42pp; English.
 XX
 CC This sequence represents the human nucleotide pyrophosphohydrolase,
 CC designated NTPPH-1, of the invention. NTPPH-1 antagonists, antibodies,
 CC agonists, proteins, complementary sequences or vectors can be used to
 CC treat and identify arthropathies (e.g. calcium pyrophosphate dihydrate
 CC deposition disease, degenerative joint disease, fibromyalgias,
 CC haemochromatosis, osteoarthritis, progressive systemic sclerosis,
 CC pseudogout, psoriasis, Rheumatoid arthritis and lupus erythematosus);
 CC immunological disorders (e.g. AIDS, allergies, anaemia, asthma,
 CC ulcerative colitis, dermatomyositis, diabetes mellitus, emphysema,
 CC glomerulonephritis, gout, multiple sclerosis, osteoporosis and
 CC pancreatitis), trauma; complications of cancer, haemodialysis, and
 CC extracorporeal circulation; viral, bacterial, fungal, parasitic,
 CC protozoal, and helminthic infections; and cancer (e.g. adenocarcinoma,

CC lymphoma, melanoma, myeloma, sarcoma, leukaemia, or teratocarcinoma of
 CC the bone and bone marrow, brain, breast, cervix, gastrointestinal tract,
 CC kidney, liver, lung, ovary, testis and skin).

SO Sequence 1184 AA;

AAW74445 Length: 1218 April 1, 2002 16:31 Type: P Check: 9834 ..

```

1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSWVGTRKA WVFELVLEV
51 TSVLGRQTML TQSVRRYQPG KKNPSIFAPK ADLTLESPEW TTMNIDIPG
101 GKGDYERLDA IREYYGDRVC ARPLRLAERT TDWTPAGSTG QVYHGSPEG
151 FMCINREQRP GQNCNNTVR PLCPPGSLRR DTERIWPMS PWSKCSAAG
201 QTGVQTRIRI CLAEWVSLCS EASEGQCHM GODCTACDLT CPMQOVNADC
251 DACMCOEML HGAWSLPGGA PASGAAYLL TKTPLLTQT DSDGRFRIPG
301 LCPDGKSLK ITKVRFAPIV LIMPRTSLKA ATIKAEFRA ETPYMWNPPE
351 TKRARGOSV SLCCKATGKP RPDKYFWYHN DTLDPISLYK HESKLVLRKL
401 QOHQAGEYFC KAQSDAGAVK SKVAQLIVIA SDETPCNPVP ESYLIRLPHD
451 CPOANTNSFY YDVGRCPVKT CAGQDNGIR CRDAVQNCG ISKIEEREIO
501 CSGYTLPTKV AKECSCQCT ETRSIVRGRV SAADNGEPMR FGHVYMGNSR
551 VSMGYKGFCT TLHVQDTER LVLTFFVDRLO KFNNTTKVLP FNKKGSAVFH
601 EIKMKCRKEP ITLEAMETNI IPLGEVVGED PMAELEISR SFYQNGEPEY
651 IGKVKASVTF LDPRNISTAT AAOCTDLNFIN DEGDFEPLRT YGMSVDFRD
701 EYTSLEPLNAG KVKVHLDSTQ VKMPEHISTV KLMSINPDGT LMEBEGDFKF
751 ENQRRNKRED RTFLVGNLEI RERRLFNLDV PESRRCFVKV RAYISERLPL
801 SEQIOGVVIS VINLEPRTGF LSNPRAMGRF DSVITGPNGA CVPAFCDDQS
851 PDVASAYVLA SLAGEELQAV ESSPKFNPNA IGVPOPYLTK LNYRTDHD
901 PRVKRTAFOI SMAKPRNSA EESNGPIYAF ENLRACEEAR PSAHFRFYQ
951 IEGDRYDINT VPENEDDPMs WTEDYLAAMP KMEFRACYI KVKIVGPLEV
1001 NVRSNMGCT HRTVGRKLYG IRDVRSTRDR DQPNVSACL EFKCSGMLYD
1051 QDRVORTLVK VIIPGSCRA SVNPMLEHYL VNHLPYLVANN DTSEYTMAR
1101 LDPLGHNTGI YTYVDQDPT AKELIAGRCF DGTSGSSSI MKNVCAVLT
1151 FNCVERQYGR QSAFOYLQST PAQSPAAGTV QGRVPSRQO RASRGQROS
1201 GVVASLREPR VAQOPLIN

```

!!AA_SEQUENCE 1.0
 ID AAW92709 standard; peptide: 11 AA.

AAW92709;

30-APR-1999 (first entry)

Human tachykinin agonist beta-amyloid peptide fragment #55.

Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

Alzheimer's disease; Down's syndrome; amyloidosis; human;

hereditary cerebral haemorrhage; non-inherited congenital anglopathy.

Homo sapiens.

XX

Key Location/Qualifiers
 Modified-site 9
 /label= Megly
 /note= "N-methyl-glycine (sarcosine)"
 Modified-site 11
 /note= "Residue is Met(O2)"

US5876948-A.

02-MAR-1999.

27-JUL-1991; 91US-0737371.

29-JUL-1991; 91US-0737371.

27-JUL-1990; 90US-0559173.

(CHIL-) CHILDRENS MEDICAL CENT.

Yankner BA;

WPI: 1999-189630/16.

Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amyloid peptide neurotoxic effect on neuronal cells

Disclosure: Column 35-36; 28pp; English.

This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease, Down's syndrome, and the syndromes of hereditary cerebral haemorrhage with amyloidosis and non-inherited congenital anglopathy with cerebral haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human beta-amyloid peptide fragments.

Sequence 11 AA;

AAW92709 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSRPKPOQ FFGIX

!!AA_SEQUENCE 1.0
 ID AAW92711 standard; peptide: 8 AA.

AAW92711;

30-APR-1999 (first entry)

Human tachykinin agonist beta-amyloid peptide fragment #57.

Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

Alzheimer's disease; Down's syndrome; amyloidosis; human;

hereditary cerebral haemorrhage; non-inherited congenital anglopathy.

Homo sapiens.

US5876948-A.

02-MAR-1999.

27-JUL-1991; 91US-0737371.

29-JUL-1991; 91US-0737371.

27-JUL-1990; 90US-0559173.

(CHIL-) CHILDRENS MEDICAL CENT.

Yankner BA;

WPI: 1999-189630/16.

XX

PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PS Disclosure: Column 35-36; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX Sequence 8 AA;

SO AAM92711 Length: 42 April 1, 2002 16:31 Type: P Check: 860 ..

1 SCARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FF

!!AA_SEQUENCE 1.0
ID AAM92715 standard; peptide; 11 AA.
AC AAM92715;
XX 30-APR-1999 (first entry)
XX Human tachykinin agonist beta-amyloid peptide fragment #61.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 10
FT /label= Mewet
FT /note= "N-methyl-leucine"
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
PI
XX WPI: 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure: Column 37-38; 28pp; English.

AAM92715 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SCARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGM

!!AA_SEQUENCE 1.0
ID AAM92716 standard; peptide; 11 AA.
AC AAM92716;
XX 30-APR-1999 (first entry)
XX Human tachykinin agonist beta-amyloid peptide fragment #62.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
PI
XX WPI: 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure: Column 37-38; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

SO AAM92716 Length: 45 April 1, 2002 16:31 Type: P Check: 898 ..

1 SCARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGPM

!!AA_SEQUENCE 1.0
ID AAM92717 standard; peptide; 11 AA.
AC AAM92717;
XX 30-APR-1999 (first entry)
XX Human tachykinin agonist beta-amyloid peptide fragment #63.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 11
FT /label= Mewet

```

FT      /note= "N-methyl-methionine"
XX
XX      US5876948-A.
XX
XX      02-MAR-1999.
XX
XX      27-JUL-1991; 91US-0737371.
XX
XX      29-JUL-1991; 91US-0737371.
XX      27-JUL-1990; 90US-0559173.
XX
XX      (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX      Yankner BA;
XX
XX      WPI; 1999-189630/16.
XX
XX      Screening for neurotoxin inhibitors - by testing compounds for their
XX      effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX      Disclosure; Column 37-38; 28pp; English.
XX
XX      This invention describes a method for screening compounds for inhibiting
XX      a neurotoxin. The method involves incubating tachykinin agonists with
XX      neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX      used for identifying compounds for treating diseases characterised by an
XX      undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX      Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX      with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX      haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX      beta-amyloid peptide fragments.
XX
XX      Sequence 11 AA;
XX
XX      AAW92717 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..
XX
XX      1 SQARNDBOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGIX
XX
XX      !!AA_SEQUENCE 1.0
XX      ID AAW92718 standard; peptide: 11 AA.
XX
XX      AAW92718;
XX
XX      30-APR-1999 (first entry)
XX
XX      Human tachykinin agonist beta-amyloid peptide fragment #64.
XX
XX      Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX      Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX      hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX      Homo sapiens.
XX
XX      US5876948-A.
XX
XX      02-MAR-1999.
XX
XX      27-JUL-1991; 91US-0737371.
XX
XX      29-JUL-1991; 91US-0737371.
XX      27-JUL-1990; 90US-0559173.
XX
XX      (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX      Yankner BA;
XX
XX      WPI; 1999-189630/16.
XX
XX      Screening for neurotoxin inhibitors - by testing compounds for their
XX      effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX      Disclosure; Column 37-38; 28pp; English.
XX

```

```

CC      This invention describes a method for screening compounds for inhibiting
CC      a neurotoxin. The method involves incubating tachykinin agonists with
CC      neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC      used for identifying compounds for treating diseases characterised by an
CC      undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC      Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC      with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC      haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC      beta-amyloid peptide fragments.
XX
XX      Sequence 11 AA;
XX
XX      AAW92718 Length: 45 April 1, 2002 16:31 Type: P Check: 857 ..
XX
XX      1 SQARNDBOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLP
XX
XX      !!AA_SEQUENCE 1.0
XX      ID AAW92719 standard; peptide: 11 AA.
XX
XX      AAW92719;
XX
XX      30-APR-1999 (first entry)
XX
XX      Human tachykinin agonist beta-amyloid peptide fragment #65.
XX
XX      Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX      Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX      hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX      Homo sapiens.
XX
XX      Key Location/Qualifiers
XX      Modified-site 9 /label= Methyl
XX      FT /note= "N-methyl-glycine"
XX
XX      US5876948-A.
XX
XX      02-MAR-1999.
XX
XX      27-JUL-1991; 91US-0737371.
XX
XX      29-JUL-1991; 91US-0737371.
XX      27-JUL-1990; 90US-0559173.
XX
XX      (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX      Yankner BA;
XX
XX      WPI; 1999-189630/16.
XX
XX      Screening for neurotoxin inhibitors - by testing compounds for their
XX      effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX      Disclosure; Column 39-40; 28pp; English.
XX
XX      This invention describes a method for screening compounds for inhibiting
XX      a neurotoxin. The method involves incubating tachykinin agonists with
XX      neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX      used for identifying compounds for treating diseases characterised by an
XX      undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX      Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX      with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX      haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX      beta-amyloid peptide fragments.
XX
XX      Sequence 11 AA;
XX
XX      AAW92719 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
XX
XX      1 SQARNDBOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
XX
XX      !!AA_SEQUENCE 1.0
XX

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```

ID AAW92720 standard; peptide; 11 AA.
XX
XX AAW92720;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #66.
DE
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 10
FT /label= Melen
FT /note= "N-methyl-leucine"
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI
XX
XX WPI; 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 39-40; 28pp; English.
PS
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX
XX Sequence 11 AA;
SQ
AAW92720 Length: 45 April 1, 2002 16:31 Type: P Check: 722
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAW92721 standard; peptide; 11 AA.
XX
XX AAW92721;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #67.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 11
FT /label= Melen
FT

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FT
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI
XX
XX WPI; 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 39-40; 28pp; English.
PS
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX
XX Sequence 11 AA;
SQ
AAW92721 Length: 45 April 1, 2002 16:31 Type: P Check: 898
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGPM
11AA_SEQUENCE 1.0
ID AAW92708 standard; peptide; 11 AA.
XX
XX AAW92708;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #54.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 7
FT /note= "Modification results in p-chloro-Phe"
FT Modified-site 8
FT /note= "Modification results in p-chloro-Phe"
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI
XX
XX WPI; 1999-189630/16.
DR

```


XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure: Column 33-34; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAW92708 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBQOE ZGHSQILKMF PSTWYSQOT HERSRPRQO FFGLM

!!AA_SEQUENCE 1.0
ID AAW92677 standard; peptide; 11 AA.
XX
AC AAW92677;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #23.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure: Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAW92677 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..

1 SQARNDBQOE ZGHSQILKMF PSTWYSQOT HERSRPRQO FFGLM

!!AA_SEQUENCE 1.0
ID AAW92678 standard; peptide; 11 AA.
XX
AC AAW92678;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #24.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 9 /note="D-form residue"
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure: Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAW92678 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..

1 SQARNDBQOE ZGHSQILKMF PSTWYSQOT HERSRPRQO FFGLM

!!AA_SEQUENCE 1.0
ID AAW92679 standard; peptide; 11 AA.
XX
AC AAW92679;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #25.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.

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XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 21-22; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
AAM92679 Length: 45 April 1, 2002 16:31 Type: P Check: 254 ..
1 SQARNDBQCE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAM92680 standard; peptide; 11 AA.
XX
XX AAM92680;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #26.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 8
XX FT /note= "Residue is N-methyl-phenylalanine"
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 21-22; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
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CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
AAM92680 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBQCE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAM92681 standard; peptide; 11 AA.
XX
XX AAM92681;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #27.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 8
XX FT /note= "Residue is N-methyl-glycine"
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 21-22; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
AAM92681 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBQCE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAM92682 standard; peptide; 11 AA.
XX
```

```

AC AAM92682;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #28.
DE
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
XX
XX Disclosure; Column 21-22; 28pp; English.
XX
XX
XX This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
XX
XX AAM92682 Length: 45 April 1, 2002 16:31 Type: P Check: 4
XX
XX 1 SCARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPCQ FFCIM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAM92683 standard; peptide; 11 AA.
XX
XX AAM92683;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #29.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 5 /note= "Residue is homocysteine"
XX Modified-site 9 /note= "Residue is homocysteine"
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX

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PF 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 23-24; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
XX
XX AAM92683 Length: 45 April 1, 2002 16:31 Type: P Check: 1726
XX
XX 1 SCARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPXQ FFCIM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAM92684 standard; peptide; 11 AA.
XX
XX AAM92684;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #30.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 5 /note= "Residue is homocysteine"
XX Modified-site 10 /note= "Residue is homocysteine"
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 23-24; 28pp; English.
XX

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CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAW92664 Length: 45 April 1, 2002 16:31 Type: P Check: 1523 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRPXQ FPGXM

11AA_SEQUENCE 1.0
ID AAW92685 standard; peptide; 11 AA.

AC AAW92685;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #31.

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 23-24; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting

XX a neurotoxin. The method involves incubating tachykinin agonists with

XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

XX used for identifying compounds for treating diseases characterised by an

XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

XX with amyloidosis and non-inherited congenophilic angiodopathy with cerebral

XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

XX beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAW92665 Length: 45 April 1, 2002 16:31 Type: P Check: 9726 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRPXQ FPGLC

11AA_SEQUENCE 1.0

ID AAW92686 standard; peptide; 11 AA.

AC AAW92686;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #32.
DE
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified-site 5 /note= "Residue is homocysteine"

FT Modified-site 11 /note= "Residue is homocysteine"

FT FT

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 23-24; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting

XX a neurotoxin. The method involves incubating tachykinin agonists with

XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

XX used for identifying compounds for treating diseases characterised by an

XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

XX with amyloidosis and non-inherited congenophilic angiodopathy with cerebral

XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

XX beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAW92686 Length: 45 April 1, 2002 16:31 Type: P Check: 1490 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRPXQ FPGIX

11AA_SEQUENCE 1.0

ID AAW92665 standard; peptide; 9 AA.

AC AAW92665;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #11.

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

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PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 15-16; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 9 AA;
AAW92665 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFG
!!AA_SEQUENCE 1.0
ID AAW92666 standard; peptide; 11 AA.
XX
AC AAW92666;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #12.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 15-16; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

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XX
SQ Sequence 11 AA;
AAW92666 Length: 45 April 1, 2002 16:31 Type: P Check: 1501 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO YFGLM
!!AA_SEQUENCE 1.0
ID AAW92667 standard; peptide; 11 AA.
XX
AC AAW92667;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #13.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note="Residue is ethionine"
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 15-16; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;
AAW92667 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFG
!!AA_SEQUENCE 1.0
ID AAW92668 standard; peptide; 11 AA.
XX
AC AAW92668;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #14.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

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KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 11 /Label= Nle
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA:
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 15-16; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA:
AAW92668 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..
1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPKPOQ FFGIX
!!AA_SEQUENCE 1.0
ID AAW92674 standard; peptide; 11 AA.
XX
AC AAW92674;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #20.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA:
XX
DR WPI; 1999-189630/16.

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XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA:
AAW92674 Length: 45 April 1, 2002 16:31 Type: P Check: 464 ..
1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPKPOQ FFALM
!!AA_SEQUENCE 1.0
ID AAW92675 standard; peptide; 11 AA.
XX
AC AAW92675;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #21.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 9 /note="D-form residue"
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA:
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA:

```

AAW92675 Length: 45 April 1, 2002 16:31 Type: P Check: 464 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFLM

!!AA_SEQUENCE 1.0

ID AAW92676 standard; peptide: 11 AA.

AC AAW92676;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #22.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 9 /label= Megly /note= "N-methyl-glycine (Sarcosine)"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 19-20; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenital angiodopathy with cerebral haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.

CC Sequence 11 AA;

AAW92676 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFLM

!!AA_SEQUENCE 1.0

ID AAW92731 standard; peptide: 11 AA.

AC AAW92731;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #77.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 43-44; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenital angiodopathy with cerebral haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.

CC Sequence 11 AA;

AAW92731 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFLM

!!AA_SEQUENCE 1.0

ID AAW92656 standard; peptide: 11 AA.

AC AAW92656;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #2.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

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XX DR WPI: 1999-189630/16.
XX XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX XX
XX PS Disclosure: Column 11-12: 28pp: English.
XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX XX
SQ Sequence 11 AA:

AAW92656 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRRKPOQ WFWLM

!!AA_SEQUENCE 1.0
ID AAW92657 standard; peptide: 11 AA.
XX XX
XX AC AAW92657;
XX XX
XX DT 30-APR-1999 (first entry)
XX XX
XX DE Human tachykinin agonist beta-amyloid peptide fragment #3.
XX XX
XX KW Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment:
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
XX XX
XX PN US5876948-A.
XX XX
XX PD 02-MAR-1999.
XX XX
XX PF 27-JUL-1991: 91US-0737371.
XX XX
XX PR 29-JUL-1991: 91US-0737371.
XX PR 27-JUL-1990: 90US-0559173.
XX XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX XX
XX PI Yankner BA;
XX XX
XX DR WPI: 1999-189630/16.
XX XX
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX XX
XX PS Disclosure: Column 11-12: 28pp: English.
XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

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CC CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC CC beta-amyloid peptide fragments.
XX XX
XX SQ Sequence 11 AA:

AAW92657 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRRKPOQ WFWLM

!!AA_SEQUENCE 1.0
ID AAW94412 standard; peptide: 12 AA.
XX XX
XX AC AAW94412;
XX XX
XX DT 15-APR-1999 (first entry)
XX XX
XX DE Cancer protease-sensitive amino acid linker PAP-215 and PAP-216.
XX XX
XX KW Ricin-like toxin; cancer; viral infection; parasitic infection;
KW linker; B chain; A chain; protease; fungal infection; malaria;
KW leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
KW rhinovirus; laryngotracheitis; poliomyelitis; varicella zoster;
KW cystic fibrosis; multiple sclerosis.
XX XX
XX OS Unidentified.
XX OS Synthetic.
XX XX
XX PN W09849311-A2.
XX XX
XX PD 05-NOV-1998.
XX XX
XX PF 30-APR-1998: 98WO-CA00394.
XX XX
XX PR 29-OCT-1997: 97US-0063715.
XX PR 30-APR-1997: 97US-0045148.
XX XX
XX PA (DNOC-) DE NOVO ENZYME CORP.
XX XX
XX PI Borgford T;
XX XX
XX DR WPI: 1999-009431/01.
XX XX
XX PT New nucleic acid encoding ricin-like toxin with an interchain linker
PT cleaved by protease - is specific for diseased cells, useful for,
PT e.g. killing selectively cancer or infected cells
XX XX
XX PS Claim 24; Fig 21: 352pp: English.
XX XX
XX CC The present invention describes new purified and isolated nucleic acids
XX CC (I) encoding: (i) the A and B chains of a ricin-like toxin (II); and
XX CC (ii) a heterologous linker, joining the two chains and including a
XX CC cleavage recognition site for a disease-specific protease (III). Also
XX CC described are: (1) plasmids or baculovirus transfer vectors that contain
XX CC (I); and (2) recombinant protein (IV) consisting of the A and B chains
XX CC of (II) joined by the specified linker. (IV), produced by expression of
XX CC (I) in host cells, are used to inhibit or kill diseased cells that
XX CC produce (III), particularly for treating cancers (e.g. leucocyte
XX CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
XX CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
XX CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngotracheitis,
XX CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
XX CC sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is
XX CC toxic specifically for (III)-expressing cells and does not depend for
XX CC specificity on a cell-binding component. When used to treat virus-
XX CC infected cells, transcytosis and cytotoxicity of (IV) are increased by
XX CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
XX CC some viruses exploit to avoid immune detection), so selectively and
XX CC safely are further improved. (IV) are not toxic until chain A is
XX CC released and this occurs only in target cells. The present sequence
XX CC represents a specifically claimed cancer protease-sensitive amino acid
XX CC linker from the present invention.

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SQ Sequence 12 AA;
AAW94412 Length: 46 April 1, 2002 16:31 Type: P Check: 4310 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLMN
!!AA_SEQUENCE 1.0
ID AAW79662 standard; peptide; 11 AA.
XX
AC AAW79662;
XX
DT 02-MAR-1999 (first entry)
XX
DE Substance P derivative having complex glycosylation.
XX
KM Substance P; mannose; glycosylation; solubility.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..4 /note= "optionally the first four residues may be
FT Region deleted, leaving SP(5-11)"
FT Modified-site 5
FT /note= "the side chain amide group is N-substituted
FT with N-acetyl-D-glucosamine (GlcNAc) which in turn
FT is extended in the 4-position with a complex type
FT sugar chain, a high mannose type sugar chain or a
FT mixed type sugar chain"
FT 11
FT /note= "Met-NH2, i.e. C-terminal amide"
FT
PN JP10306099-A.
XX
PD 17-NOV-1998.
XX
PF 28-NOV-1997; 97JP-0343979.
XX
PR 04-MAR-1997; 97JP-0065372.
XX
PA (NOCK) 2H NOGUCHI KENKYUSHO.
XX
DR WPI; 1999-054306/05.
XX
DT
XX
PT New substance P derivatives with side chain containing sugar - has
XX improved solubility
XX
PS Claim 1; Page 2; 8pp; Japanese.
XX
CC The sequence represents the peptide portion of a new Substance P
CC derivative having complex glycosylation on the Gln(5) position. The
CC derivative has improved solubility compared with Substance P.
XX
SQ Sequence 11 AA;
AAW79662 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM

FT Modified-site 6
FT /note= "the side chain amide group is N-substituted
FT with N-acetyl-D-glucosamine (GlcNAc) which in turn
FT is extended in the 4-position with a complex type
FT sugar chain, a high mannose type sugar chain or a
FT mixed type sugar chain"
FT 11
FT /note= "Met-NH2, i.e. C-terminal amide"
FT
PN JP10306099-A.
XX
PD 17-NOV-1998.
XX
PF 28-NOV-1997; 97JP-0343979.
XX
PR 04-MAR-1997; 97JP-0065372.
XX
PA (NOCK) 2H NOGUCHI KENKYUSHO.
XX
DR WPI; 1999-054306/05.
XX
DT
XX
PT New substance P derivatives with side chain containing sugar - has
XX improved solubility
XX
PS Claim 1; Page 2; 8pp; Japanese.
XX
CC The sequence represents the peptide portion of a new Substance P
CC derivative having complex glycosylation on the Gln(6) position. The
CC derivative has improved solubility compared with Substance P.
XX
SQ Sequence 11 AA;
AAW79663 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAB18483 standard; peptide; 11 AA.
XX
AC AAB18483;
XX
DT 15-JAN-2001 (first entry)
XX
DE Peptide substrate used to test prolyl-tripeptidyl peptidase activity.
XX
KM Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
KM gingivitis; periodontitis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "hydrogen attached"
FT Modified-site 11 /note= "amidated residue"
FT
PN W0200052147-A2.
XX
PD 08-SEP-2000.
XX
PF 03-MAR-2000; 2000WO-US05551.
XX
PR 05-MAR-1999; 99US-0123148.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (TRAV/) TRAVIS J.
PA (POTE/) POTEPA J.
PA (BANB/) BANBULA A.
XX
PI Travis J, Potempa J, Banbula A;
XX
DR WPI; 2000-594181/56.
XX

PT Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
 PT for identifying its inhibitor which is useful for protecting an animal
 PT from a periodontal disease such as gingivitis and periodontitis
 XX
 PS Example 4; Page 37; 58pp; English.
 CC
 CC The present sequence represents a substrate which was used to test
 CC the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The
 CC prolyl tripeptidyl-peptide has an antidiolytic activity, and cleaves
 CC a peptide bond in a target polypeptide having at least 4 amino acids.
 CC This bond is between a proline and an amino acid attached to the
 CC alpha-carboxyl group end of the proline. The polypeptide is useful for
 CC identifying inhibitors. These inhibitors are then useful for reducing
 CC the growth of bacterium or for protecting an animal from a periodontal
 CC disease such as gingivitis and periodontitis caused by Porphyromonas
 CC gingivalis.
 CC
 SQ Sequence 11 AA;
 AAB18483 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBQOE ZGHSQILKMF PSTWVSQOT HERSRPRPQQ FFGLM
 !!AA-SEQUENCE 1.0
 ID AAB23027 standard; peptide; 11 AA.
 AC AAB23027;
 XX
 DT 16-JAN-2001 (first entry)
 XX
 DE Human/rat tachykinin Substance P.
 XX
 KM Substance P; tachykinin; human; rat; magnesium binding defect;
 KM sodium sensitive essential hypertension; insulin resistance;
 KM type 2 diabetes; antibody; immunoassay; quantification.
 XX
 OS Homo sapiens.
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11 /note="C-terminal amide"
 FT
 XX
 PN WO200054053-A1.
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US03707.
 XX
 PR 10-MAR-1999. 99US-0265690.
 XX
 PA (WELL/) WELLS I C.
 XX
 PI Wells IC;
 XX
 DR WPI; 2000-587457/55.
 XX
 PT Detecting magnesium binding defects associated with abnormal
 PT physiological states such as sodium-sensitive essential hypertension
 PT and type 2 insulin-resistant diabetes mellitus, comprises measuring a
 PT specific pentapeptide in blood -
 XX
 PS Disclosure: Page 5; 21pp; English.
 CC The invention relates to a method for detecting magnesium binding
 CC defects. The method comprises quantitating a tachykinin C-terminal
 CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
 CC AAB23026) in blood using an antibody specific for the generalised
 CC mammalian tachykinin C-terminal pentapeptide
 CC Phe-(Phe/Val)-Gly-Leu-Met-NH2 (AAB23028). The method is useful for
 CC detecting cellular magnesium binding defects which are associated with
 CC abnormal physiological states such as sodium-sensitive essential
 CC hypertension and type 2 diabetes mellitus. The present sequence

CC represents the tachykinin Substance P from human and rat. C-terminal
 CC fragments (AAB23025, AAB23026) of the present sequence may be assayed
 CC according to the method of the invention.
 XX
 SQ Sequence 11 AA;
 AAB23027 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBQOE ZGHSQILKMF PSTWVSQOT HERSRPRPQQ FFGLM
 !!AA-SEQUENCE 1.0
 ID AAB08303 standard; peptide; 11 AA.
 AC AAB08303;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of Substance P analogue SPL.
 XX
 KM Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;
 KM VIP1; VIP2; VIP3; BOM1; bombesin; SPL; substance P; MuJ-7; tumour growth;
 KM tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
 KM leukaemia; lymphoma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note="D-form residue"
 FT
 FT Misc-difference 5 /note="D-form residue"
 FT
 FT Misc-difference 7 /note="D-form residue"
 FT
 FT Misc-difference 9 /note="D-form residue"
 FT
 XX
 PN WO200047221-A1.
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-US03559.
 XX
 PR 11-FEB-1999; 99US-0248381.
 XX
 PA (NAIM-) NAT INST IMMUNOLOGY.
 PA (DABU-) DABUR RES FOUND.
 PA (CORD/) CORD J I.
 XX
 PI Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;
 PI Singh AT;
 XX
 DR WPI; 2000-549083/50.
 XX
 PT Novel therapeutically active composition comprising at least 5
 PT peptides, useful for treating angiogenesis especially as a result of
 PT adenocarcinomas -
 XX
 PS Disclosure: Page 8; 42pp; English.
 CC The present sequence represents an analogue of Substance P. The
 CC specification describes therapeutically active compositions comprising
 CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and
 CC at least four analogues chosen from vasoactive intestinal peptide (VIP) 1
 CC (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a VIP
 CC receptor antagonist), BOM1 (a bombesin antagonist), and SPL (a substance
 CC P antagonist). The combination of these 7 analogues is known as MuJ-7.
 CC MuJ-7 is used as an anticancer drug to restrict tumour growth and spread
 CC by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits
 CC metastasis through its antiangiogenic activity in all cancers. The
 CC peptides are useful for the treatment and prevention of angiogenesis,
 CC especially as a result of adenocarcinomas of the colon, breast, lung,
 CC prostate, kidney, leukaemias or lymphomas.
 XX

SQ Sequence 11 AA;
AAB08303 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPQ WFWLL
!!AA_SEQUENCE 1.0
ID AAB08313 standard; peptide: 11 AA.
XX AAB08313;
AC
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of an antiangiogenic peptide.
XX
KM Vasactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;
KM VIP1; VIP2; VIP3; BOM1; bombesin; SP1; substance P; MuJ-7; tumour growth;
KM tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
KM leukaemia; lymphoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 5 /label= A1b
FT /note= "alpha-aminoisobutyric acid"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 10 /label= A1b
FT /note= "alpha-aminoisobutyric acid"
FT Modified-site 11 /note= "amidated residue"
FT
FT
XX WO200047221-A1.
PN
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000MO-US03559.
XX
PR 11-FEB-1999; 99US-0248381.
XX
PA (NAIM-) NAT INST IMMUNOLOGY.
PA (DABU-) DABUR RES FOUND.
PA (CORD/) CORD J I.
XX
PI Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;
PI Singh AT;
PI
DR WPI; 2000-549083/50.
XX
XX
PT Novel therapeutically active composition comprising at least 5
PT peptides, useful for treating angiogenesis especially as a result of
PT adenocarcinomas -
XX
XX
PS Claim 11; Page 31; 42pp; English.
XX
CC AAB08304-15 represent peptides which have an antiangiogenic effect. The
CC specification describes therapeutically active compositions comprising
CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and
CC at least four analogues chosen from vasoactive intestinal peptide (VIP)
CC 1 (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a
CC VIP receptor antagonist), BOM1 (a bombesin antagonist), and SP1 (a
CC substance P antagonist). The combination of these 7 analogues is known as
CC MuJ-7. MuJ-7 is used as an anticancer drug to restrict tumour growth and
CC spread by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits
CC metastasis through its antiangiogenic activity in all cancers. The
CC peptides are useful for the treatment and prevention of angiogenesis,
CC especially as a result of adenocarcinomas of the colon, breast, lung,

CC prostate, kidney, leukemias or lymphomas.
XX
SQ Sequence 11 AA;
AAB08313 Length: 45 April 1, 2002 16:31 Type: P Check: 2863 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPQ WFWLL
!!AA_SEQUENCE 1.0
ID AAB06257 standard; peptide: 17 AA.
XX AAB06257;
AC
XX
DT 16-OCT-2000 (first entry)
XX
DE Substance P analogue #1.
XX
XX
KM Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; SSP-SAP;
KM sapotin; SAP; analgesic; anti-inflammatory; neuroprotective;
KM anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KM tranquiliser; immunosuppressive; anti-migraine; cytostatic;
KM substance P antagonist; cytotoxic; ribosome inactivator;
KM prostaglandin antagonist; cancer; respiratory disease; asthma;
KM allergic rhinitis; ophthalmic disease; conjunctivitis;
KM allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KM gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KM carcinoma; lupus erythematosus conjunctivitis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 17 /note= "linked to Sarlme(02)-amide"
FT
FT
PN US6063758-A.
XX
PD 16-MAY-2000.
XX
PF 09-JUL-1997; 97US-0890157.
XX
PR 09-JUL-1997; 97US-0890157.
XX
PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.
XX
PI Lappi DA, Wiley RG;
PI
DR WPI; 2000-430049/37.
XX
XX
PT New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example sapotin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -
XX
XX
PS Claim 1; Column 2; 21pp; English.
XX
XX
CC The present sequence is an analogue of substance P (SP), which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Sapotin (SAP), a
CC ribosome-inactivating protein, to produce SSP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal disorders (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.
XX
SQ Sequence 17 AA;

AAB06257 Length: 51 April 1, 2002 16:31 Type: P Check: 1860 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSCYGGG GGGRRPRPQOF

51 F

!!AA_SEQUENCE 1.0
ID AAB06258 standard; peptide; 20 AA.
XX

AC AAB06258:

DT 16-OCT-2000 (first entry)

DE Substance P analogue #2.

XX Substanece P: SP, neurokinin-1 receptor; NK-1R; nociception; NTF-SAP;
KW Saporin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquilliser; immunosuppressive; anti-migraine; cytostatic;
KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis..

XX Synthetic.

FH Key Location/Qualifiers

FT Modified-site 20 /note="C-terminal amide"

PN US6063758-A.

PD 16-MAY-2000.

PF 09-JUL-1997; 97US-0890157.

PR 09-JUL-1997; 97US-0890157.

PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.

PI Lappi DA, Wiley RG;

DR WPI; 2000-430049/37.

XX New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -

PS Claim 1; Column 2; 21pp; English.

XX The present sequence is an analogue of substance P (SP). SP, which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce NTF-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.

XX Sequence 20 AA;

AAB06258 Length: 54 April 1, 2002 16:31 Type: P Check: 3738 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSCYGGG GGGRRPRPQOF

51 FGILM

!!AA_SEQUENCE 1.0
ID AAB06260 standard; peptide; 11 AA.
XX

AC AAB06260:

DT 16-OCT-2000 (first entry)

DE Substance P.

XX Substanece P: SP, neurokinin-1 receptor; NK-1R; nociception; saporin; SAP;
KW analgesic; anti-inflammatory; neuroprotective; anti-asthmatic;
KW anti-allergic; dermatological; anti-ulcer; tranquilliser;
KW immunosuppressive; anti-migraine; cytostatic; substance P antagonist;
KW cytotoxic; ribosome inactivator; prostaglandin antagonist; cancer;
KW respiratory disease; asthma; allergic rhinitis; ophthalmic disease;
KW conjunctivitis; allergic dermatitis; psoriasis; ulcerative colitis;
KW Crohn's disease; gastrointestinal disorder; anxiety; psychosis;
KW rheumatoid arthritis; carcinoma; lupus erythematosus conjunctivitis.

XX unidentified.

FH Key Location/Qualifiers

FT Modified-site 11 /note="C-terminal amide"

PN US6063758-A.

PD 16-MAY-2000.

PF 09-JUL-1997; 97US-0890157.

PR 09-JUL-1997; 97US-0890157.

PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.

PI Lappi DA, Wiley RG;

DR WPI; 2000-430049/37.

XX New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -

PS Disclosure; Column 14; 21pp; English.

XX The present sequence is substance P (SP), which binds to the neurokinin-1
CC receptor (NK-1R). SP is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce SP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.

XX Sequence 11 AA;

AAB06260 Length: 45 April 1, 2002 16:31 Type: P Check: 1196 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRRPWW FGILM

!!AA_SEQUENCE 1.0
ID AAG05042 standard; Protein; 314 AA.
XX
AC AAG05042;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1298.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
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PR 30-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 04-MAY-1999; 990S-0132407.
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PR 07-MAY-1999; 990S-0132487.
PR 11-MAY-1999; 990S-0132863.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.
PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
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PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
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PR 04-JUN-1999; 990S-0137502.
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PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.
PR 10-JUN-1999; 990S-0138847.
PR 14-JUN-1999; 990S-0138119.
PR 16-JUN-1999; 990S-0139452.
PR 17-JUN-1999; 990S-0139453.
PR 18-JUN-1999; 990S-0139492.
PR 18-JUN-1999; 990S-0139454.
PR 18-JUN-1999; 990S-0139455.
PR 18-JUN-1999; 990S-0139456.
PR 18-JUN-1999; 990S-0139457.
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PR 18-JUN-1999; 990S-0139459.
PR 18-JUN-1999; 990S-0139460.
PR 18-JUN-1999; 990S-0139461.
PR 18-JUN-1999; 990S-0139462.
PR 18-JUN-1999; 990S-0139463.
PR 18-JUN-1999; 990S-0139750.
PR 18-JUN-1999; 990S-0139763.
PR 21-JUN-1999; 990S-0139817.
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PR 23-JUN-1999; 990S-0140353.
PR 23-JUN-1999; 990S-0140354.
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PR 28-JUN-1999; 990S-0140823.
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PR 30-JUN-1999; 990S-0141287.
PR 01-JUL-1999; 990S-0141842.
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PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142390.
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PR 19-JUL-1999; 990S-0144325.
PR 19-JUL-1999; 990S-0144331.
PR 19-JUL-1999; 990S-0144332.
PR 19-JUL-1999; 990S-0144333.
PR 19-JUL-1999; 990S-0144334.
PR 19-JUL-1999; 990S-0144335.
PR 20-JUL-1999; 990S-0144632.
PR 20-JUL-1999; 990S-0144632.
PR 21-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0145086.
PR 22-JUL-1999; 990S-0145085.
PR 22-JUL-1999; 990S-0145087.
PR 22-JUL-1999; 990S-0145089.
PR 22-JUL-1999; 990S-0145192.
PR 23-JUL-1999; 990S-0145145.
PR 23-JUL-1999; 990S-0145218.
PR 23-JUL-1999; 990S-0145224.
PR 26-JUL-1999; 990S-0145276.
PR 27-JUL-1999; 990S-0145913.
PR 27-JUL-1999; 990S-0145918.
PR 27-JUL-1999; 990S-0145919.
PR 28-JUL-1999; 990S-0145951.
PR 02-AUG-1999; 990S-0146386.
PR 02-AUG-1999; 990S-0146388.
PR 02-AUG-1999; 990S-0146389.
PR 03-AUG-1999; 990S-0147038.
PR 04-AUG-1999; 990S-0147204.
PR 04-AUG-1999; 990S-0147302.
PR 05-AUG-1999; 990S-0147192.
PR 05-AUG-1999; 990S-0147260.
PR 06-AUG-1999; 990S-0147303.
PR 06-AUG-1999; 990S-0147416.
PR 09-AUG-1999; 990S-0147493.
PR 09-AUG-1999; 990S-0147935.
PR 10-AUG-1999; 990S-0148171.
PR 11-AUG-1999; 990S-0148319.
PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148365.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149317.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.

PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0149930.
PR 26-AUG-1999; 99US-0150566.
PR 27-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
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PR 25-OCT-1999; 99US-0161406.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
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PR 29-OCT-1999; 99US-0162228.
PR 01-NOV-1999; 99US-0162891.
PR 01-NOV-1999; 99US-0162894.
PR 01-NOV-1999; 99US-0162895.
PR 02-NOV-1999; 99US-0163091.
PR 02-NOV-1999; 99US-0163092.
PR 03-NOV-1999; 99US-0163093.
PR 03-NOV-1999; 99US-0163348.
PR 03-NOV-1999; 99US-0163249.
PR 03-NOV-1999; 99US-0163379.
PR 04-NOV-1999; 99US-0163379.
PR 04-NOV-1999; 99US-0163380.
PR 08-NOV-1999; 99US-0164381.
PR 08-NOV-1999; 99US-0164146.
PR 08-NOV-1999; 99US-0164150.
PR 08-NOV-1999; 99US-0164151.

PR 09-NOV-1999; 99US-0164259.
PR 09-NOV-1999; 99US-0164260.
PR 10-NOV-1999; 99US-0164317.
PR 10-NOV-1999; 99US-0164318.
PR 10-NOV-1999; 99US-0164319.
PR 10-NOV-1999; 99US-0164321.
PR 10-NOV-1999; 99US-0164544.
PR 10-NOV-1999; 99US-0164545.
PR 10-NOV-1999; 99US-0164548.
PR 12-NOV-1999; 99US-0164870.
PR 12-NOV-1999; 99US-0164871.
PR 12-NOV-1999; 99US-0164959.
PR 12-NOV-1999; 99US-0164960.
PR 12-NOV-1999; 99US-0164961.
PR 12-NOV-1999; 99US-0164962.
PR 15-NOV-1999; 99US-0164926.
PR 15-NOV-1999; 99US-0164927.
PR 15-NOV-1999; 99US-0164929.
PR 16-NOV-1999; 99US-0165661.
PR 16-NOV-1999; 99US-0165669.
PR 16-NOV-1999; 99US-0165671.
PR 17-NOV-1999; 99US-0165911.
PR 17-NOV-1999; 99US-0165918.
PR 17-NOV-1999; 99US-0165919.
PR 18-NOV-1999; 99US-0166157.
PR 18-NOV-1999; 99US-0166158.
PR 18-NOV-1999; 99US-0166173.
PR 19-NOV-1999; 99US-0166411.
PR 19-NOV-1999; 99US-0166412.
PR 19-NOV-1999; 99US-0166419.
PR 19-NOV-1999; 99US-0166419.
PR 22-NOV-1999; 99US-0166733.
PR 22-NOV-1999; 99US-0166750.
PR 23-NOV-1999; 99US-0167362.
PR 24-NOV-1999; 99US-0167233.
PR 24-NOV-1999; 99US-0167234.
PR 24-NOV-1999; 99US-0167235.
PR 24-NOV-1999; 99US-0167382.
PR 30-NOV-1999; 99US-0167902.
PR 30-NOV-1999; 99US-0167904.
PR 30-NOV-1999; 99US-0167908.
PR 01-DEC-1999; 99US-0168231.
PR 01-DEC-1999; 99US-0168232.
PR 01-DEC-1999; 99US-0168233.
PR 02-DEC-1999; 99US-0168546.
PR 02-DEC-1999; 99US-0168548.
PR 02-DEC-1999; 99US-0168549.
PR 03-DEC-1999; 99US-0168673.
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XX (CERE-) CERES INC.
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XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI; 2000-507395/46.
DR N-PSDB; AAC32966.
XX
XX
XX New sequence determined DNA fragments (SDPs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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XX Claim 19; SEQ ID 1298; 344bp + CD-ROM; English.
XX
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CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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PA (CERE-) CERES INC.
XX
PI Alexandrov N., Brover V., Chen X., Subramanian G., Troukhan ME;
PI Zheng L., Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB; AAC32966.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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PS Claim 19; SEQ ID 1299; 344bp + CD-ROW; English.
XX
CC The present sequence is a putative protein frgment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
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 XX
 PA (CERE-) CERES INC.
 XX
 PI Alexandrov N., Brover V., Chen X., Subramanian G., Troukhan ME;
 PI zheng L., Dumas J;
 XX
 XX WPI: 2000-507395/46.
 DR N-PSDB; AAC32966.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 XX
 PS Claim 19; SEQ ID 1300; 344pp + CD-ROM; English.

XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX

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XX AAG06751:

XX 17-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A7.

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PA (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI: 2000-507395/46.
DR N-PSDB: AAC33599.
XX
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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XX
PS Claim 19; SEQ ID 3640; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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DT 17-OCT-2000 (first entry)
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
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 XX (CERE-) CERES INC.
 PA Alexandrov N, Brower V, Chen X, Subramanian G, Troukhan ME;
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 PI
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 DR WPI: 2000-507395/46.
 DR N-PSDB; AWC33599.
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 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 XX
 PS Claim 19; SEQ ID 3641; 344pp + CD-ROM; English.
 XX
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 CC sequence, for controlling the behaviour of a gene within the chromosome
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
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DT 17-OCT-2000 (first entry)
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
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PR 21-JUN-1999; 99US-0139817.
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PR 20-JUL-1999; 99US-0144864.
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PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
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PR 28-JUL-1999; 99US-0145951.
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PR 02-AUG-1999; 99US-0146388.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.

PR 18-AUG-1999;	99US-0149426.
PR 20-AUG-1999;	99US-0149722.
PR 20-AUG-1999;	99US-0149723.
PR 20-AUG-1999;	99US-0149929.
PR 23-AUG-1999;	99US-0149902.
PR 23-AUG-1999;	99US-0149930.
PR 25-AUG-1999;	99US-0150566.
PR 26-AUG-1999;	99US-0150884.
PR 27-AUG-1999;	99US-0151065.
PR 27-AUG-1999;	99US-0151066.
PR 27-AUG-1999;	99US-0151080.
PR 30-AUG-1999;	99US-0151303.
PR 31-AUG-1999;	99US-0151438.
PR 01-SEP-1999;	99US-0151930.
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PR 13-SEP-1999;	99US-0153758.
PR 13-SEP-1999;	99US-0154018.
PR 16-SEP-1999;	99US-0154039.
PR 20-SEP-1999;	99US-0154779.
PR 22-SEP-1999;	99US-0155139.
PR 23-SEP-1999;	99US-0155486.
PR 24-SEP-1999;	99US-0155659.
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PR 29-SEP-1999;	99US-0156596.
PR 04-OCT-1999;	99US-0157117.
PR 05-OCT-1999;	99US-0157753.
PR 06-OCT-1999;	99US-0157865.
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PR 13-OCT-1999;	99US-0159294.
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PR 14-OCT-1999;	99US-0159329.
PR 14-OCT-1999;	99US-0159330.
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PR 21-OCT-1999;	99US-0160741.
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PR 21-OCT-1999;	99US-0160770.
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PR 22-OCT-1999;	99US-0160981.
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PR 25-OCT-1999;	99US-0161405.
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PR 28-OCT-1999;	99US-0161920.
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PR 01-NOV-1999;	99US-0162891.
PR 01-NOV-1999;	99US-0162894.
PR 01-NOV-1999;	99US-0162895.
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PR 03-NOV-1999;	99US-0163093.
PR 03-NOV-1999;	99US-0163248.
PR 03-NOV-1999;	99US-0163249.
PR 03-NOV-1999;	99US-0163281.
PR 04-NOV-1999;	99US-0163379.
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PR 04-NOV-1999;	99US-0163381.
PR 08-NOV-1999;	99US-0164146.
PR 08-NOV-1999;	99US-0164150.
PR 08-NOV-1999;	99US-0164151.
PR 09-NOV-1999;	99US-0164259.
PR 09-NOV-1999;	99US-0164260.
PR 10-NOV-1999;	99US-0164317.
PR 10-NOV-1999;	99US-0164318.
PR 10-NOV-1999;	99US-0164319.
PR 10-NOV-1999;	99US-0164321.
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PR 12-NOV-1999;	99US-0164870.
PR 12-NOV-1999;	99US-0164871.
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PR 12-NOV-1999;	99US-0164960.
PR 12-NOV-1999;	99US-0164961.
PR 12-NOV-1999;	99US-0164962.
PR 15-NOV-1999;	99US-0164926.
PR 15-NOV-1999;	99US-0164927.
PR 15-NOV-1999;	99US-0164929.
PR 16-NOV-1999;	99US-0165661.
PR 16-NOV-1999;	99US-0165669.
PR 16-NOV-1999;	99US-0165671.
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PR 17-NOV-1999;	99US-0165918.
PR 17-NOV-1999;	99US-0165919.
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PR 19-NOV-1999;	99US-0166411.
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PR 22-NOV-1999;	99US-0166733.
PR 22-NOV-1999;	99US-0166750.
PR 23-NOV-1999;	99US-0167362.
PR 24-NOV-1999;	99US-0167233.
PR 24-NOV-1999;	99US-0167234.
PR 24-NOV-1999;	99US-0167235.
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PR 30-NOV-1999;	99US-0167902.
PR 30-NOV-1999;	99US-0167904.
PR 30-NOV-1999;	99US-0167908.
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PR 01-DEC-1999;	99US-0168232.
PR 01-DEC-1999;	99US-0168233.
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PR 02-DEC-1999;	99US-0168549.
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PR 03-DEC-1999;	99US-0168674.
PR 07-DEC-1999;	99US-0168675.
PR 07-DEC-1999;	99US-0169278.
PR 07-DEC-1999;	99US-0169298.
PR 08-DEC-1999;	99US-0169302.
PR 08-DEC-1999;	99US-0169691.
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PR 16-DEC-1999;	99US-0171098.
PR 16-DEC-1999;	99US-0171107.
PR 19-JAN-2000;	2000US-0176866.
PR 19-JAN-2000;	2000US-0176867.
PR 19-JAN-2000;	2000US-0176910.
PR 26-JAN-2000;	2000US-0178166.
PR 27-JAN-2000;	2000US-0177666.
PR 27-JAN-2000;	2000US-0178544.
PR 27-JAN-2000;	2000US-0178545.
PR 27-JAN-2000;	2000US-0178546.
PR 28-JAN-2000;	2000US-0178547.
PR 28-JAN-2000;	2000US-0178754.
PR 28-JAN-2000;	2000US-0178755.
PR 01-FEB-2000;	2000US-0179388.
PR 01-FEB-2000;	2000US-0179395.

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PR 04-FEB-2000; 20000US-0180207.
PR 07-FEB-2000; 20000US-0180695.
PR 07-FEB-2000; 20000US-0180696.
PR 09-FEB-2000; 20000US-0181214.
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PR 10-FEB-2000; 20000US-0181476.
PR 10-FEB-2000; 20000US-0181551.
PR 15-FEB-2000; 20000US-0182477.
PR 15-FEB-2000; 20000US-0182478.
PR 15-FEB-2000; 20000US-0182512.
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XX
PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB: AAC33599.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 3642; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
CC
XX
SO Sequence 256 AA;
AG06753 Length: 290 April 1, 2002 16:31 Type: P Check: 4240 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSOOT HERSMLTDLT PPEYEDTIPM
51 WAVPIICLV PICIFIIVYY YRQVDVLDLH ALLGIGFSL VTGVTDSIK
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151 SMSFAGLTEL AWYLSGRIKY FDRRGVAKL CLVFLPILS ILIGISRVDD
201 YWHHTDVF GAIGIFVAS FSVLHFFPYR YDENGMAPHA YFRMLAENST
251 GRATTMTGTG SRGMLNDVPE PCNSASSPHD RHRESTDSDF
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ID AAG10034 standard; Protein: 327 AA.
XX
AC AAG10034;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8196.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX
OS Arabidopsis thaliana.
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EN EP1033405-A2.
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PD 06-SEP-2000.
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PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139495.
PR 18-JUN-1999; 99US-0139496.
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PR 18-JUN-1999; 99US-0139498.
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PR 18-JUN-1999; 99US-0139501.
PR 18-JUN-1999; 99US-0139502.
PR 18-JUN-1999; 99US-0139503.
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PR 18-JUN-1999; 99US-0139529.
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PR 18-JUN-1999; 99US-0139531.
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PR 18-JUN-1999; 99US-0139539.
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PR 18-JUN-1999; 99US-0139541.
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PR 18-JUN-1999; 99US-0139543.
PR 18-JUN-1999; 99US-0139544.
PR 18-JUN-1999; 99US-0139545.
PR 18-JUN-1999; 99US-0139546.
PR 18-JUN-1999; 99US-0139547.
PR 18-JUN-1999; 99US-0139548.
PR 18-JUN-1999; 99US-0139549.
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PR 18-JUN-1999; 99US-0139552.
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PR 18-JUN-1999; 99US-0139571.
PR 18-JUN-1999; 99US-0139572.
PR 18-JUN-1999; 99US-0139573.
PR 18-JUN-1999; 99US-0139574.
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PR 18-JUN-1999; 99US-0139592.
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PR 30-NOV-1999; 99US-0167902.
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PR 07-DEC-1999; 99US-0169302.
PR 08-DEC-1999; 99US-0169692.
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PR 19-JAN-2000; 2000US-0176910.
PR 26-JAN-2000; 2000US-0178166.
PR 27-JAN-2000; 2000US-0177666.
PR 27-JAN-2000; 2000US-0178544.
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PR 27-JAN-2000; 2000US-0178546.
PR 27-JAN-2000; 2000US-0178547.
PR 28-JAN-2000; 2000US-0178754.
PR 28-JAN-2000; 2000US-0178754.
PR 01-FEB-2000; 2000US-0178755.
PR 01-FEB-2000; 2000US-0179388.
PR 01-FEB-2000; 2000US-0179395.
PR 03-FEB-2000; 2000US-0180039.
PR 03-FEB-2000; 2000US-0180139.
PR 04-FEB-2000; 2000US-0180206.
PR 04-FEB-2000; 2000US-0180207.
PR 07-FEB-2000; 2000US-0180695.
PR 07-FEB-2000; 2000US-0180696.
PR 09-FEB-2000; 2000US-0181214.
PR 09-FEB-2000; 2000US-0181228.
PR 10-FEB-2000; 2000US-0181476.
PR 10-FEB-2000; 2000US-0181551.
PR 15-FEB-2000; 2000US-0182477.
PR 15-FEB-2000; 2000US-0182478.
PR 15-FEB-2000; 2000US-0182512.
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XX (CERE-) CERES INC.
PA Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
XX Zheng L, Dumas J;
PI WPI; 2000-507395/46.
XX DR N-PSDB; AAC34872.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX Claim 19; SEQ ID 8196; 344bp + CD-ROW; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
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XX
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SO
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DT 17-OCT-2000 (first entry)
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XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
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PR 23-MAR-1999;	990S-0125788.
PR 25-MAR-1999;	990S-0126264.
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PR 21-APR-1999;	990S-0130449.
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PR 14-MAY-1999;	990S-0134219.
PR 14-MAY-1999;	990S-0134221.
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PR 28-MAY-1999;	990S-0136782.
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PR 08-JUN-1999;	990S-0138094.
PR 10-JUN-1999;	990S-0138540.
PR 10-JUN-1999;	990S-0138847.
PR 14-JUN-1999;	990S-0139119.
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PR 16-JUN-1999;	990S-0139453.
PR 17-JUN-1999;	990S-0139492.
PR 18-JUN-1999;	990S-0139454.
PR 18-JUN-1999;	990S-0139455.
PR 18-JUN-1999;	990S-0139456.
PR 18-JUN-1999;	990S-0139457.
PR 18-JUN-1999;	990S-0139458.
PR 18-JUN-1999;	990S-0139459.
PR 18-JUN-1999;	990S-0139460.
PR 18-JUN-1999;	990S-0139461.
PR 18-JUN-1999;	990S-0139462.
PR 18-JUN-1999;	990S-0139463.
PR 18-JUN-1999;	990S-0139750.
PR 18-JUN-1999;	990S-0139763.
PR 21-JUN-1999;	990S-0139817.
PR 22-JUN-1999;	990S-0139899.
PR 23-JUN-1999;	990S-0140353.
PR 23-JUN-1999;	990S-0140354.
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PR 28-JUN-1999;	990S-0140823.
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PR 13-JUL-1999;	990S-0143542.
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PR 19-JUL-1999;	990S-0144331.
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PR 19-JUL-1999;	990S-0144333.
PR 19-JUL-1999;	990S-0144334.
PR 19-JUL-1999;	990S-0144335.
PR 20-JUL-1999;	990S-0144352.
PR 20-JUL-1999;	990S-0144632.
PR 20-JUL-1999;	990S-0144884.
PR 21-JUL-1999;	990S-0144814.
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PR 21-JUL-1999;	990S-0145088.
PR 22-JUL-1999;	990S-0145085.
PR 22-JUL-1999;	990S-0145087.
PR 22-JUL-1999;	990S-0145089.
PR 22-JUL-1999;	990S-0145192.
PR 23-JUL-1999;	990S-0145145.
PR 23-JUL-1999;	990S-0145218.
PR 23-JUL-1999;	990S-0145276.
PR 26-JUL-1999;	990S-0145913.
PR 27-JUL-1999;	990S-0145918.
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PR 02-AUG-1999;	990S-0146386.
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PR 09-AUG-1999;	990S-0147935.
PR 10-AUG-1999;	990S-0148171.
PR 11-AUG-1999;	990S-0148319.
PR 12-AUG-1999;	990S-0148341.
PR 13-AUG-1999;	990S-0148565.
PR 13-AUG-1999;	990S-0148684.
PR 16-AUG-1999;	990S-0149368.
PR 17-AUG-1999;	990S-0149175.
PR 18-AUG-1999;	990S-0149426.
PR 20-AUG-1999;	990S-0149722.
PR 20-AUG-1999;	990S-0149723.
PR 20-AUG-1999;	990S-0149929.
PR 23-AUG-1999;	990S-0149902.
PR 23-AUG-1999;	990S-0149930.
PR 25-AUG-1999;	990S-0150566.
PR 26-AUG-1999;	990S-0150884.
PR 27-AUG-1999;	990S-0151065.
PR 27-AUG-1999;	990S-0151066.
PR 27-AUG-1999;	990S-0151080.
PR 30-AUG-1999;	990S-0151303.
PR 31-AUG-1999;	990S-0151438.
PR 01-SEP-1999;	990S-0151930.
PR 07-SEP-1999;	990S-0152363.
PR 10-SEP-1999;	990S-0153070.
PR 13-SEP-1999;	990S-0153758.
PR 15-SEP-1999;	990S-0154018.
PR 16-SEP-1999;	990S-0154039.
PR 20-SEP-1999;	990S-0154779.
PR 22-SEP-1999;	990S-0155139.
PR 23-SEP-1999;	990S-0155486.
PR 24-SEP-1999;	990S-0155659.
PR 28-SEP-1999;	990S-0156456.
PR 29-SEP-1999;	990S-0156596.
PR 04-OCT-1999;	990S-0157117.
PR 05-OCT-1999;	990S-0157753.
PR 06-OCT-1999;	990S-0157865.

PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.
PR 29-OCT-1999; 99US-0162228.
PR 01-NOV-1999; 99US-0162891.
PR 01-NOV-1999; 99US-0162894.
PR 01-NOV-1999; 99US-0162895.
PR 02-NOV-1999; 99US-0163091.
PR 02-NOV-1999; 99US-0163092.
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PR 03-NOV-1999; 99US-0163248.
PR 03-NOV-1999; 99US-0163249.
PR 03-NOV-1999; 99US-0163281.
PR 04-NOV-1999; 99US-0163379.
PR 04-NOV-1999; 99US-0163380.
PR 04-NOV-1999; 99US-0163381.
PR 08-NOV-1999; 99US-0164146.
PR 08-NOV-1999; 99US-0164150.
PR 08-NOV-1999; 99US-0164151.
PR 09-NOV-1999; 99US-0164259.
PR 09-NOV-1999; 99US-0164260.
PR 10-NOV-1999; 99US-0164317.
PR 10-NOV-1999; 99US-0164318.
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PR 10-NOV-1999; 99US-0164545.
PR 10-NOV-1999; 99US-0164548.
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PR 12-NOV-1999; 99US-0164959.
PR 12-NOV-1999; 99US-0164960.
PR 12-NOV-1999; 99US-0164961.
PR 12-NOV-1999; 99US-0164962.
PR 15-NOV-1999; 99US-0164926.
PR 15-NOV-1999; 99US-0164927.
PR 15-NOV-1999; 99US-0164929.
PR 16-NOV-1999; 99US-0165661.
PR 16-NOV-1999; 99US-0165669.
PR 16-NOV-1999; 99US-0165671.
PR 17-NOV-1999; 99US-0165911.
PR 17-NOV-1999; 99US-0165918.
PR 17-NOV-1999; 99US-0165919.
PR 18-NOV-1999; 99US-0166157.

PR 18-NOV-1999; 99US-0166158.
PR 18-NOV-1999; 99US-0166173.
PR 19-NOV-1999; 99US-0166411.
PR 19-NOV-1999; 99US-0166412.
PR 19-NOV-1999; 99US-0166413.
PR 22-NOV-1999; 99US-0166733.
PR 22-NOV-1999; 99US-0166750.
PR 23-NOV-1999; 99US-0167362.
PR 24-NOV-1999; 99US-0167233.
PR 24-NOV-1999; 99US-0167234.
PR 24-NOV-1999; 99US-0167235.
PR 30-NOV-1999; 99US-0167382.
PR 30-NOV-1999; 99US-0167902.
PR 30-NOV-1999; 99US-0167904.
PR 30-NOV-1999; 99US-0167908.
PR 01-DEC-1999; 99US-0168231.
PR 01-DEC-1999; 99US-0168232.
PR 01-DEC-1999; 99US-0168233.
PR 02-DEC-1999; 99US-0168546.
PR 02-DEC-1999; 99US-0168548.
PR 02-DEC-1999; 99US-0168549.
PR 03-DEC-1999; 99US-0168673.
PR 03-DEC-1999; 99US-0168674.
PR 03-DEC-1999; 99US-0168675.
PR 07-DEC-1999; 99US-0169278.
PR 07-DEC-1999; 99US-0169298.
PR 07-DEC-1999; 99US-0169302.
PR 08-DEC-1999; 99US-0169691.
PR 08-DEC-1999; 99US-0169692.
PR 16-DEC-1999; 99US-0171098.
PR 16-DEC-1999; 99US-0171107.
PR 16-DEC-1999; 99US-0171114.
PR 19-JAN-2000; 2000US-0176866.
PR 19-JAN-2000; 2000US-0176867.
PR 19-JAN-2000; 2000US-0176910.
PR 26-JAN-2000; 2000US-0178166.
PR 27-JAN-2000; 2000US-0177666.
PR 27-JAN-2000; 2000US-0178544.
PR 27-JAN-2000; 2000US-0178545.
PR 27-JAN-2000; 2000US-0178546.
PR 27-JAN-2000; 2000US-0178547.
PR 28-JAN-2000; 2000US-0178754.
PR 28-JAN-2000; 2000US-0178755.
PR 01-FEB-2000; 2000US-0179388.
PR 01-FEB-2000; 2000US-0179395.
PR 03-FEB-2000; 2000US-0180039.
PR 03-FEB-2000; 2000US-0180139.
PR 04-FEB-2000; 2000US-0180206.
PR 04-FEB-2000; 2000US-0180207.
PR 07-FEB-2000; 2000US-0180695.
PR 07-FEB-2000; 2000US-0180696.
PR 09-FEB-2000; 2000US-0181214.
PR 09-FEB-2000; 2000US-0181228.
PR 10-FEB-2000; 2000US-0181476.
PR 10-FEB-2000; 2000US-0181551.
PR 15-FEB-2000; 2000US-0182477.
PR 15-FEB-2000; 2000US-0182478.
PR 15-FEB-2000; 2000US-0182512.
PR 15-FEB-2000; 2000US-0182516.
PR 17-FEB-2000; 2000US-0183165.
PR 17-FEB-2000; 2000US-0183166.

PA (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI; 2000-507395/46.
DR N-PSDB; AAC34872.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination

PT sequences -
PS Claim 19; SEQ ID 8197; 344pp + CD-ROM; English.
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
SQ Sequence 302 AA;
AAG10035 Length: 336 April 1, 2002 16:31 Type: P Check: 8399 ..
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151 IKVATRRPRP NFYWRCPFDG KELYDALGV VCHGKAQEVK EGHKSPSGH
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8198.
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 29-MAR-1999; 99US-0126785.
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PR 30-APR-1999; 99US-0132048.
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PR 21-MAY-1999; 99US-0135353.
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PR 25-MAY-1999; 99US-0136021.
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PR 28-MAY-1999; 99US-0136782.
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PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139454.
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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 PA (CERE-) CERES INC.
 XX
 PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 PI Zheng L, Dumas J;
 XX
 DR WPI: 2000-507395/46.
 DR N-PSDB: AAC36049.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 PS
 PS Claim 19; SEQ ID 12362; 344pp + CD-ROM; English.
 XX
 CC The present sequence is a putative protein fragment from
 CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
 CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
 CC library which could then be sequenced, allowing the putative protein
 CC sequence(s) to be obtained. This sequence may be useful for protein
 CC identification and for aiding in the elucidation of signal transduction
 CC and metabolic pathways. Its coding sequence has a use in the control of
 CC gene expression as a promoter, coding sequence, 3' UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
 CC the identification of a particular organism.
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KW Protein identification; signal transduction pathway; metabolic pathway;
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termination sequence.
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XX
PA (CERE-) CERES INC.
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB; AAC36049.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 12363; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
CC
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151 CEPDGKALYD SLGDVICHGD KSVIRGSHKS PPSGHTSMSE SGLGLSLYL
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 12364.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
PN EPI033405-A2.
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PD 06-SEP-2000.
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PR 10-FEB-2000; 2000US-0181551.
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PR 15-FEB-2000; 2000US-0182478.
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(CERE-) CERES INC.

PA Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;

PI WPI: 2000-507395/46.
PI N-PSDB: AAC36228.

PT New sequence determined DNA fragments (SDFs) from different plant
species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,

PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 13018; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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51 QHRMREAQUG GHTLRSHGNT VARTHMHWI ILVLVILEC VLLIHPFYR
101 FVGKDMWTDL SYELKSNTVP IWSVPVYAML LPLVIFIFIY FRRRDYDLH
151 HAVLGILYSV LYTAVLTDAI KNAVGRPRPD FFWRCFPDCK ALYDSLGDVI
201 CHGDKSVIRE GHKSFPSCGT SMSFSGLGFL SLVLSGKIQ AFDKGHVAKL
251 CIYLFLLEFA ALVGISRVDD YMHMWDVFA GGLGLAIST ICYLQFFPPP
301 YHTEGNGPVA YFOVLEAARV QGAANGAQQ PPRQVNNGE EDCGFAGLHL
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DT 17-OCT-2000 (first entry)
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 24-NOV-1999;	99US-0167234.
PR 24-NOV-1999;	99US-0167235.

PR 19-MAY-1999;	99US-0134941.	PR 28-JUL-1999;	99US-0145951.
PR 20-MAY-1999;	99US-0135124.	PR 02-AUG-1999;	99US-0146386.
PR 21-MAY-1999;	99US-0135353.	PR 02-AUG-1999;	99US-0146388.
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PR 27-MAY-1999;	99US-0136392.	PR 04-AUG-1999;	99US-0147204.
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PR 01-JUN-1999;	99US-0137222.	PR 05-AUG-1999;	99US-0147199.
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PR 07-JUN-1999;	99US-0137724.	PR 06-AUG-1999;	99US-0147416.
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PR 18-JUN-1999;	99US-0139463.	PR 26-AUG-1999;	99US-0150884.
PR 18-JUN-1999;	99US-0139750.	PR 27-AUG-1999;	99US-0151086.
PR 18-JUN-1999;	99US-0139763.	PR 27-AUG-1999;	99US-0151066.
PR 21-JUN-1999;	99US-0139817.	PR 27-AUG-1999;	99US-0151080.
PR 22-JUN-1999;	99US-0139899.	PR 30-AUG-1999;	99US-0151303.
PR 23-JUN-1999;	99US-0140353.	PR 31-AUG-1999;	99US-0151438.
PR 23-JUN-1999;	99US-0140354.	PR 01-SEP-1999;	99US-0151930.
PR 24-JUN-1999;	99US-0140695.	PR 07-SEP-1999;	99US-0152363.
PR 28-JUN-1999;	99US-0140823.	PR 10-SEP-1999;	99US-0153070.
PR 29-JUN-1999;	99US-0140991.	PR 13-SEP-1999;	99US-0153758.
PR 30-JUN-1999;	99US-0141287.	PR 15-SEP-1999;	99US-0154018.
PR 01-JUL-1999;	99US-0141842.	PR 16-SEP-1999;	99US-0154039.
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PR 06-JUL-1999;	99US-0142390.	PR 23-SEP-1999;	99US-0155486.
PR 08-JUL-1999;	99US-0142803.	PR 24-SEP-1999;	99US-0155659.
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PR 12-JUL-1999;	99US-0142977.	PR 29-SEP-1999;	99US-0156596.
PR 13-JUL-1999;	99US-0143542.	PR 04-OCT-1999;	99US-0157117.
PR 14-JUL-1999;	99US-0143624.	PR 05-OCT-1999;	99US-0157753.
PR 15-JUL-1999;	99US-0144005.	PR 06-OCT-1999;	99US-0157865.
PR 16-JUL-1999;	99US-0144085.	PR 07-OCT-1999;	99US-0158029.
PR 16-JUL-1999;	99US-0144086.	PR 08-OCT-1999;	99US-0158232.
PR 19-JUL-1999;	99US-0144325.	PR 12-OCT-1999;	99US-0158369.
PR 19-JUL-1999;	99US-0144331.	PR 13-OCT-1999;	99US-0159293.
PR 19-JUL-1999;	99US-0144332.	PR 13-OCT-1999;	99US-0159294.
PR 19-JUL-1999;	99US-0144333.	PR 13-OCT-1999;	99US-0159295.
PR 19-JUL-1999;	99US-0144334.	PR 14-OCT-1999;	99US-0159329.
PR 19-JUL-1999;	99US-0144335.	PR 14-OCT-1999;	99US-0159330.
PR 20-JUL-1999;	99US-0144352.	PR 14-OCT-1999;	99US-0159331.
PR 20-JUL-1999;	99US-0144632.	PR 14-OCT-1999;	99US-0159637.
PR 20-JUL-1999;	99US-0144864.	PR 14-OCT-1999;	99US-0159638.
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PR 26-JUL-1999;	99US-0145276.	PR 25-OCT-1999;	99US-0161404.
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PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.
 PR 29-OCT-1999; 99US-0162143.
 PR 29-OCT-1999; 99US-0162228.
 PR 01-NOV-1999; 99US-0162891.
 PR 01-NOV-1999; 99US-0162894.
 PR 01-NOV-1999; 99US-0162895.
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 PR 03-NOV-1999; 99US-0163248.
 PR 03-NOV-1999; 99US-0163249.
 PR 03-NOV-1999; 99US-0163281.
 PR 04-NOV-1999; 99US-0163379.
 PR 04-NOV-1999; 99US-0163380.
 PR 04-NOV-1999; 99US-0163381.
 PR 08-NOV-1999; 99US-0164146.
 PR 08-NOV-1999; 99US-0164150.
 PR 08-NOV-1999; 99US-0164151.
 PR 09-NOV-1999; 99US-0164259.
 PR 09-NOV-1999; 99US-0164260.
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 PR 10-NOV-1999; 99US-0164545.
 PR 10-NOV-1999; 99US-0164548.
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 PR 12-NOV-1999; 99US-0164871.
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 PR 12-NOV-1999; 99US-0164960.
 PR 12-NOV-1999; 99US-0164961.
 PR 12-NOV-1999; 99US-0164962.
 PR 15-NOV-1999; 99US-0164926.
 PR 15-NOV-1999; 99US-0164927.
 PR 15-NOV-1999; 99US-0164929.
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 PR 16-NOV-1999; 99US-0165671.
 PR 17-NOV-1999; 99US-0165911.
 PR 17-NOV-1999; 99US-0165918.
 PR 17-NOV-1999; 99US-0165919.
 PR 18-NOV-1999; 99US-0166157.
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 PR 19-NOV-1999; 99US-0166411.
 PR 19-NOV-1999; 99US-0166412.
 PR 19-NOV-1999; 99US-0166419.
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 PR 22-NOV-1999; 99US-0166750.
 PR 23-NOV-1999; 99US-0167362.
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 PR 24-NOV-1999; 99US-0167234.
 PR 24-NOV-1999; 99US-0167235.
 PR 24-NOV-1999; 99US-0167382.
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 PR 30-NOV-1999; 99US-0167904.
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 PR 01-DEC-1999; 99US-0168232.
 PR 01-DEC-1999; 99US-0168233.
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 PR 02-DEC-1999; 99US-0168548.
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 PR 03-DEC-1999; 99US-0168674.
 PR 03-DEC-1999; 99US-0168675.
 PR 07-DEC-1999; 99US-0169278.

PR 07-DEC-1999; 99US-0169298.
 PR 07-DEC-1999; 99US-0169302.
 PR 08-DEC-1999; 99US-0169691.
 PR 08-DEC-1999; 99US-0169692.
 PR 16-DEC-1999; 99US-0171098.
 PR 16-DEC-1999; 99US-0171107.
 PR 19-JAN-2000; 99US-0171114.
 PR 19-JAN-2000; 2000US-0176866.
 PR 19-JAN-2000; 2000US-0176867.
 PR 19-JAN-2000; 2000US-0176910.
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 PR 27-JAN-2000; 2000US-0177666.
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 PR 27-JAN-2000; 2000US-0178545.
 PR 27-JAN-2000; 2000US-0178546.
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 PR 28-JAN-2000; 2000US-0178755.
 PR 01-FEB-2000; 2000US-0179388.
 PR 01-FEB-2000; 2000US-0179395.
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 PR 03-FEB-2000; 2000US-0180139.
 PR 04-FEB-2000; 2000US-0180206.
 PR 04-FEB-2000; 2000US-0180207.
 PR 07-FEB-2000; 2000US-0180695.
 PR 07-FEB-2000; 2000US-0180696.
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 PR 09-FEB-2000; 2000US-0181228.
 PR 10-FEB-2000; 2000US-0181476.
 PR 10-FEB-2000; 2000US-0181551.
 PR 15-FEB-2000; 2000US-0182477.
 PR 15-FEB-2000; 2000US-0182478.
 PR 15-FEB-2000; 2000US-0182512.
 PR 15-FEB-2000; 2000US-0182516.
 PR 17-FEB-2000; 2000US-0183165.
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 PA (CERE-) CERES INC.
 PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 PI Zheng L, Dumas J;
 XX WPI, 2000-507395/46.
 DR N-PSDB; AAC36228.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 XX
 PS Claim 19; SEQ ID 13020; 344pp + CD-ROM; English.
 XX
 CC The present sequence is a putative protein fragment from
 CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
 CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
 CC library which could then be sequenced, allowing the putative protein
 CC sequence(s) to be obtained. This sequence may be useful for protein
 CC identification and for aiding in the elucidation of signal transduction
 CC and metabolic pathways. Its coding sequence has a use in the control of
 CC gene expression as a promoter, coding sequence, 3' UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
 CC the identification of a particular organism.
 CC
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KM termination sequence.
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PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
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PR 19-APR-1999; 99US-0130077.
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PR 19-JUL-1999; 99US-0144334.
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PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
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PR 23-JUL-1999; 99US-0145218.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
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PR 12-NOV-1999;	99US-0164959.
PR 12-NOV-1999;	99US-0164960.
PR 12-NOV-1999;	99US-0164961.
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PR 22-NOV-1999;	99US-0166750.
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PR 24-NOV-1999;	99US-0167233.
PR 24-NOV-1999;	99US-0167234.
PR 24-NOV-1999;	99US-0167235.
PR 24-NOV-1999;	99US-0167382.
PR 30-NOV-1999;	99US-0167902.
PR 30-NOV-1999;	99US-0167904.
PR 30-NOV-1999;	99US-0167908.
PR 01-DEC-1999;	99US-0168231.
PR 01-DEC-1999;	99US-0168232.
PR 01-DEC-1999;	99US-0168233.
PR 02-DEC-1999;	99US-0168546.
PR 02-DEC-1999;	99US-0168548.
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PR 03-DEC-1999;	99US-0168675.
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PR 07-DEC-1999;	99US-0169298.
PR 07-DEC-1999;	99US-0169302.
PR 08-DEC-1999;	99US-0169691.
PR 08-DEC-1999;	99US-0169692.
PR 16-DEC-1999;	99US-0171098.
PR 16-DEC-1999;	99US-0171107.
PR 16-DEC-1999;	99US-0171114.
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PR 26-JAN-2000;	2000US-0178166.
PR 27-JAN-2000;	2000US-0177666.
PR 27-JAN-2000;	2000US-0178544.
PR 27-JAN-2000;	2000US-0178545.

PR 27-JAN-2000; 200005-0178546.
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PR 28-JAN-2000; 200005-0178754.
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PR 15-FEB-2000; 200005-0182516.
PR 17-FEB-2000; 200005-0183165.
PR 17-FEB-2000; 200005-0183166.

XX (CERE-) CERES INC.

PI Alexandrov N, Brower V, Chen X, Subramanian G, Troukhan ME;

PI Zheng L, Dumas J;

DR WPI; 2000-507395/46.

DR N-PSDB; AAC36351.

XX New sequence determined DNA fragments (SDFs) from different plant

PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,

PT protein coding sequences, untranslated regions, or as 3' termination

PT sequences -

PS Claim 19; SEQ ID 13483; 344pp + CD-ROM; English.

XX The present sequence is a putative protein fragment from

CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out

CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA

CC library which could then be sequenced, allowing the putative protein

CC sequence(s) to be obtained. This sequence may be useful for protein

CC identification and for aiding in the elucidation of signal transduction

CC and metabolic pathways. Its coding sequence has a use in the control of

CC gene expression as a promoter, coding sequence, 3'UTR or termination

CC sequence, for controlling the behaviour of a gene within the chromosome,

CC as a tool for use in genetic mapping, including a use in hybridisation

CC assays, for recognition or isolation of similar DNA fragments, or for

CC the identification of a particular organism.

XX Sequence 314 AA;

AA013842 Length: 348 April 1, 2002 16:31 Type: P Check: 1334

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151 IKNAVGRPRP DFEWRCFPD KALYDSLGDV ICHGDKSVIR EGHKSPSGH
201 TSMFSFGIGF LSLYLSGKIQ AFDGKGHVAK LCIYILPLLF AALVGISRDV
251 DYWHHMDVAF AGGILGLAIS TICCYIQFPP PYHTEGKCPY AYYOVLFAAR
301 VOGAANGAVQ QPPPOVNGGE EEDGGFMGLH LVDPFTMRRE EDVETGRG

11AA SEQUENCE 1.0
ID AA013843 standard; Protein: 299 AA.
XX
AC AA013843;

XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 13484.
XX
DE Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
PN
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PD 06-SEP-2000.
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PE 25-FEB-2000; 2000EP-0301439.
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PR	01-NOV-1993;	99US-0162896.
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PR	04-NOV-1993;	99US-0163380.
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PR	09-NOV-1993;	99US-0164259.
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PR	17-FEB-2000; 20000US-0183166.
PA	(CERE-) CERES INC.
XX	
PI	Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI	Zheng L, Dumas J;
XX	
DR	WPI: 2000-507395/46.
DR	N-PSDB: AAC36351.
XX	
PT	New sequence determined DNA fragments (SDFs) from different plant
PT	species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT	protein coding sequences, untranslated regions, or as 3' termination
PT	sequences -
XX	
PS	Claim 19; SEQ ID 13484; 344pp + CD-ROM; English.
XX	
CC	The present sequence is a putative protein fragment from
CC	Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC	RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC	library which could then be sequenced, allowing the putative protein
CC	sequence(s) to be obtained. This sequence may be useful for protein
CC	identification and for aiding in the elucidation of signal transduction
CC	and metabolic pathways. Its coding sequence has a use in the control of
CC	gene expression as a promoter, coding sequence, 3'UTR or termination
CC	sequence, for controlling the behaviour of a gene within the chromosome,
CC	as a tool for use in genetic mapping, including a use in hybridisation
CC	assays, for recognition or isolation of similar DNA fragments, or for
CC	the identification of a particular organism.
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101	IFIFIFYFRRR DUYDLHAYL GLIYSVLYTA VLTDAIKNAV GRPRDPFEMR
151	CEPDSKALYD SLGDVICHGD KSVIRGSHS FPSGHTSMSE SGAGPLSLYL
201	SKRIAPFGGK GHVAKLCITV LPLFLPALYG ISRVDYDINH WQDYFAGGLL
251	GLAISTICYL QFPPRPYHTE GNGPYAVFQV LEARVQGA NGAVQDPPQ
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XX	
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DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 13485.
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KW	protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.

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PR 17-FEB-2000; 2000US-0183165.
PR 17-FEB-2000; 2000US-0183166.

(CERE-) CERES INC.

XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX

DR WPI: 2000-507395/46.
DR N-PSDB: AAC36351.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences ..
XX
PS Claim 19; SEQ ID 13485; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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AAC13844 Length: 326 April 1, 2002 16:31 Type: P Check: 3694 ..

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101 RRRDYYDLHH AVLGILYSVL VTAVLDAIK NAVGRPRDF FWRCEPDDKA
151 LYDSLGDVYC HGDKSVIREG HKSFPSGHTS WFSFGIGFLS LYLSEKIDAF
201 DCKGHVAKLC IVILPLLEFA LVGISRVDDY WHHMDVDFNG GLLGIAISTI
251 CYLQFIPIPPY HTEGMPYAY FOVLEARVO GAANGAVOOP PPOVNGBEE
301 DGFAGKLIHV DNPTMRRED VETGRG

11AA_SEQUENCE 1.0
ID AAC14936 standard; Protein: 314 AA.
XX
AC AAC14936;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14986.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW terminator sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-f2.
XX
PD 06-SEP-2000.
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PE 25-FEB-2000; 2000EP-0301439.
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(CERE-) CERES INC.
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Zheng L, Dumas J;
WPI: 2000-507395/46.
N-PSDB: AAC36760.
New sequence determined DNA fragments (cDNAs) from different plant
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protein coding sequences, untranslated regions, or as 3' termination
sequences -
PS Claim 19; SEQ ID 14987; 344bp + CD-ROM; English.
XX The present sequence is a putative protein fragment from
XX Arabidopsis thaliana. Its coding sequence was isolated by carrying out
XX RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
XX library which could then be sequenced, allowing the putative protein
XX sequence(s) to be obtained. This sequence may be useful for protein
XX identification and for aiding in the elucidation of signal transduction
XX and metabolic pathways. Its coding sequence has a use in the control of
XX gene expression as a promoter, coding sequence, 3'UTR or termination
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XX as a tool for use in genetic mapping, including a use in hybridisation
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XX (CERE-) CERES INC.

PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;

XX WPI: 2000-507395/46.
DR N-PSDB; AAC36760.

PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -

XX Claim 19; SEQ ID 14988; 344pp + CD-ROM; English.

XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.

XX Sequence 292 AA;

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XX Arabidopsis thaliana protein fragment SEQ ID NO: 18829.
DE Protein identification; signal transduction pathway; metabolic pathway;
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XX
XX (CERE-) CERES INC.
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XX Alexandrov N, Broyer V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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XX Claim 19; SEQ ID 18829; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein frgment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
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CC sequence, for controlling the behaviour of a gene within the chromosome,
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ID AG17707 standard; Protein: 299 AA.
XX
XX AG17707;
XX
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18830.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX

```


PI Alexandrov H, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR MPI: 2000-507395/46.
N-PSDB: AAC37833.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or *Arabidopsis thaliana*, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 18830; 344pp + CD-ROM; English.
XX
PS The present sequence is a putative protein fragment from
CC *Arabidopsis thaliana*. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
SQ Sequence 299 AA;

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1 SQARNDBCE ZGHSQILKMF PSTWVSQOT HERSMTVART HHHWIIIVL

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151 CFPDGAALVD SLGDVICHGD KSVIREGHS FPSGHTSMSF SGLGFLSYL

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ID AAG17708 standard; Protein: 292 AA.

XX AAG17708;

XX 17-OCT-2000 (first entry)

DE *Arabidopsis thaliana* protein fragment SEQ ID NO: 18831.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS *Arabidopsis thaliana*.

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XX (CERE-) CERES INC.
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XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences.
XX
PS Claim 19; SEQ ID 18831; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from

CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 24762.
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KW termination sequence.
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XX		
PA	(CERE-) CERES INC.	
PI	Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;	
PI	Zheng L, Dumas J;	
XX		
DR	WPI: 2000-507395/46.	
DR	N-PDB: AAC39473.	
XX		
PT	New sequence determined DNA fragments (SDFs) from different plant	
PT	species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,	
PT	protein coding sequences, untranslated regions, or as 3' termination	
PT	sequences -	
XX		
PS	Claim 19;. SEQ ID 24762; 344bp + CD-ROM; English.	
XX		
XX	The present sequence is a putative protein fragment from	
CC	Arabidopsis thaliana. Its coding sequence was isolated by carrying out	
CC	RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA	
CC	library which could then be sequenced, allowing the putative protein	
CC	sequence(s) to be obtained. This sequence may be useful for protein	
CC	identification and for aiding in the elucidation of signal transduction	
CC	and metabolic pathways. Its coding sequence has a use in the control of	
CC	gene expression as a promoter, coding sequence, 3' UTR or termination	
CC	sequence, for controlling the behaviour of a gene within the chromosome	
CC	as a tool for use in genetic mapping, including a use in hybridisation	
CC	assays, for recognition or isolation of similar DNA fragments, or for	
CC	the identification of a particular organism.	
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DT 17-OCT-2000 (first entry)

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KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EPI033405-A2.

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PR 07-DEC-1999; 9905-0169298.
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PR 08-DEC-1999; 9905-0169691.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
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PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.
PR 29-OCT-1999; 99US-0162228.
PR 01-NOV-1999; 99US-0162894.
PR 01-NOV-1999; 99US-0162895.
PR 01-NOV-1999; 99US-0163091.
PR 02-NOV-1999; 99US-0163092.
PR 02-NOV-1999; 99US-0163093.
PR 03-NOV-1999; 99US-0163248.
PR 03-NOV-1999; 99US-0163249.
PR 03-NOV-1999; 99US-0163281.
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PR 04-NOV-1999; 99US-0163380.
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PR 08-NOV-1999: 99US-0164146.
PR 08-NOV-1999: 99US-0164150.
PR 08-NOV-1999: 99US-0164151.
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PR 09-NOV-1999: 99US-0164260.
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PR 16-NOV-1999: 99US-0165869.
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PR 22-NOV-1999: 99US-0166750.
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PR 24-NOV-1999: 99US-0167233.
PR 24-NOV-1999: 99US-0167234.
PR 24-NOV-1999: 99US-0167235.
PR 24-NOV-1999: 99US-0167382.
PR 30-NOV-1999: 99US-0167902.
PR 30-NOV-1999: 99US-0167904.
PR 30-NOV-1999: 99US-0167908.
PR 01-DEC-1999: 99US-0168231.
PR 01-DEC-1999: 99US-0168232.
PR 01-DEC-1999: 99US-0168233.
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PR 02-DEC-1999: 99US-0168546.
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PR 03-DEC-1999: 99US-0168675.
PR 07-DEC-1999: 99US-0169278.
PR 07-DEC-1999: 99US-0169298.
PR 07-DEC-1999: 99US-0169302.
PR 08-DEC-1999: 99US-0169691.
PR 08-DEC-1999: 99US-0169692.
PR 16-DEC-1999: 99US-0171098.
PR 16-DEC-1999: 99US-0171107.
PR 16-DEC-1999: 99US-0171114.
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PR 19-JAN-2000: 2000US-0176867.
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PR 27-JAN-2000: 2000US-0177666.
PR 27-JAN-2000: 2000US-0178544.
PR 27-JAN-2000: 2000US-0178545.
PR 27-JAN-2000: 2000US-0178546.
PR 28-JAN-2000: 2000US-0178547.
PR 28-JAN-2000: 2000US-0178754.
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PR 03-FEB-2000: 2000US-0180039.
PR 03-FEB-2000: 2000US-0180139.
PR 04-FEB-2000: 2000US-0180206.
PR 04-FEB-2000: 2000US-0180207.
PR 07-FEB-2000: 2000US-0180695.
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PR 09-FEB-2000: 2000US-0181214.
PR 09-FEB-2000: 2000US-0181228.
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PR 15-FEB-2000: 2000US-0182478.
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XX
XX (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
PI WPI: 2000-507395/46.
DR N-PSDB: AAC39473.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX Claim 19; SEQ ID 24764; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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AAAG22001 length: 333 April 1, 2002 16:31 Type: P Check: 69
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101 IFIFIFERRR DYYDLHNAVL GLYSVLVTA VLTDAIKNAV GRPPDFEWR
151 CEPQKALYD SLGDVICHGD KSVIREGHS FPSGHTSMSE SGLGFLSYL
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AC AAC30400;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 36337.
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KW Protein identification; signal transduction pathway; metabolic pathway;

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PR 17-FEB-2000; 2000US-0183165.
XX 17-FEB-2000; 2000US-0183166.
PA (CERE-) CERES INC.
PI Alexandrov N, Broyer V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB; AAC62647.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 36337; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for adding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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151 IKDAVGRPRP DFWRCPPDGG IGIFHNVTKN VLCTGAKVY KEHGKSPSG
201 HTSWSFAGLG FLSLYLSGKI RVFDQRGHVA KLCIVILPLL VVALVGSRY
251 DDVWHHMDV FCGAIIIGLVY ATECYLQFRR PRYPBDGMP HAVFQMLADS
301 RNDVQDSAGM NHLSVROTEL ESVR
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AC AAG30401;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 36338.
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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OS Arabidopsis thaliana.
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XX
XX
PA (CERE-) CERES INC.
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Lomas J;
XX
XX MPI; 2000-507395/46.
DR N-PSDB; AAC42647.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination

PT sequences -
XX
XX Claim 19; SEQ ID 36338; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KW Protein identification; signal transduction pathway; metabolic pathway;
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KW termination sequence.
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CC assays, for recognition or isolation of similar DNA fragments, or for
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PR 16-DEC-1999; 99US-0171107.
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PR 01-FEB-2000; 2000US-0179388.
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PR 03-FEB-2000; 2000US-0180039.
PR 03-FEB-2000; 2000US-0180139.
PR 04-FEB-2000; 2000US-0180206.
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PR 07-FEB-2000; 2000US-0180695.
PR 07-FEB-2000; 2000US-0180696.
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PR 09-FEB-2000; 2000US-0181228.
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PR 10-FEB-2000; 2000US-0181551.
PR 15-FEB-2000; 2000US-0182477.
PR 15-FEB-2000; 2000US-0182478.
PR 15-FEB-2000; 2000US-0182512.
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XX
XX (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI: 2000-507395/46.
DR N-PSDB: AAC42695.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX Claim 19; SEQ ID 36513; 344bp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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XX 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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XX Arabidopsis thaliana.
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PR 01-APR-1959; 990S-0127462.
PR 06-APR-1959; 990S-0128234.
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XX The present sequence is a putative protein fragment from
CC *Arbidopsis thaliana*. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.

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AC AAG38755;

DT 18-OCT-2000 (first entry)

DE Arabidopsis; thaliana protein fragment SEQ ID NO: 47858.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR	25-FEB-1993;	990S-0121825.
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PR 16-DEC-1999; 99US-0171098.
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PR 10-FEB-2000; 2000US-0181476.
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XX
PA (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI; 2000-507395/46.
DR N-PSDB; AAC45813.
XX
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 47858; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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XX 06-SEP-2000.
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PR 28-SEP-1999;	990S-0156458.
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PA (CERE-) CERES INC.
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PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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DR WPI: 2000-507395/46.
DR N-PSDB: AAC45813.
XX
PT New sequence determined DNA fragments (SDPs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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PS
PS Claim 19: SEQ ID 47859; 344pp + CD-ROM; English.
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CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KM termination sequence.
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XX
PA (CERE-) CERES INC.
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PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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DR N-PSDB: AAC47339.
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CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
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PA (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX WPI: 2000-507395/46.
DR N-PSDB; AAC47339.
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
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PT sequences -
XX
PS Claim 19; SEQ ID 53457; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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PR 29-OCT-1999; 99US-0162143.
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PR 19-NOV-1999; 99US-0166419.
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PR	17-FEB-2000;	2000US-0183166.
PA	(CERE-) CERES INC.	
XX	Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;	
PI	Zheng L, Dumas J;	
PI	WPI: 2000-507395/46.	
DR	N-PSDB: AAC50204.	
XX		
PT	New sequence determined DNA fragments (SDFs) from different plant	
PT	species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,	
PT	protein coding sequences, untranslated regions, or as 3' termination	
PT	sequences -	
PS	Claim 19; SEQ ID 63963; 344pp + CD-ROM; English.	
XX		
CC	The present sequence is a putative protein fragment from	
CC	Arabidopsis thaliana. Its coding sequence was isolated by carrying out	
CC	Rt-PCR on all of the mRNA obtained from the plant, and creating a cDNA	
CC	library which could then be sequenced, allowing the putative protein	
CC	sequence(s) to be obtained. This sequence may be useful for protein	
CC	identification and for aiding in the elucidation of signal transduction	
CC	and metabolic pathways. Its coding sequence has a use in the control of	
CC	gene expression as a promoter, coding sequence, 3'UTR or termination	
CC	sequence, for controlling the behaviour of a gene within the chromosome	
CC	as a tool for use in genetic mapping, including a use in hybridisation	
CC	assays, for recognition or isolation of similar DNA fragments, or for	
CC	the identification of a particular organism.	

XX	Sequence	59 AA:	
SO	Length:	93	April 1, 2002 16:31 Type: P Check: 9507 ..
AA050469	1 SQARNDBQCG ZGHSQILKMF PSTWVYSQOT HERSMALAPL PQAOVQLLVI		
	51 QTLAVQTLEV RILVVLAPLG DLGGVGDPF ALGARPHML YFF		
IIAA	SEQUENCE 1.0		
ID	AA96513 standard; Protein: 826 AA.		
XX	AA96513:		
AC			
XX	12-SEP-2000	(first entry)	
DE			
XX	Human Zs1g43	polypeptide.	
XX			
KW	Zs1g43:	receptor; chromosome 17q21.1; recombinant production;	
KW	gene therapy.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..25	
FT		/label= signal_peptide	
FT	Protein	26..826	
FT		/label= mature_protein	
FT	Domain	26..315	
FT		/label= extracellular_domain	
FT	Domain	316..340	
FT		/label= transmembrane_domain	
FT	Domain	341..826	
FT		/label= intracellular_domain	
PN	WO200031259-A1.		
PD			
XX	02-JUN-2000.		
XX			
PF	15-NOV-1999;	99WO-US27040.	
PR	23-NOV-1998;	98US-0200417.	
XX			
PA	(Zymo) ZYMOGENETICS INC.		
XX			
PI	Sheppard PO, Lok S;		
DR	WPI: 2000-400069/34.		
DR	N-PSDB: AAA29367, AAA29368.		
XX			
XX			
PT	Isolated Zs1g43 polypeptides and nucleic acids useful for detecting		
PT	Zs1g43 gene expression in samples and for screening for modulators of		
XX	Zs1g43 activity		
PS	Claim 1; Page 81-83; 88pp; English.		
XX			
CC	This is a putative receptor, Zs1g43. The gene is strongly expressed		
CC	in heart, liver, skeletal muscle, adrenal gland, kidney and pancreatic		
CC	tissues. The Zs1g43 gene resides on human chromosome 17 at 17q21.1. The		
CC	Zs1g43 coding sequences may be used to detect Zs1g43 gene expression in		
CC	samples and to analyze Zs1g43 gene structure according to standard		
CC	methodologies (e.g. polymerase chain reaction (PCR) amplification). They		
CC	may also be used for the recombinant production of Zs1g43 polypeptides		
CC	either in vitro (e.g. in a fermentation culture) or in vivo (e.g. as part		
CC	of a gene therapy protocol for rectifying inappropriate Zs1g43 expression		
CC	in a patient). The proteins may be used to identify and produce agonists		
CC	and antagonists (especially antibodies which may then be used to modulate		
CC	Zs1g43 expression and activity. Antibodies specific for Zs1g43 may also		
CC	be used to detect the presence of Zs1g43 gene expression products		
CC	according to standard methods (e.g. enzyme linked immunosorbant assays		
CC	(ELISAs) (claimed).		
XX	Sequence	826 AA:	

AAV6513 Length: 860 April 1, 2002 16:31 Type: P Check: 8290 ..

1 SOARDBCOE ZGHSQILKMF PSTWVYSQOT HERSMPPASG PSVLARLLPL

51 LGLLGSASR APGKSPEPP SPOEILIKYO VVSGELVPL ARASYDVGN

101 RFLAAGTSD SEGVATLPLS YRLGTWLVLT AARPGFLINS VPMWRDKPL

151 YASVSLYLP ERPAFLILYE DLVHLLGSP GARSOPLOVF QRRARLPEVS

201 STYSOLMASL TPASTOEMR APPAFLGTEA SSSGNSWME LMPLTAVSVH

251 LITGNGTEVP LSGPIHLSLP VPSETRALTY GTSIPAWRMD PKSGIWMANG

301 TGVIRKEGRQ LYWTFVSEPOL GYVVAAMASP TAGLVTTISG IQDIGTYHTI

351 FLUTLIALA LLVLILCLL IYYCRRRCLK PROQRKLQL SGPSDGNKRD

401 QATSMSQLHL ICGGLEPAP SGDPEAPPG PLHSAFSSSR DLASRDOFF

451 RTKPSASRP AAPSGARG ESAGLGARS ABGPGLEPG LEHRGPGSG

501 AAFLHEPPS PPPPDHYLG HKGAEGKTP DELLSQVDQ LARPSLQQA

551 GQLICGSID HIKDNYRNV MPTLVIPAHY VRLGGEAGAA GVGDEPAPPE

601 GTAPGPAAAF PDDPQRPQM PGHSGPGEQ GGGGGEWGCA GRAAPVGSV

651 TIPVLFNST MAOLNGELQA LTEKKLELG VKPHPAMFV SLDGSRNSQV

701 RHSTYIDLQAG GGARSTDAFL DSGVDVHEAR PARRRAREE RERAPAPAP

751 PPPAPPRAL SEDTEPSSSE SRTGLCSPED NSLTFPLIDEV AAPEGRAATV

801 PRGRGRSRGD SSRSSASELR RDSLTSPED E LGAEVGDEAG DKKSPWQRE

851 ERPLMVFNVK

!!AA_SEQUENCE 1.0

ID AAV58787 standard; Protein: 290 AA.

AC AAV58787;

XX

DT 08-MAY-2000 (first entry)

XX

DE Arabidopsis phosphatidic acid phosphatase ATPAP1.

XX

XX ATPAP1: phosphatidic acid phosphatase; PAP; diacylglycerol;

KM lipid; oilseed; vegetable oil; transgenic plant.

XX

OS Arabidopsis thaliana.

XX

PN WO200005385-A1.

XX

PD 03-FEB-2000.

XX

PF 22-JUL-1999; 99WO-US16892.

XX

PR 24-JUL-1998; 98US-0122315.

XX

PA (CALJ) CALGENE LLC.

XX

PI Lassner MW, Ruezinsky D;

XX

XX WPI: 2000-182706/16.

DR N-PSDB: AA258188.

XX

PT New polynucleotide encoding phosphatase protein useful for modifying

XX the lipid composition in plant cells -

PS Example 1; Fig 2; 49pp; English.

XX

CC The present sequence is that of Arabidopsis thaliana phosphatidic

CC acid phosphatase ATPAP1, as deduced from a cDNA clone (see AA258188)

CC isolated from an Arabidopsis EST database on the basis of homology

CC to conserved regions (see AAV58720-21) of mouse, rat, human and

CC yeast PAPs. The invention provides novel plant PAP nucleic acids

CC and PAP polypeptides active in the formation of diacylglycerol from

CC phosphatidic acid. Also provided are methods of using PAP nucleic

CC acids, in sense or antisense orientation, to modify or alter lipid

CC compositions or lipid levels in transgenic plants.

XX

SQ Sequence 290 AA:

AAV58787 Length: 324 April 1, 2002 16:31 Type: P Check: 2030 ..

1 SOARDBCOE ZGHSQILKMF PSTWVYSQOT HERSMPEIHL GAHTIRSGV

51 TVARFHMHDV LILLILVIE IVLVNIEPPH REVGEDMLTD LRYPLQDNFI

101 PFWAVPLIAY VLPEAVICVY YFIRNDVYDL HHAILGLRS VLITGVITDA

151 IKDANGRRPP DFEWRCFPDG IGIFHNNTKN VLCTGAKDV KEGHKSFPSG

201 HTSWSPAGIG FLSLYLSGKI RVFDQRGHA KLCIVILPLL VAALGVSRV

251 DDYWHHMDDV FGAIIGLTV ATFCYLOFPF PRYDPDGWGP HAYFQMLADS

301 RNDVDSAGM NHLSVQTEL ESVR

!!AA_SEQUENCE 1.0

ID AAV58788 standard; Protein: 348 AA.

AC AAV58788;

XX

DT 08-MAY-2000 (first entry)

XX

DE Arabidopsis phosphatidic acid phosphatase ATPAP2.

XX

XX ATPAP2: phosphatidic acid phosphatase; PAP; diacylglycerol;

KM lipid; oilseed; vegetable oil; transgenic plant.

XX

OS Arabidopsis thaliana.

XX

PN WO200005385-A1.

XX

PD 03-FEB-2000.

XX

PF 22-JUL-1999; 99WO-US16892.

XX

PR 24-JUL-1998; 98US-0122315.

XX

PA (CALJ) CALGENE LLC.

XX

PI Lassner MW, Ruezinsky D;

XX

XX WPI: 2000-182706/16.

DR N-PSDB: AA258189.

XX

PT New polynucleotide encoding phosphatase protein useful for modifying

XX the lipid composition in plant cells -

PS Example 1; Fig 3; 49pp; English.

XX

XX The present sequence is that of Arabidopsis thaliana phosphatidic

CC acid phosphatase ATPAP2, as deduced from DNA (see AA258189) isolated

CC from an Arabidopsis EST database on the basis of homology to

CC Arabidopsis ATPAP1 (see AAV58787). The invention provides novel

CC plant PAP nucleic acids and PAP polypeptides active in the

CC formation of diacylglycerol from phosphatidic acid. Also provided

CC are methods of using PAP nucleic acids, in sense or antisense

CC orientation, to modify or alter lipid compositions or lipid levels

CC in transgenic plants.

XX

SQ Sequence 348 AA:

AAV58788 Length: 382 April 1, 2002 16:31 Type: P Check: 1560 ..

1 SOARNDBCE ZGHSQILKMF PSTWVYSOOT HERSHASATF LFNLLSSLSR

51 DLHFLTFITIS FESSLLEFWRN SQDEAQRGR MOEIDLVSHT IKSIGGRVAS

101 KKHNDWIIIV ILIAIEIGLN LISPFYRYVG KDMATDLKYP FKDNTPVIMS

151 VPHYAVLLPI IVFCFYLKR TCYVDLHHSI LGLLFAVLIT GYITDSIKVA

201 TGRPRNPFYW RCFPDGKELY DALGVVCHG KAAEVKEGK SPPSGHTSWS

251 FAGLFLSLY LSGIKAFNN EGHVAKLCLV IFFLLAACIV GISRVDDYWH

301 HMQDVFAGAL IGTVAFCY RQFYPNPYHE EGMGPAYFR AAOEGVPT

351 SSQNGDALRA MSLQMDSTSL ENMESGTSTA PR

!!AA_SEQUENCE 1.0

ID AAV58789 standard; Protein: 314 AA.

AC AAV58789;

DT 08-MAY-2000 (first entry)

DE Arabidopsis phosphatidic acid phosphatase ATPAP3.

XX

XX

XX ATPAP2; phosphatidic acid phosphatase; PAP; diacylglycerol;

KW lipid; oilseed; vegetable oil; transgenic plant.

XX

XX Arabidopsis thaliana.

OS

XX

XX W0200005385-A1.

PN

XX

PD 03-FEB-2000.

XX

XX

PF 22-JUL-1999; 99WO-US16892.

XX

XX

PR 24-JUL-1998; 98US-0122315.

XX

XX (CALJ) CALGENE LLC.

PA

XX

PI Lasserer MW, Ruezinsky D;

XX

XX WPI: 2000-182706/16.

DR N-PSDB: AAZ58190.

XX

XX

XX New polynucleotide encoding phosphatase protein useful for modifying

PT the lipid composition in plant cells -

XX

XX

PS Example 1; Fig 4; 49pp; English.

XX

XX The present sequence is that of Arabidopsis thaliana phosphatidic

CC acid phosphatase ATPAP3, as deduced from DNA (see AAZ58190) isolated

CC from an Arabidopsis EST database on the basis of homology to

CC Arabidopsis ATPAP1 (see AAV58787). The invention provides novel

CC plant PAP nucleic acids and PAP polypeptides active in the

CC formation of diacylglycerol from phosphatidic acid. Also provided

CC are methods of using PAP nucleic acids, in sense or antisense

CC orientation, to modify or alter lipid compositions or lipid levels

CC in transgenic plants.

XX

XX

SO Sequence 314 AA;

AAV58789 Length: 348 April 1, 2002 16:31 Type: P Check: 1234 ..

1 SOARNDBCE ZGHSQILKMF PSTWVYSOOT HERSMREAO LGGHTRSHGM

51 TWAATHMHDM IIVLVVILE CVLLIHFPY RFYGRKMDMD LSYPLKSTIV

101 PWSVSVYAM LLPVITFTI YFRRDVYDL HNAVLGLYS VLVTAVALTDA

151 IKNAVGRPR DEFWRCPFDG KALYDSLGV ICHGDKSVIR EGHKSPSGH

201 TSWSFSGLGF LSLYLSGKIQ AFDGKHVAK LCIVILPLF AALVGISRPD

251 DYWHMQDYF AGGLGLAIS TICLYOFPP PYHTEGMPY AYFVLEAAR

301 VOGAANGAVQ QPPPOVNNGE EEDGFMGLH LVDNPTMRRE EDVETGRG

!!AA_SEQUENCE 1.0

ID AAV58790 standard; Protein: 310 AA.

AC AAV58790;

DT 08-MAY-2000 (first entry)

DE Corn phosphatidic acid phosphatase.

XX

XX

XX phosphatidic acid phosphatase; PAP; diacylglycerol;

KW lipid; oilseed; vegetable oil; transgenic plant; maize; corn.

XX

XX

XX Zea mays.

OS

XX

XX W0200005385-A1.

PN

XX

PD 03-FEB-2000.

XX

XX

PF 22-JUL-1999; 99WO-US16892.

XX

XX

PR 24-JUL-1998; 98US-0122315.

XX

XX (CALJ) CALGENE LLC.

PA

XX

PI Lasserer MW, Ruezinsky D;

XX

XX WPI: 2000-182706/16.

DR N-PSDB: AAZ58191.

XX

XX

XX New polynucleotide encoding phosphatase protein useful for modifying

PT the lipid composition in plant cells -

XX

XX

PS Example 1; Fig 5; 49pp; English.

XX

XX The present sequence is that of corn phosphatidic acid phosphatase

CC (PAP), as deduced from DNA (see AAZ58191) isolated from a corn EST

CC database on the basis of homology to an Arabidopsis PAP (see

CC AAV58787). The invention provides novel plant PAP nucleic acids and

CC PAP polypeptides active in the formation of diacylglycerol from

CC phosphatidic acid. Also provided are methods of using PAP nucleic

CC acids, in sense or antisense orientation, to modify or alter lipid

CC compositions or lipid levels in transgenic plants.

XX

XX

SO Sequence 310 AA;

AAV58790 Length: 344 April 1, 2002 16:31 Type: P Check: 5033 ..

1 SOARNDBCE ZGHSQILKMF PSTWVYSOOT HERSMADQLG SYTIRSHMI

51 LARLHYMDI ILLLAVIDG LNTIEPFHR FVCKDMMTDL RYPMKGNIVP

101 FMAVPLIGII LPMAIFVGIV FKKNFYDLH HGLIGILYSV LITAVITDAI

151 KDVGFRPRD FFWRCFPMGN DYYDNITGV ICGVKSVIK EGHKSPSGH

201 SSMVFAGLOF LAWYLACKLT AFDRKGHIK LCIVFLPLT AALVAVSRVD

251 DYWHMQDYF AGGLGLTVA SFCLQFFPY PRDGDALMPH AVAVRLAEEG

301 NSRNASYSV RPTETETVDI PGHGAITLR ETLNDVESG ARRL

!!AA_SEQUENCE 1.0

ID AAV58791 standard; Protein: 343 AA.

AC AAV58791;

XX 08-MAY-2000 (first entry)
 XX Soybean phosphatidic acid phosphatase soyPAP1.
 DE Phosphatidic acid phosphatase; PAP; soyPAP1; diacylglycerol;
 KW lipid; oilseed; vegetable oil; transgenic plant; soybean.
 XX
 OS Glycine max.
 PN W0200005385-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-US16892.
 XX
 PR 24-JUL-1998; 98US-0122315.
 XX
 PA (CALJ) CALGENE LLC.
 XX
 PI Lasserer MW, Ruezinsky D;
 XX WPI: 2000-182706/16.
 DR N-PSDB; AA258193.
 XX
 PT New polynucleotide encoding phosphatase protein useful for modifying
 the lipid composition in plant cells -
 XX
 PS Example 1; Fig 8; 49pp; English.
 XX
 CC The present sequence is that of soybean phosphatidic acid
 phosphatase soyPAP1, as deduced from DNA (see AA258193) isolated from
 a soybean EST database on the basis of homology to an Arabidopsis
 PAP (see AA258787). The invention provides novel plant PAP nucleic
 acids and PAP polypeptides active in the formation of diacylglycerol
 from phosphatidic acid. Also provided are methods of using PAP
 nucleic acids, in sense or antisense orientation, to modify or alter
 lipid compositions or lipid levels in transgenic plants.
 CC
 SO Sequence 343 AA;
 AAY58791 Length: 377 April 1, 2002 16:31 Type: P Check: 9121 ..
 1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSMASWMD LRPFRRQSV
 51 RTRRQEFETR EVOLGSHTVS SHGYAVARTN KHDMLILLLL VLYISLXTI
 101 HFRHREVGKD MMTDLKYPLK SNTVPAMAIR IYAILLPITV FLGYIIRRD
 151 VYDLHNAVIG LIFSVLITAV FTEAIKNAVQ RPRDPFWRMC FRDGKDYDK
 201 WGDVICHQDQ KVIKEGYKSF PSCHTSGSFS GLGFLSLVLS GKIAFDRKG
 251 HVAKLCIVFL PLLVASLVGI SRVDYWHMH QDVFAAGLLG LTVATFCYLQ
 301 FEPPEYHSEG WGPYAYFRML EESRGMTQYP SVONSGOAOQ AEAQAEQOE
 351 QGLHGCWGLT LSRDHAAALN DCESGRG
 !!AA_SEQUENCE 1.0
 ID AAY58792 standard; Protein: 322 AA.
 XX
 AC AAY58792;
 XX
 DT 08-MAY-2000 (first entry)
 XX
 DE Soybean phosphatidic acid phosphatase soyPAP2.
 XX
 KW Phosphatidic acid phosphatase; PAP; soyPAP2; diacylglycerol;
 lipid; oilseed; vegetable oil; transgenic plant; soybean.
 XX
 OS Glycine max.
 XX

PN W0200005385-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-US16892.
 XX
 PR 24-JUL-1998; 98US-0122315.
 XX
 PA (CALJ) CALGENE LLC.
 XX
 PI Lasserer MW, Ruezinsky D;
 XX WPI: 2000-182706/16.
 DR N-PSDB; AA258194.
 XX
 PT New polynucleotide encoding phosphatase protein useful for modifying
 the lipid composition in plant cells -
 XX
 PS Example 1; Fig 7; 49pp; English.
 XX
 CC The present sequence is that of soybean phosphatidic acid
 phosphatase soyPAP2, as deduced from DNA (see AA258194) isolated from
 a soybean EST database on the basis of homology to an Arabidopsis
 PAP (see AA258787). The invention provides novel plant PAP nucleic
 acids and PAP polypeptides active in the formation of diacylglycerol
 from phosphatidic acid. Also provided are methods of using PAP
 nucleic acids, in sense or antisense orientation, to modify or alter
 lipid compositions or lipid levels in transgenic plants.
 CC
 SO Sequence 322 AA;
 AAY58792 Length: 356 April 1, 2002 16:31 Type: P Check: 5772 ..
 1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSAPEIOL GMNTRISHT
 51 RVARTNMHDW LILLLVITD AVNLILQPH RFVGGMMTD LRYLKANT
 101 RFMAVPIAI LPLAVFLVY YFIRKDYVDL NHAINGLLFS VLITAVMTDA
 151 IKDANVRPRP DFWRCFRPDG KGVFDPVTN VLCTGDKGI KEHGKSPSG
 201 HTSWSFAGLV YLAWYLSGKL RAFDRGHVA KICLVFLPIL VAAMIAVSrv
 251 DDYWHNMQDV FAGALIGMII ASFCYLQFPR PYVDVGWCP HAYOMLAES
 301 RNGAOPSTVN NEIHVOSAE LQAVSLYIPR QHDAOTRGNS WDSSPMLGAS
 351 QNVRTH
 !!AA_SEQUENCE 1.0
 ID AAY54319 standard; Protein: 2074 AA.
 XX
 AC AAY54319;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE Amino acid sequence of a murine PCTG4 protein.
 XX
 KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
 mental retardation; autism; depression; bipolar affective disorder;
 hypothyroidism; OPA gene; neuropsychiatric disorder.
 KW
 OS Mus sp.
 XX
 PN W09955915-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-US09365.
 XX
 PR 29-APR-1998; 98US-0083465.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Philibert RA, Gims ET;
 XX WPI: 2000-126357/11.
 DR
 XX
 PT Identification of polymorphisms in the PCTG4 region of Xq13 for
 PT diagnosing mental retardation or autism -
 XX
 PS Example 7; Page 81-84; 100pp; English.
 XX
 CC The present sequence represents a murine PCTG4 protein. Polymorphisms
 CC in the human PCTG4 region of chromosome Xq13 are associated with
 CC mental retardation, autism, depression, bipolar affective disorder or
 CC hypothyroidism. One 12 bp insertion polymorphism occurs within the
 CC coding region of the human OPA gene, and introduces a 4 amino acid
 CC insertion in a putative OPA domain. This domain has been shown to be
 CC involved in tissue specific expression. Another polymorphism consists
 CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp
 CC polymorphism. Another polymorphism consists of a dinucleotide repeat
 CC approximately 4.5 kb downstream of the 12 bp polymorphism. The
 CC specification describes a method for screening for polymorphisms in a
 CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related
 CC sequences within the q13 region of the X chromosome have polymorphisms
 CC associated with neuropsychiatric disorders. The methods can be used to
 CC screen for the presence of a heritably linked form of mental retardation,
 CC autism, depression, bipolar affective disorder or hypothyroidism.
 CC
 XX
 SQ Sequence 2074 AA;

AAV54319 Length: 2108 April 1, 2002 16:31 Type: P Check: 165 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSMNOKDN FMLVTARSOS
 51 AINTWFTDLA GTRPLTHLAK KVFIFSKKEE VEGYLAKTIV PYMAANLIK
 101 MTCAYYAAMS ETKVKKKNTA DPTEWTOII TKYLMEOLOK MAEYYRQPA
 151 GSGCGGSGTIG PLPHDVEMAI RQWDYNEKLA LFMQDGMLD RHEFLTWLE
 201 CPEKRPBED ELKLKLLPL LRTSGEYVOS AYSRLRAY CTRRLALDLD
 251 GVSSHSHSVI AAGTSSSLPT TPAPOPPTS TPSTPESDL MCPORPLVF
 301 GLSCILQITL LCCPSALVMH YSLTDSRIKT GSPLDHLPIA PSNLPMPGN
 351 SAFIQOVAK LREIEQOIKE RGAAVEVRMS FDKCEATAG FTIGRVLHTL
 401 EYLDHSFEER SDFSNSLDSL CNRIFGLGPR KDGHETSSDD DAVVSLCEW
 451 AVSCRSGRH RAMVYAKLE KROAIEAER CGESEADEK GSVASGLSA
 501 PSAPIFQVYL LQFLDTQAPM LTPRSESER VEFNVLVLE CELIRHVES
 551 HNMVTCCLIS RGLDAFGAPG PRPPSPFDDP TDDPERKEAE GSSSSKLEDP
 601 GLSEMDIDP SSTVLFEDEME KPDFSLFSPT MPCGKSPS PEKPDVEKEV
 651 KPPAKEKEEG TLGILYDQPR HVOYATHFPI POBESCSHEC NORLVLEFGV
 701 GKORDARHA IKKITKDLK VLNRKGTAEI DQLAIVPLN PGDLTFEGE
 751 DGQRRRRNRP EAPPTAEDIF AKFOHLSHYD QHOVTAQVSR NVLQIITSFA
 801 LGMSTHLLV QHVOFIDLM EYSLISGLI DPAIQLNLE SVVEALLLK
 851 SSDLVGSYTT SLCLIAVAVL RHYHACLIIN ODQMAQVEG LCGVYKQGN
 901 RSDGSABRC ILAVLYDLYT SCSHLSKSKG ELFPDSCSV KNITVCNVEP
 951 SESNRRMAPE FMDITLENPA AHFTYTGIG KSLSEPNANR YSFVCNALMH
 1001 VCVGHHDPR VNDIAILCAE LTGYCKSLA EWLGVLKALC CSSNNGTCGF

1051 NDLCNVDS DLSFHDSLAT FVALIAROC LLEDLIRCA AIPSLNAAC
 1101 SEQSEBGAR LTRIRILLHF KTRPOLNPGOS DONKTVGIR SSCRRHLLAA
 1151 SONRIVDGA VAVLKAAYVL GDAELKSGF TVPGTEELP EEEGGGSSG
 1201 RROGGRNISV ETASLDVYAK YVLRISIQOE WYGERCLASL CEDSNDIQDP
 1251 VLSSAQORL MQLICYPHRL LDNEGENPO RQRIKRIKN LDQWTMOSS
 1301 LELDLMIKOT PNTENSLLE NIARATIEVF QQSAETGSSS GSTASNPSS
 1351 .SKTRVLSL ERSGVWLVA PLIAKPTSVQ GHVLAAGEE LEKQHLGSS
 1401 SRKEKDROK QKMSLSQOP FLSTVLTCLK GODEBREGL ASLHSQHQI
 1451 VINMRENOYL DCKPKQLMH EALKRLNV GMPFTVGRS TQOTTEMAQL
 1501 LLEITISGTV DMOSSNLELT TVLDMLSVLI NGTLAADSS ISQSMEEK
 1551 RAYMLVKKL QKDLGERQSD SLEKVHQLP LPKQNRDVIY CEPQSLIDT
 1601 KGNKIAGEFS IFKKEGLQVS TKOKISPMWL FEGIKPSTAP LSWAMEGTVR
 1651 VDRVARGEE QORLLYTHY LRPRRAYYL EPLPLPEDE EPPAPALLEP
 1701 EKKAPEPKT DKROAAPST EERKKKSTKG KKRSPATKN EDYMGGRS
 1751 GPYGVTPPD LLMHNPDSI SHLSYROSSM GLYTQNPPLP AGGRVDPYR
 1801 PVRLPMOKLP TRPYPGVLP TTWSTVAGLE PSSYKTSYVR QOQPTVPOQ
 1851 RLRLQLOOSQ GMLGSSVHQ MPSSSYGLQ TSQLSPSLQ GYTSYVHG
 1901 LQHTGPADP TRHLQRPBG YVHQAPTYG HGLISTORPS HQTLQOTPM
 1951 GTMTPLSAOG VQAGVRSTSI LPEQOQOQOQ OQOQOQOQOQ
 2001 QOQOQOQHIR QOQOQOQMLR QOQOQOQOQO QOQOQOQOQO
 2051 QOQQAAPPQ QPOSQPOFOR QGLQOTQOQO QTAALVRLQI QQLSNTQOP
 2101 STNIFGRY
 11AA-SEQUENCE 1.0
 ID AAY54320 standard; Protein: 2023 AA.
 XX AC
 XX AAY54320;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE Amino acid sequence of a human PCTG4 protein.
 XX
 KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
 KW mental retardation; autism; depression; bipolar affective disorder;
 KW hypothyroidism; OPA gene; neuropsychiatric disorder.
 XX
 OS Homo sapiens.
 XX
 PN W09955915-A2.
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-US09365.
 XX
 PR 29-APR-1998; 98US-0083465.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Philibert RA, Gims ET;
 XX

DR WPI: 2000-126357/11.
 XX Identification of polymorphisms in the PCTG4 region of Xq13 for
 PT diagnosing mental retardation or autism -
 XX Example 7: Page 81-84; 100pp; English.
 PS
 CC The present sequence represents a human PCTG4 protein. Polymorphisms
 CC in the human PCTG4 region of chromosome Xq13 are associated with
 CC mental retardation, autism, depression, bipolar affective disorder or
 CC hypothyroidism. One 12 bp insertion polymorphism occurs within the
 CC coding region of the human OPA gene, and introduces a 4 amino acid
 CC insertion in a putative OPA domain. This domain has been shown to be
 CC involved in tissue specific expression. Another polymorphism consists
 CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp
 CC polymorphism. Another polymorphism consists of a dinucleotide repeat
 CC approximately 4.5 kb downstream of the 12 bp polymorphism. The
 CC specification describes a method for screening for polymorphisms in a
 CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related
 CC sequences within the q13 region of the X chromosome have polymorphisms
 CC associated with neuropsychiatric disorders. The methods can be used to
 CC screen for the presence of a heritably linked form of mental retardation,
 CC autism, depression, bipolar affective disorder or hypothyroidism.
 CC
 SQ Sequence 2023 AA;

AAV54320 Length: 2057 April 1, 2002 16:31 Type: P Check: 8484 ..

1 SQARNBCE ZGHSQILKMF PSTWVSQOT HERSMRAWL IKMTCAYAA
 51 ISETKVKRRH VDFEMEMTOI ITKYLMEOQ KMAEYRPG AGSGGGSTI
 101 GPLPHDEVA IROMDYTEKL AMFMFOQDGL DRHEFLTWVL ECFEKIRPGE
 151 DELIKLLPL LRYSGEFVQ SAYLSRLAY FCTRLALQL DGVSSSHSHV
 201 ISAGSTFPL TPAPQPTPS STPTSPFSDL LMCPOHRLV FGLSCILQTI
 251 LCCPSALW HYSLTDSRIK TGSPLDLPI APSNLPMEG NSAFYQGVRA
 301 KLRLEIQIK ERQAVEVRM SFDKQCEATA GFTTGRVILHT LEVLDSHSFE
 351 RSDFSNLS LCNRIPLGP SKDGHEISSD DDAVVSILCE WAVSCKRGR
 401 HRAWVAKL EKQAELEAE RGESEADE KGIASSLS APAPIFQDV
 451 LLOFLDTQAP MLTDPRESE RVEFPNLVL FCELRHDFV SHNMYCTLI
 501 SRGLAFGAP GPRPSPFDD PADDEHREA EGSSSSKLED PGLSEMDID
 551 PSSSVLFEDM EKPDFSLFSP TMPGCKGSP SPEKPDVEKE VKPPKKEIE
 601 GTLGVLYDOP RHVQVATHP IPQESCSHE CNQRLVVLFG VGRQDDARH
 651 AIKKITKIL KVLNRKTAE TDQLAPIVL NPGDLTEFG EDQKRRNR
 701 PEAFPTAEDI FAKFOHLSHY DQHOVTAQVS RNVLQITSF ALGMSHTLPL
 751 VQHVQFIPL MEYSISISGL IDEFATQLNE LSVVEAEILL KSSDLVGSYT
 801 TSLICIAVAV LRHYHACLIL NQDMAQVEE GLCGVVKGM NRSDGSAER
 851 CILAYLVLY TSCSHLKNF GELFSDPCK VKNTIYCAVE PPSNMMAP
 901 ERMIDITENP AHTFTYTG I GKSUSENPAN RYFVCNALM HVCVGHHPD
 951 RVNDIATICA ELTGCKSLIS AEMLGVLKAL CCSSNNGTCG FNDLLCNVDY
 1001 SDSLFSHSLA TFAVAILIARQ CILLEDLIRC AAIPLSLNAA CSFODSPPGA
 1051 RLTCRILLHL FKTPOINPCQ SDGNKPWGI RSSCDRHLLA ASQNRIVDGA
 1101 VFAVLKAVF LGDAELKSGS FVTGTGTEEL PEEGGGSGS GRQGRNIS

1151 VETASLDVYA KYVLRISICQ EWWGERCLKS LCEDSNLDQ PVLSSAQAR
 1201 LMOLICTPHR LDNEDGENP QORIRKRILO NLDQOTAROS SLELOLMIKO
 1251 TPNNEMNSL ENIAKATIEV FOOSAETGSS SGSTASNMPS SSKTKPYLSS
 1301 LERSGVMLVA PLIAKLPTSV QGHVLKAGE ELEKGHIGS SSRKERDROK
 1351 QKSNLSLSQO PFLSLVLTCL KQDEQREGL LLSLSYOHQ IVNMMDQY
 1401 LDDCKPRLM HEALKLRLNL VGMFDTYQR STQQTTEAM ILLEIISGT
 1451 VDMQSNMELF TYVLDMLSVL INGTLAADS SISGSMEN KRAYMLAK
 1501 LOKLGEROS DSLEKVRQL PLPKOTRDYI TCEPQSLID TKGNKTAGFD
 1551 SIFKEGLOV STOKISPMQ LFEGLKPSAP LSWMGFTVR VDRRVARGEE
 1601 QORLLYHTH LRPRPARYL EPLPLPEDE EPAPTLLEP EKKAPPEPKT
 1651 DKPQAAFPST EERKKSTKG KRSOPATKT EDYKMGERS GPGVTVYPPD
 1701 LLAHPNPGSI THLNROGSI GLYTQNOPLP AGGPRVDPYR PVRLPMOKLP
 1751 TRPTYPGVLP TMTGVMGLE PSSYKTSYR QQCPAVPQO RLROQLQSQ
 1801 GMLGQSSVHQ MTPSSSYGLQ TSQYTPYVS HVGLOQHTGP AGTWPPSYIS
 1851 SQPYOSTHPS TNP TLVDPTR HLOQRPBGV HQQAPTYGNG LSTORSHQ
 1901 TLQOTPMIST MTPMSAQVQ AGVRSALIP EQQQQQQQQQ QQQQQQQQQQ
 1951 QQQQQQQQYHI RQQQQQQQILR QQQQQQQQQQ QQQQQQQQQQ QQQQQQHQQQ
 2001 QQQQAAFPQP QPQSQPQFOR QGLQOTQOQO QTAALVROLQ QQLSNTQPOP
 2051 STNIFGR
 11AA SEQUENCE 1.0
 ID AAY6657 standard; protein; 1184 AA.
 XX
 AC AAY6657;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1188.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO963088-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-051252.
 XX
 PR 02-JUN-1998; 98US-0087607.
 PR 02-JUN-1998; 98US-0087609.
 PR 02-JUN-1998; 98US-0087759.
 PR 03-JUN-1998; 98US-0087827.
 PR 04-JUN-1998; 98US-0088021.
 PR 04-JUN-1998; 98US-0088025.
 PR 04-JUN-1998; 98US-0088028.
 PR 04-JUN-1998; 98US-0088029.
 PR 04-JUN-1998; 98US-0088030.
 PR 04-JUN-1998; 98US-0088033.
 PR 04-JUN-1998; 98US-0088326.
 PR 05-JUN-1998; 98US-0088167.
 PR 05-JUN-1998; 98US-0088202.
 PR 05-JUN-1998; 98US-0088212.

PR	05-JUN-1993	98US-0086821
PR	09-JUN-1993	98US-0086855
PR	10-JUN-1993	98US-0086872
PR	10-JUN-1993	98US-0086870
PR	10-JUN-1993	98US-0086873
PR	10-JUN-1993	98US-0086874
PR	10-JUN-1993	98US-0086878
PR	10-JUN-1993	98US-0086873
PR	10-JUN-1993	98US-0086874
PR	10-JUN-1993	98US-0086871
PR	10-JUN-1993	98US-0086810
PR	10-JUN-1993	98US-0086811
PR	10-JUN-1993	98US-0086824
PR	10-JUN-1993	98US-0086825
PR	10-JUN-1993	98US-0086826
PR	12-JUN-1993	98US-0089105
PR	16-JUN-1993	98US-0089440
PR	16-JUN-1993	98US-0089512
PR	16-JUN-1993	98US-0089514
PR	17-JUN-1993	98US-0089532
PR	17-JUN-1993	98US-0089538
PR	17-JUN-1993	98US-0089598
PR	17-JUN-1993	98US-0089599
PR	17-JUN-1993	98US-0089600
PR	17-JUN-1993	98US-0089653
PR	18-JUN-1993	98US-0089601
PR	18-JUN-1993	98US-0089607
PR	18-JUN-1993	98US-0089608
PR	19-JUN-1993	98US-0089947
PR	19-JUN-1993	98US-0089952
PR	22-JUN-1993	98US-0090246
PR	22-JUN-1993	98US-0090252
PR	22-JUN-1993	98US-0090254
PR	23-JUN-1993	98US-0090349
PR	23-JUN-1993	98US-0090355
PR	24-JUN-1993	98US-0090429
PR	24-JUN-1993	98US-0090431
PR	24-JUN-1993	98US-0090435
PR	24-JUN-1993	98US-0090444
PR	24-JUN-1993	98US-0090445
PR	24-JUN-1993	98US-0090451
PR	24-JUN-1993	98US-0090472
PR	24-JUN-1993	98US-0090535
PR	24-JUN-1993	98US-0090538
PR	24-JUN-1993	98US-0090540
PR	24-JUN-1993	98US-0090557
PR	25-JUN-1993	98US-0090576
PR	25-JUN-1993	98US-0090678
PR	25-JUN-1993	98US-0090688
PR	25-JUN-1993	98US-0090690
PR	25-JUN-1993	98US-0090691
PR	25-JUN-1993	98US-0090694
PR	25-JUN-1993	98US-0090695
PR	25-JUN-1993	98US-0090696
PR	26-JUN-1993	98US-0090682
PR	26-JUN-1993	98US-0090683
PR	01-JUL-1993	98US-0091358
PR	01-JUL-1993	98US-0091360
PR	01-JUL-1993	98US-0091364
PR	02-JUL-1993	98US-0091474
PR	02-JUL-1993	98US-0091486
PR	02-JUL-1993	98US-0091487
PR	02-JUL-1993	98US-0091519
PR	02-JUL-1993	98US-0091526
PR	02-JUL-1993	98US-0091528
PR	02-JUL-1993	98US-0091633
PR	02-JUL-1993	98US-0091646
PR	02-JUL-1993	98US-0091673
PR	07-JUL-1993	98US-0091978

PR	17-JUN-1998;	98US-0091982;
PR	09-JUL-1998;	98US-0092188;
PR	10-JUL-1998;	98US-0092472;
PR	20-JUL-1998;	98US-0093339;
PR	30-JUL-1998;	98US-0094651;
PR	04-AUG-1998;	98US-0095282;
PR	04-AUG-1998;	98US-0095285;
PR	04-AUG-1998;	98US-0095302;
PR	04-AUG-1998;	98US-0095318;
PR	04-AUG-1998;	98US-0095325;
PR	04-AUG-1998;	98US-0095919;
PR	10-AUG-1998;	98US-0096012;
PR	10-AUG-1998;	98US-0096143;
PR	11-AUG-1998;	98US-0096146;
PR	12-AUG-1998;	98US-0096329;
PR	17-AUG-1998;	98US-0096357;
PR	17-AUG-1998;	98US-0096766;
PR	17-AUG-1998;	98US-0096773;
PR	17-AUG-1998;	98US-0096791;
PR	17-AUG-1998;	98US-0096867;
PR	17-AUG-1998;	98US-0096891;
PR	17-AUG-1998;	98US-0096894;
PR	17-AUG-1998;	98US-0097022;
PR	19-AUG-1998;	98US-0097141;
PR	20-AUG-1998;	98US-0097218;
PR	24-AUG-1998;	98US-0097661;
PR	26-AUG-1998;	98US-0097951;
PR	26-AUG-1998;	98US-0097959;
PR	26-AUG-1998;	98US-0097954;
PR	26-AUG-1998;	98US-0097955;
PR	26-AUG-1998;	98US-0097971;
PR	26-AUG-1998;	98US-0097974;
PR	26-AUG-1998;	98US-0097978;
PR	26-AUG-1998;	98US-0097979;
PR	26-AUG-1998;	98US-0097986;
PR	26-AUG-1998;	98US-0098014;
PR	31-AUG-1998;	98US-0098525;
PR	16-SEP-1998;	98US-0100634;
PR	12-JAN-1999;	99US-0115565;
PA	(GETH) GENENTECH INC.	
PI	Baker K., Chen J., Goddard A.	
PI	Wood W.,	
XX	WPI: 2000-072883/06.	
XX	N-PSDB; AAZ6485.	
DR		
XX		
PT	Membrane-bound proteins and	
XX		
PS	claim 12; Fig 72; 822pp; Eng	
XX		
CC	The invention provides membra	
CC	polynucleotides encoding the	
CC	identified based on extracell	
CC	sequences have homology with	
CC	ligands and various enzymes.	
CC	molecules are useful as phar	
CC	immunoadhesins, for instance	
CC	receptor-ligand interactions	
CC	employed for screening of po	
CC	of the relevant receptor/lig	
CC	are useful as hybridization	

CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX
 SO Sequence 1184 AA:

AAV66657 Length: 1218 April 1, 2002 16:31 Type: P Check: 668 ..

1 SOARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSWVGTKA WVSFSLYLEV
 51 TSVLGRQTM L TOSVRRVQPG KKNPSIFAKP ADLIESPEBW TTFWNIDYPG
 101 GKDYERLDA IRFYGDRCV APRLEAET TDWTPAGSTG QVYHSGREG
 151 FWCINREORP GQNCNVTYR FLCPPGSLER DTERIWPMS PMSKSAACG
 201 QTGVOTFTRI CLAEWVSLCS EASEGQHGM GQDCIACLT CPMQVAVADC
 251 DACMCQDFML HGAVSLPGGA PASGAATYLL TKTPKLITQT DSDGRFRIPG
 301 LCPDGKSLK ITRVKEFPIV LTMPTSLKA ATIKAEFYRA ETPYMWNPPE
 351 TKARRAQSV SLCCKATGKP RPDKTFWYHN DTLLDPSLYK HESLVLRKL
 401 QOHQAGEYFC KAOSDAGAVK SKVAOLIVYA SDETPPCNBPV ESYLIRLPHD
 451 CFQATNSFY YDVGRCPVKI CAGQDNGIR CRDAVQNCBG ISKTEEREIQ
 501 CSGTLPYKV AKESCORCT ETRSIYRGV SAADNGEPMR FGAVYMGNSR
 551 VSMYGYKGF TLHVPODTER LVLTPEVDRLQ KEVNTTKVLP FNKKSAAVFI
 601 EIKMLRKEP ILEAMETNI IFLGEVGED PMAELEIPSR SFYRQNEPY
 651 IGKTKASVTE LDPNRISTAT AAOITLNFIN DEGTFFPLRT YGMSVDFRD
 701 EVTSEPINAG KVKVHLDSTQ VKMPEHISTV KLSMLNPDG LWESEGDPEF
 751 ENGRNRKED RTFLVGNLEI RERLEFNLV PESRCEYKV RAYSERFLP
 801 SEQIQGVVIS VINLEPRTGF LSNPRAMGRF DSVITGPNGA CVPAFCDDOS
 851 PDAVSAYVLA SLAGEELOAV ESSPKENPNA IGVPQPYLTK LNYRRTDHD
 901 PRVAKTAFQI SMAKPRNSA EESNGPIYAF ENLRACEAP PSAHFRFYQ
 951 IEGRYDYNT VPFNEDDPMS WTEYLAWMP KPMERFACYI KVKIYPLEV
 1001 NVSRNMGCT HRTVGLYK IRDVRSTRDR DQPNVSAACL EFKCSGMLYD
 1051 QDRVDRTLVK VIPQSCRA SVNPMLEHL VNHLPYAVNN DTSEYTM LAP
 1101 LDPIGHNYGI YTYTDODPRT AKETALGRCF DGTSDGSSRI MKNVGYALT
 1151 FNCVEROVR QSAFOYLQST PAOSPAAGTV QGRVPSRRQO RASRGOROG
 1201 GVVASLRFPR VAQOPLIN
 11AA_SEQUENCE 1.0
 ID AAV76061 standard; Protein: 128 AA.
 AC AAV76061;
 XX
 DE 27-MAR-2000 (first entry)
 XX
 XX Rat skin cell transmembrane protein, SEQ ID NO:316.
 XX
 KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytosolic; neuroprotective; vulerity.

XX
 OS Rattus sp.
 XX
 PN WO9955865-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-N200051.
 XX
 PR 29-APR-1998; 98US-0069726.
 PR 09-NOV-1998; 98US-0188930.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 XX WPI: 2000-072177/06.
 DR
 XX Novel polynucleotides useful for the treatment of various conditions
 PT including wounds and cancer -
 PT
 PS Claim 4; Page 186-187; 235pp; English.
 XX
 CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.
 XX
 SO Sequence 128 AA;
 AAY76061 Length: 162 April 1, 2002 16:31 Type: P Check: 24 ..
 1 SOARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSAEEGT SGENGNALG
 51 AELGVAVLLF VAFIATELTP PQQRRIQPEE LMYNPNYVE AEYPTGPMF
 101 VTAFLTPSL IPFAKFLRKA DATDSKQACL AASLALANG VFTNIKLIY
 151 GRPRPDFEYR CF
 11AA_SEQUENCE 1.0
 ID AAY32382 standard; Peptide: 11 AA.
 AC AAY32382;
 XX
 DE 28-FEB-2000 (first entry)
 XX
 XX Cell differentiation, proliferation and maintenance factor peptide.
 DE
 XX Cell differentiation; cell proliferation; cell maintenance;
 KW ectoderm-like cell; embryonic stem cell; pluripotent cell;
 KW gene therapy; cell therapy; tissue transplant; organ transplant;
 KW xerotransplant; allotransplant; concomitant transplantation;
 KW transgenic animal; substance P.
 OS Synthetic.
 XX
 PN WO9953021-A1.
 XX
 PD 21-OCT-1999.

XX 09-APR-1999; 99WO-AU00265.
XX 09-APR-1998; 98AU-0002912.
PR 23-SEP-1998; 98AU-0006097.
XX (BRES-) BRESAGEN LTD.
XX
PI Bettes MD, Rathjen PD, Rathjen J;
XX WPI; 2000-061970/05.
DR
XX
XX New isolated biologically active factor capable of influencing
PT differentiation, proliferation or maintenance of pluripotent cells
PS
PS Claim 3; Page 123; 189pp; English.
XX
XX This sequence represents a peptide (substance P free acid) that can
CC form the low mol.wt. component of a novel biologically active factor
CC that is capable of influencing the differentiation, proliferation
CC and/or maintenance of pluripotent cells. The factor consists of a
CC low mol.wt. component selected from Pro, Pro-Ala, Ala-Pro-Gly,
CC Pro-Or-Pro, Pro-Gly, Gly-Pro-Ala, Gly-Pro-Or-Pro, a peptide given in
CC AA32378-82, or a protease digested (including collagenase digested)
CC collagen fragment, and a high mol.wt. component such as fibronectin.
CC The biologically active factor is obtained from conditioned media of
CC hepatic or hepatoma cells or cell lines or extraembryonic endodermal
CC cells or cell lines. The factor is capable of causing the
CC transition of pluripotent cells (e.g. embryonic stem cells in
CC adherent culture and in suspension culture) to pluripotent cells
CC having different properties, more specifically primitive
CC ectoderm-like (EPL) cells. The factor is also capable of
CC maintaining and supporting proliferation of these cells in vitro.
CC It also allows the isolation and maintenance of EPL cells derived
CC from in vitro and in vivo primitive ectoderm. These cells can be
CC used in allo-, concomitant- or xeno-transplantation, cell therapy,
CC tissue and organ augmentation or replacement, and gene therapy.
CC They can also be used for producing chimeric or transgenic animals.
XX
SQ Sequence 11 AA;
AA32382 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAY53610 standard; Protein: 214 AA.
XX
AC AAY53610;
XX
DT 11-FEB-2000 (first entry)
XX
DE The nitrile hydratase alpha subunit of *Bacillus* sp. BR449.
XX
XX *Bacillus* sp. BR449; nitrile hydratase; alpha subunit; beta subunit;
KW nitrile; amide; acrylonitrile; acrylamide; amidase.
XX
OS *Bacillus* sp.
XX
PN WO9955719-A1.
XX
PD 04-NOV-1999.
XX
PE 30-MAR-1999; 99WO-US06888.
XX
PR 29-APR-1998; 98US-0083485.
PR 10-FEB-1999; 99US-0248528.
XX
PA (UNMS) UNIV MICHIGAN STATE.
XX
PI Ortel PJ, Padmakumar R, Kim SH;
XX WPI; 2000-013413/01.

DR N-PSDB; AA236225, AA230407.
XX
XX Isolated nucleic acids encoding nitrile hydratase and amidase from
PT thermophilic *Bacillus*, useful for conversion of acrylonitrile to
PT acrylamide -
XX
XX
XX Claim 31; Fig 11; 71pp; English.
XX
XX The present sequence represents the alpha subunit of a nitrile hydratase
CC of *Bacillus* sp. BR449 (ATCC 202119). The BR449 nitrile hydratase is
CC optimally active at greater than 55 degrees Celsius, and stable at
CC greater than 60 degrees Celsius. The enzyme contains cobalt, and converts
CC nitriles to amides without significant production of its corresponding
CC acid. As the BR449 nitrile hydratase, unlike known nitrile hydratases,
CC does not require a low temperature, cooling is not necessary and both
CC reaction rate and product solubility are improved. The enzyme also has
CC high resistance to substrate inhibition, allowing a high concentration
CC of acrylonitrile in the reaction mixture. The nitrile hydratase and cells
CC that express it, are used to convert acrylonitrile to acrylamide, a
CC starting material for polymers, and may also be used to hydrate many
CC other nitriles. The enzymatic production of acrylamide from acrylonitrile
CC generates fewer waste products and requires less energy than the
CC conventional copper-catalysed process. An associated amidase is used to
CC convert amides to the corresponding acid. The nitrile hydratase
CC polynucleotide is used to produce transformants for recombinant
CC production of the nitrile hydratase without expression of the associated
CC amidase.
XX
SQ Sequence 214 AA;
AAY53610 Length: 248 April 1, 2002 16:31 Type: P Check: 4816 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSMTIDOK NTNIDPREPH
51 HHPRQSQWE ARAKALESLS IEKGHLSSDA IERVYKHVEH ELGPMNGAKV
101 VAKAWTDPAF KQRLDEPET VLKELGYGL OGEHRYVEN TDYHNVVVC
151 TLCSCYPWPL LGLPPSWYKE PAYRARVYKE PQVYKEFL DLPSVEIRV
201 WDSSEIRFM VLPORPECTE GMTHEELAKL VTRDSMIGVA KIEPLKLR
!!AA_SEQUENCE 1.0
ID AAM23571 standard; Protein: 157 AA.
XX
AC AAM23571;
XX
DT 12-OCT-2001 (first entry)
XX
DE Arabidopsis EST encoded protein SEQ ID NO: 1096.
XX
KW Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
OS Arabidopsis thaliana.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PE 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX MPI: 2001-476164/51.
DR N-PSDB; AAH98230.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PS antibodies and research use -
XX
PS Claim 20; Page 821-822; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 157 AA;

AA023571 Length: 191 April 1, 2002 16:31 Type: P Check: 7240 ..

1 SOARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSMFEVIAF LSPLSLFLA
51 KFLKKADTRD SRQACLAASL ALALNGVFTN TIKLIYGRPR PDFEYRCPFD
101 GLAHSIDLACT GDKDVNENGR KSPFSGHSSF AFAGLAFASF YLAGKLHCFT
151 POGRGKSWRF CAPLSPLFLA AVIALSRCTD YKHHMOGPPK W

!!AA_SEQUENCE 1.0
ID AAA0285 standard; Protein; 566 AA.

XX AAA0285;

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3430.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemoknetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Qa, Zhou P, Goodrich R, Drmanac RT;
XX MPI: 2001-442253/47.
DR N-PSDB; AAI59441.
XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -
XX
PS Example 5; SEQ ID NO 3430; 10078pp; English.
XX

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA038642-AA042213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemoknetic activity, hemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 566 AA;

AA040285 Length: 600 April 1, 2002 16:31 Type: P Check: 2082 ..

1 SOARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSMDEGCT PLLPDSLIVYO
51 IFLSLGPAVY LAAGLVCKQW QAVSRDEFM REQFYTYOV ARDYVRHRA
101 MSWYEEFORL YDTPVCVEVQ TLREHTDOVL HLFSSHGXQ FASCSDCTV
151 KIMSDLRTIS LLHSADMRPY NWSYQFSQF NKDDSLLLAS GVFLGPHNSS
201 SEIYAVISLD SFALLSRPN KPYDVEGCWL TETSLISGMV HRIGITSCS
251 VLMLNNAFOD VESENVVYK RLFKIONLNA SVYRTVMAD CSRFDPDL
301 LEAGDPATSP CRIFDLGSDN EEVYAGPAPA HAKEGLRHFL DYLEGRAPQ
351 QLSERKLETK VALLAQGHT KPERRSATGA KSYLIFFTG CLTYSPHIG
401 IKOLLEPHONT TAGPYLGEGR GSDAFDLDL HVIDIHGII GMGLSPDNRY
451 LVVNSRAMPN GAVVADPMQ PPIAEIDL VFDLKTREY RALRAHAY
501 TRNDECFEFL LDVSRDFVAS GAEDRHGYM DRHYNICLAR LRHEVYNSV
551 VSPQEQELL LTASDDATIK AMRSPRTMY LQAPRRPRT PFSWLASQRR

!!AA_SEQUENCE 1.0
ID AAA02450 standard; Protein; 85 AA.

XX AAA02450;

XX 22-OCT-2001 (first entry)

DE Human kidney related polypeptide SEQ ID NO 319.

XX Human; kidney antigen; immunosuppressive; antiarthritis; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotrophic; cerebroprotective;
KW noctropic; neuroprotective; antibacterial; virocidic; fungicide;
KW ophthalmological; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; vulnerability; anticonvulsant; antiparasitic;
KW gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection.

XX Homo sapiens.

XX WO200155323-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01343.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209457.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225457.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0234200.
PR 14-SEP-2000; 2000US-0234201.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239933.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-488784/53.
DR N-PSDB: AAI63004.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,

PT treating and/or preventing human diseases and disorders -
 XX
 XX Claim 11: SEQ ID NO 319; 564pp + Sequence Listing; English.
 XX
 CC The invention relates to novel kidney related polynucleotides
 CC (AA162971-AA163793) and the encoded polypeptides (AA42417-AA42691)
 CC collectively known as kidney antigens and the use of such kidney antigens
 CC for detecting disorders of the kidney, especially kidney cancer and
 CC kidney cancer metastases. The polynucleotides and proteins are also
 CC useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. The genes are isolated from a range
 CC of human tissues disclosed in the specification. The nucleic acids,
 CC proteins, antibodies and (ant)agonists are useful in the diagnosis,
 CC treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
 CC and other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
 CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 85 AA:
 AA42450 Length: 119 April 1, 2002 16:31 Type: P Check: 7719 ..
 1 SQARNDBCEQ ZGHSQILKMF PSTWVYSQOT HERSKPSDLF ILESHYQKF
 51 PASQLAGITG HAPSWLAIEFC IFSRDVSPC WSGMSGNSRP QVDLPXNASQ
 101 SGWGFSTVGH PRPGIYFVX
 11AA-SEQUENCE 1.0
 ID AAU12377 standard; Protein: 1184 AA.
 XX
 AC AAU12377;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO1188 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PE 01-DEC-2000; 2000WO-US32678.
 XX
 XX 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 XX (GENTECH) GENENTECH INC.
 PA
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;
 PI Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WPI: 2001-408281/43.
 DR N-PSDB: AAS21449.
 DR
 DR
 DR
 XX
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 XX
 PS Claim 12; Fig 412; 813pp; English.
 XX
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 XX
 SQ Sequence 1184 AA;
 AAU12377 Length: 1218 April 1, 2002 16:31 Type: P Check: 668 ..
 1 SQARNDBCEQ ZGHSQILKMF PSTWVYSQOT HERSWGTGA WFSPLVLEY
 51 TSVLGRQTMV TQSVRRVQPG KKNPSIFAKP ADLIESPGEW TTFMFIDIPG
 101 GKDYERLDA IRFYGDRCV APRLRLEART TMTFAGSTG QVHGSPREG
 151 FVCLNREQRP GONCSNVTYR FLCPPGSLR DTERIWPMS PMSKSAACG
 201 QTCVQTRTRI CLAEVSLCS EASEEGCHM GDDCTACDLT CPMGVNADC
 251 DACMCOEFLM HGAVSLPGA PASGAATYLL TTPKLLTQT DSDGRRIRIG
 301 LCPDGSLIK ITKVFAPIV LTMPTSLKA ATIKAEFVA ETPYVWNP
 351 TKARRAGQSV SLCKAIGKP RPDKIYWHN DTLIDPSLYK HESKIVLKL
 401 OQHAGEYFC KAQSDAGAV SKVAQLITVA SDETPCNPV ESYLIRLPHD

451 CFQNNATNSFY YDVGRCPVKT CAGQDNGIR CRDAVQNCQG ISKTEEREIQ
 501 CSGTYLPTKV AKESCCORCT EFRSIVRGV SAADNGEPMR FGHVYMNSR
 551 VSMGYKATF TLHYPDTER LVLTFFVDRIG KFNVTTKVLK FNKGSVFI
 601 EIKMLRKEP TLEAMETNI IPLGEVGED PMAELEIPSR SFYQNGEPEY
 651 IGKVASVTF LDPNNISTAT AAOQDLNFIN DEGDFEPLRT YGMSVDFRD
 701 EYTSPELWAG KVKYHLDSTQ VKMPEHISTY KLMSLNPDIG LMEEGDFKE
 751 ENQRRNKRED RTFLVGNLEI RERRLFNLV PESRCFVKV RAYSERFLP
 801 SEQIQ3VVIS VINLEPRTGF LSNPRAMGRF DSVITGPNGA CVPAFCDQS
 851 PDAYSAYVLA SLAGEELOAV ESSPKFNPN IGVPPQYLNK LMYRTIHED
 901 PRVKKTAFOI SMAKPRPNSA EESNGPIYAF ENLRACEAP PSAAHFREYQ
 951 IEGDRYDNT VPFNEDDPMs WTEDYLAMP KMEFRACYI KVKIVGPLEV
 1001 NVRSNNMGT HRTVVGKLYG IRDVRSTRDR DQPNVSACL EFKSGMLYD
 1051 QDRVDRTLVK VIPQSCSRA SVNPMLEHYL VNHPLAVNN DTSEYTM LAP
 1101 LDPLGHNYGI YTYPDODPRT AKELALGRCF DGTSDGSSRI MKNVGVALT
 1151 FNCVERQYGR QSAFOYLOST PAQSPAAGTY QGRVPSRRQ RASRGQNG
 1201 GVVASLRPR VAQPLIN

11AA-SEQUENCE 1.0
 ID AAG62768 standard; peptide: 11 AA.

AC AAG62768;
 DT 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P.
 KM Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 OS Unidentified.
 FH Key Location/Qualifiers
 FT Modified-site 11 /note- "amidated residue"
 PN WO200153336-A1.
 PD 26-JUL-2001.
 PF 17-JAN-2001; 2001WO-US01529.
 PR 19-JAN-2000; 2000US-0489667.
 PA (ALLR) ALLERGAN SALES INC.
 PI Donovan S;
 DR WPI: 2001-451900/48.
 PT Agent useful for treating pain comprises a clostridial neurotoxin (or
 PS component) attached to a targeting moiety
 XX Disclosure: Page 61; 77pp; English.
 CC The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin

CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P, and is used in the course of the invention.
 SO Sequence 11 AA;

AAG62768 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGIM

11AA-SEQUENCE 1.0
 ID AAG62769 standard; peptide: 12 AA.

AC AAG62769;
 DT 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P precursor.
 KM Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 OS Unidentified.
 PN WO200153336-A1.
 PD 26-JUL-2001.
 PF 17-JAN-2001; 2001WO-US01529.
 PR 19-JAN-2000; 2000US-0489667.
 PA (ALLR) ALLERGAN SALES INC.
 PI Donovan S;
 DR WPI: 2001-451900/48.

PT Agent useful for treating pain comprises a clostridial neurotoxin (or
 PS component) attached to a targeting moiety

PS Disclosure: Page 62; 77pp; English.

CC The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.

SO Sequence 12 AA;

AAG62769 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGIMG

11AA-SEQUENCE 1.0
 ID AAG62770 standard; peptide: 13 AA.

AC AAG62770;
 DT 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P precursor.
 KM Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 XX

OS Unidentified.
 XX WO200153336-A1.
 PN 26-JUL-2001.
 XX 17-JAN-2001; 2001WO-US01529.
 PF 19-JAN-2000; 2000US-0489667.
 XX (ALLR) ALLERGAN SALES INC.
 XX Donovan S;
 XX WPI; 2001-451900/48.
 DR Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX Disclosure; Page 62; 77pp; English.
 PS The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.
 CC
 SQ Sequence 13 AA;
 AAG62770 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGLMGR

!!AA_SEQUENCE 1.0
 ID AAG62771 standard; peptide: 14 AA.
 XX AAG62771;
 XX 17-SEP-2001 (first entry)
 DT Amino acid sequence of substance P precursor.
 DE Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 KM Unidentified.
 OS
 XX WO200153336-A1.
 PN 26-JUL-2001.
 PD 17-JAN-2001; 2001WO-US01529.
 PF 19-JAN-2000; 2000US-0489667.
 XX (ALLR) ALLERGAN SALES INC.
 PA Donovan S;
 XX WPI; 2001-451900/48.
 DR Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX Disclosure; Page 63; 77pp; English.
 PS The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected

CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.
 CC
 SQ Sequence 14 AA;
 AAG62771 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGLMGR

!!AA_SEQUENCE 1.0
 ID AAG62772 standard; peptide: 12 AA.
 XX AAG62772;
 AC 17-SEP-2001 (first entry)
 DT Amino acid sequence of carboxy-ester substance P precursor.
 DE Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 KW Synthetic.
 OS Key
 XX Location/Qualifiers
 FH Modified-site 12
 FT /note="methylated residue"
 FT
 XX WO200153336-A1.
 PN 26-JUL-2001.
 PD 17-JAN-2001; 2001WO-US01529.
 PF 19-JAN-2000; 2000US-0489667.
 XX (ALLR) ALLERGAN SALES INC.
 PA Donovan S;
 XX WPI; 2001-451900/48.
 DR Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX Disclosure; Page 64; 77pp; English.
 PS The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 CC
 SQ Sequence 12 AA;
 AAG62772 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGLMGR

!!AA_SEQUENCE 1.0
 ID AAG62773 standard; peptide: 13 AA.
 XX

AC AAG62773;
XX
PR 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 13
PS /note= "methylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PE 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 65; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
SQ Sequence 13 AA:
AAG62773 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSOOT HERSRPPQO FFGIMGK
11AA_SEQUENCE 1.0
ID AAG62774 standard; peptide: 14 AA.
XX
AC AAG62774;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 14
PS /note= "methylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 65; 77pp; English.

XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 66; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
SQ Sequence 14 AA:
AAG62774 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSOOT HERSRPPQO FFGIMGKR
11AA_SEQUENCE 1.0
ID AAG62775 standard; peptide: 12 AA.
XX
AC AAG62775;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
PS /note= "ethylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PE 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 67; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin

CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 XX
 SQ Sequence 12 AA;

AAG62775 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG

IIAA_SEQUENCE 1.0
 ID AAG62776 standard; peptide: 13 AA.

AC AAG62776;

DT 17-SEP-2001 (first entry)

DE Amino acid sequence of carboxy-ester substance P precursor.

KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 13 /note="ethylated residue"

XX WO200153336-A1.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

PR 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

PA (ALLR) ALLERGAN SALES INC.

PI Donovan S;

DR WPI; 2001-451900/48.

XX
 PT Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety
 XX
 PS Disclosure; Page 68; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 CC
 XX
 SQ Sequence 13 AA;

AAG62776 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG

IIAA_SEQUENCE 1.0

ID AAG62777 standard; peptide: 14 AA.

AC AAG62777;

DT 17-SEP-2001 (first entry)

XX
 DE Amino acid sequence of carboxy-ester substance P precursor.
 XX
 KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Modified-site 14 /note="ethylated residue"

XX WO200153336-A1.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

PR 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

PA (ALLR) ALLERGAN SALES INC.

PI Donovan S;

DR WPI; 2001-451900/48.

XX
 PT Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety
 XX
 PS Disclosure; Page 69; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 CC
 XX
 SQ Sequence 14 AA;

AAG62777 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

IIAA_SEQUENCE 1.0
 ID AAG62780 standard; peptide: 9 AA.

AC AAG62780;

DT 17-SEP-2001 (first entry)

DE Amino acid sequence of a substance P fragment.

KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX Unidentified.

XX WO200153336-A1.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

PR 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

PA (ALLR) ALLERGAN SALES INC.

PI Donovan S;

PI Fitzgerald DJ, Iadarola MJ;
XX
DR WPI; 2001-417560/44.
XX
PT Making cell toxin to treat chronic pain, by forming substance
PT P-pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
PT exotoxin and substance P having additional cysteine residue at its
PT N-terminus
XX
PS Disclosure; Page 10; 54pp; English.
XX
CC The present sequence represents a human substance P. The peptide is
CC used to produce a cell toxin. The cell toxin comprises a substance
CC P-pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
CC useful for ablating NK-1 receptor expressing cells, such as dorsal horn
CC cell, a stratum cell or a brain parenchyma cell, for treating chronic
CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
CC sheaths, nerve linings, meninges, pia mater cells, arachnoid membrane
CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
CC parenchymal cells, without significantly affecting basal nociceptive
CC responses. The cell toxin is thus useful for treating chronic pain or
CC tumours that binds substance P. It is also useful for neurological
CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
CC that express substance P e.g. Parkinson's disease.
CC
XX
SQ Sequence 11 AA;

AAB84527 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQOQ FFGIM

!1AA_SEQUENCE 1.0

ID AAB84528 standard; peptide; 12 AA.

AC AAB84528;

DT 05-SEP-2001 (first entry)

XX Amino acid sequence of a modified substance P.

DE Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;

KW NK-1 receptor; chronic pain; tumour; neurological dysfunction;

KW basal ganglia; cholinergic interneuron; Parkinson's disease.

XX Homo sapiens.

OS Synthetic.

XX WO200131020-A1.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-US29064.

XX 22-OCT-1999; 99US-0161159.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Fitzgerald DJ, Iadarola MJ;

XX WPI; 2001-417560/44.

XX Making cell toxin to treat chronic pain, by forming substance
XX P-pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
XX exotoxin and substance P having additional cysteine residue at its
XX N-terminus

XX Example 1; Page 10; 54pp; English.

XX The present sequence represents a modified substance P. The peptide is
XX used to produce a cell toxin. The cell toxin comprises a substance
XX P-pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
XX useful for ablating NK-1 receptor expressing cells, such as dorsal horn
XX cell, a stratum cell or a brain parenchyma cell, for treating chronic

CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
CC sheaths, nerve linings, meninges, pia mater cells, arachnoid membrane
CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
CC parenchymal cells, without significantly affecting basal nociceptive
CC responses. The cell toxin is thus useful for treating chronic pain or
CC tumours that binds substance P. It is also useful for neurological
CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
CC that express substance P e.g. Parkinson's disease.
CC
XX
SQ Sequence 12 AA;

AAB84528 Length: 46 April 1, 2002 16:31 Type: P Check: 3910 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQOQ QFGIM

!1AA_SEQUENCE 1.0

ID AAG89279 standard; Protein; 180 AA.

XX AAG89279;

DT 11-SEP-2001 (first entry)

XX Human secreted protein, SEQ ID NO: 399.

DE Human secreted protein; gene therapy; vaccine; treatment; diagnosis;

KW GENSET.

XX Homo sapiens.

XX WO200142451-A2.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-IB01938.

XX 08-DEC-1999; 99US-0169629.

XX 06-MAR-2000; 2000US-0187470.

XX (GENSET) GENSET.

XX Dumas Milne Edwards J, Bougueleret L, Jobert S;

XX WPI; 2001-367870/38.

XX N-PSDB; AAH64882.

XX Full length GENSET human nucleic acids encoding potentially secreted
XX proteins, useful in gene therapy and vaccination against a variety of
XX diseases, and for diagnosis of those diseases

XX Claim 21; Page 882-883; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding
XX potentially secreted proteins. The nucleic acids and the polypeptides
XX they encode may be used in the prevention, treatment and diagnosis of
XX diseases associated with inappropriate GENSET gene expression. For
XX example, they be used to treat disorders associated with decreased
XX GENSET gene expression by rectifying mutations or deletions in a
XX patient's genome that affect the activity of GENSET or by supplementing
XX the patient's own production of GENSET polypeptides. Conversely,
XX antisense nucleic acid molecules may be administered to down regulate
XX GENSET expression by binding with the cells' own genes and preventing
XX their expression. The sense and antisense nucleic acids may also be
XX used as DNA probes in diagnostic assays to detect and quantitate the
XX presence of similar nucleic acid sequences in samples, and hence to
XX determine which patients may be in need of restorative therapy.

XX The GENSET polypeptides may be used as antigens in the production of
XX antibodies and in assays to identify modulators (agonists and
XX antagonists) of GENSET polypeptide expression and activity. The
XX present sequence is a GENSET polypeptide of the invention.

XX Sequence 180 AA;

XX AAG89279 Length: 214 April 1, 2002 16:31 Type: P Check: 9228 ..

XX 03-MAY-2001.
PD
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
DR
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 12 AA;
0
AAB98867 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIMG
11AA_SEQUENCE 1.0
ID AAB98868 standard; Peptide; 13 AA.
XX
AC AAB98868;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #24.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 13
FT /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
PF 28-OCT-1999; 99US-0428692.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
DR
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from

CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 13 AA;
AAB98868 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIMG
11AA_SEQUENCE 1.0
ID AAB98869 standard; Peptide; 14 AA.
XX
AC AAB98869;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #25.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
DR
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 14 AA;
AAB98869 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIMG
11AA_SEQUENCE 1.0
ID AAB98870 standard; Peptide; 12 AA.
XX
AC AAB98870;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #26.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.

XX Key Location/Qualifiers
FH Modified-site 12
FT /label= OTHER
FT /note= "modified by Ome"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
XX Sequence 12 AA;

AAB98870 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLMG

!!AA_SEQUENCE 1.0
ID AAB98871 standard; Peptide; 13 AA.

AC AAB98871;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #27.

KM Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 13
FT /label= OTHER
FT /note= "modified by Ome"

PN WO200130371-A2.

PD 03-MAY-2001.

PD 27-OCT-2000; 2000WO-US29789.

PR 28-OCT-1999; 99US-0428692.

PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

WPI; 2001-397593/42.

DT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group

XX Claim 10; Page 15; 34pp; English.
PS
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
XX Sequence 13 AA;

AAB98871 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLMG

!!AA_SEQUENCE 1.0
ID AAB98872 standard; Peptide; 14 AA.

AC AAB98872;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #28.

KM Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 14
FT /label= OTHER
FT /note= "modified by Ome"

PN WO200130371-A2.

PD 03-MAY-2001.

PD 27-OCT-2000; 2000WO-US29789.

PR 28-OCT-1999; 99US-0428692.

PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

WPI; 2001-397593/42.

DT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group

PS Claim 10; Page 15; 34pp; English.

CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
XX Sequence 14 AA;

AAB98872 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLMGKR

!!AA_SEQUENCE 1.0
ID AAB98873 standard; Peptide; 12 AA.

AC AAB98873;

DT 14-AUG-2001 (first entry)

XX Chimeric analgesic peptide #29.
DE
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
KM pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /label= OTHER
FT /note= "modified by Oeth"
XX
PN W0200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
XX (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
PI WPI; 2001-397593/42.
XX
DR
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 12 AA;
AAB9873 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG
!!AA_SEQUENCE 1.0
ID AAB9874 standard; Peptide; 13 AA.
XX
AC AAB9874;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #30.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
KM pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 13
FT /label= OTHER
FT /note= "modified by Oeth"
XX
PN W0200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
XX (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
PI
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 13 AA;
AAB9874 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG
!!AA_SEQUENCE 1.0
ID AAB9875 standard; Peptide; 14 AA.
XX
AC AAB9875;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #31.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
KM pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "modified by Oeth"
XX
PN W0200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
XX (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
PI WPI; 2001-397593/42.
XX
DT New chimeric peptides used for treating pain comprise opioid receptor
DT binding group and nociceptive receptor binding group
XX
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 14 AA;
AAB9875 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

11AA_SEQUENCE 1.0
ID AAB98878 standard; Peptide: 9 AA.
XX
AC AAB98878;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #34.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Modified-site 9 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 9 AA;
AAB98878 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFG
11AA_SEQUENCE 1.0
ID AAB98879 standard; Peptide: 11 AA.
XX
AC AAB98879;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #35.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT /note= "D-form residue"
XX

FT Modified-site 11
FT /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 11 AA;
AAB98879 Length: 45 April 1, 2002 16:31 Type: P Check: 1410 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFWLM
11AA_SEQUENCE 1.0
ID AAB98880 standard; Peptide: 12 AA.
XX
AC AAB98880;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #36.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT MISC-difference 12 /note= "D-form residue"
FT Modified-site 12 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX

DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15-16; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 12 AA;
AAB98880 Length: 46 April 1, 2002 16:31 Type: P Check: 4676 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVYSOOT HERSRPKPQO FFWLMG
!!AA_SEQUENCE 1.0
ID AAB98881 standard; Peptide: 11 AA.
XX
AC AAB98881;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #37.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 11 /note= "D-form residue"
FT Modified-site 11 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 16; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 11 AA;

AAB98881 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVYSOOT HERSRPKPQO FFWLMG
!!AA_SEQUENCE 1.0
ID AAB98882 standard; Peptide: 12 AA.
XX
AC AAB98882;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #38.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 12 /note= "D-form residue"
FT Modified-site 12 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 16; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 12 AA;
AAB98882 Length: 46 April 1, 2002 16:31 Type: P Check: 5373 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVYSOOT HERSRPKPQO FFWLMG
!!AA_SEQUENCE 1.0
ID AAB82070 standard; peptide: 11 AA.
XX
AC AAB82070;
XX
DT 22-JUN-2001 (first entry)
XX
DE Substance P.
XX
KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
KW viral infection; substance P.
XX

OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200124822-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-EP09657.
XX
PR 01-OCT-1999; 99AT-0001680.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Flettman J, Maltner F, Buschle M, Melling J;
XX
DR WPI; 2001-290577/30.
XX
PT New pharmaceutical composition comprising an antigen, an
PT immunostimulating substance and a polycationic polymer, useful in
PT manufacturing vaccines
XX
PS Example 3; Page 14; 20pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC (a) an antigen; (b) an immunostimulating substance consisting of
CC neuroactive compounds, hormones, compounds having growth hormone activity
CC or their mixtures; and (c) a polycationic polymer. The composition is
CC useful in manufacturing vaccines. To illustrate the present invention, a
CC murine tyrosinase related protein-2 peptide (TRP-2 peptide; see
CC AAB82064), was used. Mice were injected subcutaneously with either the
CC TRP-2 peptide, TRP-2 peptide + poly-L-arginine 60 (pR60) or TRP-2 peptide
CC + pR60 + substance P (the present peptide). Animals were sacrificed 10
CC days post injection, and spleen tissue was harvested. Lymphocytes were
CC prepared from the spleen tissue and were re-stimulated with TRP-2 peptide
CC or with an ovalbumin-derived peptide (AAB82065), with the same major
CC histocompatibility complex (MHC) restriction serving as negative control.
CC Spots representing single T cells specific for the peptide used for
CC re-stimulation were counted. No spots were detected when the ovalbumin
CC derived peptide was used, while TRP-2 peptide + pR60 + substance P showed
CC the highest number of spots or single T cells.
XX
SQ Sequence 11 AA:
AAB82070 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFGLM
11AA_SEQUENCE 1.0
ID AAB91402 standard; Peptide: 11 AA.
XX
AC AAB91402;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:578.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR

PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 389; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA:
AAB91402 Length: 45 April 1, 2002 16:31 Type: P Check: 981 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFGLM
11AA_SEQUENCE 1.0
ID AAB91409 standard; Peptide: 11 AA.
XX
AC AAB91409;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:585.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX

PT
XX
PS Disclosure; Page 391; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
AAB91409 Length: 45 April 1, 2002 16:31 Type: P Check: 1520 ..
1 SQARNDBQGE ZGHSQILKMF PSTWVYSOOT HERSRPRQO FYGLM
11AA_SEQUENCE 1.0
ID AAB91410 standard; Peptide: 10 AA.
XX
AC AAB91410;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:586.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 391; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;
AAB91410 Length: 44 April 1, 2002 16:31 Type: P Check: 7516 ..
1 SQARNDBQGE ZGHSQILKMF PSTWVYSOOT HERSRPRQO FYGLM
11AA_SEQUENCE 1.0
ID AAB91411 standard; Peptide: 11 AA.
XX
AC AAB91411;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:587.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 392; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX

SQ Sequence 11 AA;
AAB91411 Length: 45 April 1, 2002 16:31 Type: P Check: 765 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFWLM
!!AA_SEQUENCE 1.0
ID AAB91412 standard; Peptide: 11 AA.
XX AAB91412;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:588.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy1; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200069300-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX -
PT
XX
XX Disclosure; Page 392; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
CC
XX
XX Sequence 11 AA;
SQ
AAB91412 Length: 45 April 1, 2002 16:31 Type: P Check: 1410 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFWLM
!!AA_SEQUENCE 1.0
ID AAB91413 standard; Peptide: 11 AA.
XX AAB91413;
AC
XX

DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:589.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy1; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX -
PT
XX
XX Disclosure; Page 392; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
CC
XX
XX Sequence 11 AA;
SQ
AAB91413 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFWLM
!!AA_SEQUENCE 1.0
ID AAB91414 standard; Peptide: 11 AA.
XX AAB91414;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Tachykinins peptide SEQ ID NO:590.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy1; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX

PM WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 392; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
AAB91414 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..
1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPPO WFWLL
ID AAB91415 standard; Peptide; 11 AA.
XX
AC AAB91415;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:591.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification: succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.

XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 393; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
AAB91415 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..
1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPPO FFWLL
ID AAB91422 standard; Peptide; 10 AA.
XX
AC AAB91422;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:598.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification: succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 395; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
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CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

AAB91422 Length: 44 April 1, 2002 16:31 Type: P Check: 7516 ..

1 SQARNDBQCE ZGHSQILKMF PSTWYVSQOT HERSRPPQQ FFLM

!!AA_SEQUENCE 1.0
ID AAB91423 standard; Peptide; 10 AA.

XX AAB91423;

DT 22-JUN-2001 (first entry)

XX Tachykinins peptide SEQ ID NO:599.

XX Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI: 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX -
XX Disclosure: Page 395; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

AAB91423 Length: 44 April 1, 2002 16:31 Type: P Check: 7257 ..

1 SQARNDBQCE ZGHSQILKMF PSTWYVSQOT HERSRPPQQ FFLG

!!AA_SEQUENCE 1.0
ID AAB91427 standard; Peptide; 10 AA.

XX AAB91427;

DT 22-JUN-2001 (first entry)

XX Tachykinins peptide SEQ ID NO:603.

XX Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI: 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX -
XX Disclosure: Page 396; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

AAB91427 Length: 44 April 1, 2002 16:31 Type: P Check: 7257 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPPQO FEGL
!!AA_SEQUENCE 1.0
ID AAB91429 standard; Peptide; 11 AA.
XX
AC AAB91429;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:605.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
PN 23-NOV-2000.
XX
PD 17-MAY-2000; 2000WO-US13576.
XX
PF 17-MAY-1999; 99US-0134406.
XX
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
XX WPI: 2001-112059/12.
XX
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS
XX Disclosure: Page 397; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
AAB91429 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ...

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
PN 23-NOV-2000.
XX
PD 17-MAY-2000; 2000WO-US13576.
XX
PF 17-MAY-1999; 99US-0134406.
XX
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
XX WPI: 2001-112059/12.
XX
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS
XX Disclosure: Page 398; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;
AAB91432 Length: 44 April 1, 2002 16:31 Type: P Check: 7516 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPPQO FFPLM
!!AA_SEQUENCE 1.0
ID AAB91434 standard; Peptide; 11 AA.
XX
AC AAB91434;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:610.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
PN 23-NOV-2000.
XX

PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 398; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
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CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SO Sequence 11 AA:
AAB91434 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO WFWLL
11AA_SEQUENCE 1.0
ID AAB91436 standard; Peptide: 11 AA.
XX
AC AAB91436;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:612.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.

XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 399; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
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CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SO Sequence 11 AA:
AAB91436 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
11AA_SEQUENCE 1.0
ID AAB91438 standard; Peptide: 11 AA.
XX
AC AAB91438;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:614.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 399; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently

XX AAB91449;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:625.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
PS Disclosure: Page 403; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
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CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 11 AA;
AAB91449 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SCARNDBOE ZGHSQILKMF PSTWYSQOT HERSRPPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAB91450 standard; Peptide; 11 AA.
XX
XX AAB91450;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:626.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX

OS Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
PS Disclosure: Page 403; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
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CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
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CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 11 AA;
AAB91450 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SCARNDBOE ZGHSQILKMF PSTWYSQOT HERSRPPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAB91451 standard; Peptide; 10 AA.
XX
XX AAB91451;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:627.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 24 AA;

AAB92031 Length: 58 April 1, 2002 16:31 Type: P Check: 344 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSGWTLS AGYLLGPPRK

51 PQQFWML

11AA_SEQUENCE 1.0
 ID AAB70690 standard; Protein; 175 AA.

XX AAB70690;

XX 17-MAY-2001 (first entry)

XX Human hDPP protein sequence SEQ ID NO:7.

XX Human; hDPP; diacylglycerol pyrophosphate phosphatase; DPP; detection.

XX Homo sapiens.

XX CN1271009-A.

XX 25-OCT-2000.

XX 17-MAR-2000; 2000CN-0114952.

XX 17-MAR-2000; 2000CN-0114952.

XX (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.

XX Li N, Xiao H, Liu F;

XX WPI: 2001-081384/10.

XX N-PSDB; AAF74766.

XX New human diacyl glyceropyrophosphate phosphatase protein and its code
 XX sequence -

XX Claim 4; Page 17; 19pp; Chinese.

XX The present invention describes a human diacylglycerol pyrophosphate
 CC phosphatase (DPP) designated hDPP. hDPP is expressed in normal tissue
 CC near cancerous liver cells of a human body. Also described are methods
 CC for the preparation and detection of hDPP nucleotide and protein
 CC sequences. The present sequence represents human hDPP, as given in the
 CC present invention.
 CC
 XX
 SQ Sequence 175 AA;

AAB70690 Length: 209 April 1, 2002 16:31 Type: P Check: 4219 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSMILYRN PYVEAFYPT

51 KPMFVIAFLS PLSLIFLAKF LKKADTRDSR QACIAASLAL ALNGVFTNTI

101 KLIV3PRPD PFYRCFPDGL AHSILMCTGD KDVVNIGRKS FPGHSSFAF

151 AGIAPASFLY AGKLHCFTIPQ GRGSMRCA FLSPILFAAY IALSRICDYK

201 HHMOGPFKX

11AA_SEQUENCE 1.0
 ID AAB49755 standard; peptide; 11 AA.

XX AAB49755;

XX 17-APR-2001 (first entry)

XX Complex sugar bound peptide (SBP) amino acid sequence.

XX Sugar peptide complex; SBP; sugar bound peptide; enzymatically stable.

XX Synthetic.

XX JP2000319297-A.

XX 21-NOV-2000.

XX 30-MAR-1999; 99JP-0088030.

XX 30-MAR-1999; 99JP-0088030.

XX (NOCK) ZH NOGUCHI KENKYUSHO.

XX WPI: 2001-184996/19.

XX A process for preparation of enzymically stable sugar peptide complex

XX Example 2; Page 3; 4pp; Japanese.

XX This invention relates to a process for the preparation of an
 CC enzymatically stable sugar peptide complex, and includes an in vivo
 CC stable inhibitor of peptide:N-glycanase (EC. 3.5.1.57). The process can
 CC be used for the investigation of in vivo reciprocal recognition of
 CC cell-cell and substrate-receptor interaction, and their metabolism. The
 CC present sequence represents a complex sugar bound peptide (SBP) amino
 CC acid sequence prepared by the process of the invention.
 CC
 XX
 SQ Sequence 11 AA;

AAB49755 Length: 45 April 1, 2002 16:31 Type: P Check: 736 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSKRPQO FFGIM

11AA_SEQUENCE 1.0
 ID AAB65180 standard; Protein; 1184 AA.

XX AAB65180;

XX 02-APR-2001 (first entry)

XX Human PRO1188 (UNQ602) protein sequence. SEQ ID NO:124.

XX Human; secreted and transmembrane protein; PRO; cytosolic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 KW
 XX
 OS Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US05884.
 PR 20-MAR-2000; 2000WO-US07377.
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CU, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 XX
 XX WPI: 2001-032160/04.
 DR N-PSDB: AAF44131.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 72; 935bp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 CC
 XX Sequence 1184 AA;
 SO
 AAB65180 Length: 1218 April 1, 2002 16:31 Type: P Check: 668 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWYVSGOT HERSMVGTKA WVFSEFLVEV
 51 TSVLGRQTM TQSVRRVQPG KKNPSITFAKP ADLLESPGEM TFWPNDIDYG
 101 GKGDYERLDA IREYYGDRVC ARPLRLBART TDWTPAGSTG QVYHGSPPRG
 151 FWCINREORP GONCSNYTVR FLCPPGSLRR DTERIWPMS PWSKCSAAGC
 201 QYGVQTRTRI CLAEVSLCS EASEEGQHCN GDCCTACDLT CPMGOVNADC
 251 DACMCOFPM HGAVSLPGA PASGAAILYL TKTPKLLTOT DSDGRRIRIG
 301 LCPDGKSLK ITRKVFAPIV LTMPTSLKA ATIKAEFVRA ETPYVMNPE
 351 TARRRGQSV SLCCKATGKP RPDKYFWYHN DTLLDSLYK HSKVLRLKL
 401 OOHQAGEYFC KAQSDAGAVK SKVAQLIVTA SDETPCNVP ESYLIRLPMD
 451 CFQNAINSPY YDVGRCPVKT CAGQDNGIR CRDAVONCCG ISKTEREIO

501 CSGYTLPTKV AKESCQRCCT ETRSIYGRV SAADNGBPMR FGHVYMGNSR
 551 VSKTGKGTFF TLHVPODTER LVLTFFVDRLQ KEVNTTKULP FNKKSAAVPH
 601 EIKMLRRKEP ITLEAMETNI IPGEVVGED PMAELEIPSR SEYRONGEPP
 651 ICKVKAATFE LDPNISTAT AAOQDLNFIN DEGDTPPLRT YGMFVDFRD
 701 EYTSPEPLNG KVKYHLDSQ VKPEHISTV KLSLNPDPG LMEEGDKFF
 751 ENORNRKRED RTFLVGNLEI RERLFNLDV PESRRCFVAV RAYRSERLP
 801 SQIQGVVIS VINLEPTGF LSNPRAGRF DSVITGPNGA CVPACDDQS
 851 PDAYSAYVLA SLAGELOAV ESSPKFPNA IGVPOPLYAK LMYRTDHD
 901 PRVKTAFQI SMAKRPNSA EESNGPIYAF ENLRACEAP PSAHFRFYQ
 951 IEGDRDYNT VPFNEDDPS WTEDEYLAWP KMEFRACI KYKIGPLEV
 1001 NVSRNMGT HRTYGLYIG IRDYSTRDR DQPNVSAACL EFKSGMLYD
 1051 QDRVDRTLVK VIPQSCRRRA SYNPLHEYL VNHLPYVNN DTSEYTM LAP
 1101 LDPIGHNNGI YTYDQDPRT AKELALGRCF DQTSDDSSRI MKNNGVALT
 1151 FNCVERQVR QSAFOYLOST PAOSPAAGTV QGRVPSRRQO RASRGQROG
 1201 GVVASLRFPR VAQOPLIN
 11AA_SEQUENCE 1.0
 ID AAB50544 standard; peptide: 11 AA.
 XX
 AC AAB50544;
 XX
 DT 16-MAR-2001 (first entry)
 XX
 DE Prolyl endopeptidase inhibitor substance P peptide.
 XX
 KW Prolyl endopeptidase inhibitor; PEP inhibitor; central nervous system;
 KW CNS; nootropic; brain function disorder; Alzheimer's disease; amnesia.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note="amidated"
 XX
 PN WO200071144-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 16-MAY-2000; 2000WO-JP03135.
 XX
 PR 19-MAY-1999; 99JP-0138791.
 XX
 PA (DOME-) DOME INC.
 XX
 PI Kayahara H, Tsukahara K, Inagaki T;
 XX
 DR WPI: 2001-070833/08.
 XX
 PT Prolyl endopeptidase inhibitor comprises cereal extract including new
 PT ketone compound.
 PT
 XX
 PS Disclosure; Fig 1; 27pp; Japanese.
 XX
 CC The present invention describes prolyl endopeptidase (PEP) inhibitors
 CC comprising a cereal extract. Also described are:
 CC (i) a 7-octadecenyl-7,10-henecosadienyl ketone;
 CC (ii) germinating brown rice having prolyl endopeptidase inhibitory
 CC activity for preventing and/or relieving brain function disorders; and

CC (111) foods for preventing or relieving brain function disorders
 CC comprising the above PEP inhibitor or the above germinated brown rice.
 CC The PEP inhibitors can have central nervous system (CNS) and nootropic
 CC activity. The PEP inhibitors can be used for preventing and relieving
 CC brain function disorders including Alzheimer's disease and amnesia.
 CC The present sequence represents a PEP inhibitor peptide given in the
 CC exemplification of the present invention.

XX
 XX
 SO Sequence 11 AA;

AA050344 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQOQ FFGLM

11AA_SEQUENCE 1.0

ID AAB50306 standard; peptide; 11 AA.

AC AAB50306;

DT 08-MAR-2001 (first entry)

DE Substance P.

XX Antibacterial; Botulinum toxin inhibitor; Bttxb;
 KW previn; tetanus neurotoxin; buforinin; substance P.

XX Unidentified.

PN WO200069891-A2.

XX 23-NOV-2000.

PF 15-MAY-2000; 2000WO-US13215.

PR 17-MAY-1999; 99US-0134446.

PA (USSA) US DEPT OF THE ARMY.

PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;

DR WPI: 2001-025001/03.

XX Novel Previn compounds useful for inhibiting the protease activity of
 PT Botulinum B and tetanus toxins -

PS Claim 7; Page 29; 47pp; English.

CC The present sequence was investigated in the search for Botulinum
 CC toxin inhibitors (Bttxb). Previn compounds which inhibit the enzymatic
 CC activity of Bttxb and tetanus neurotoxins were isolated. Previn
 CC may be used to construct compounds such as buforinins.

SO Sequence 11 AA;

AA050306 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQOQ FFGLM

11AA_SEQUENCE 1.0

ID AAB56000 standard; Protein; 128 AA.

AC AAB56000;

DT 08-MAR-2001 (first entry)

DE Skin cell protein, SEQ ID NO: 316.

XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
 KW nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease.

XX Ratus sf.

XX
 PN WO200069884-A2.

XX 23-NOV-2000.

PF 15-MAY-2000; 2000WO-N200075.

PR 14-MAY-1999; 99US-0312283.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

DR WPI: 2001-007495/01.

DR N-PSDB; AAC96699.

XX New isolated polynucleotide used in the identification of genetic
 PT disorders and encoding polypeptides used for treating inflammatory
 PT disease, cancer and neurological diseases -

PS Claim 4; Page 252-253; 352pp; English.

XX The present sequence is a polypeptide which is expressed in
 CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer, and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.

SO Sequence 128 AA;

AA056000 Length: 162 April 1, 2002 16:31 Type: P Check: 24 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRAEFGR SGEMGNAALG

51 AELGVAVLLF VAFIATELLP PFQRIQPEE LMIXRNPYE AXYFTGPWF

101 VIAELTPLSL IFFAKFLRKA DAIDSKOACL AASLALALNG VFTNIITKLIV

151 GRPRDPFFYR CF

```

1 FINDPATTERNS on pir: * allowing 0 mismatches
1 1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) April 1, 2002

1 SPNUB ck: 9307 len: 129 1 neurokinin 1 precursor, beta splice form [V
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 SPRTB ck: 239 len: 130 1 substance P beta precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 SPBOB ck: 421 len: 130 1 neurokinin 1 precursor, beta splice form [V
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 SPRBG ck: 1957 len: 115 1 substance P gamma precursor - rabbit
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 SPRTA ck: 2164 len: 112 1 substance P alpha precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 SPID ck: 4974 len: 11 1 substance P - horse
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLM

1 1:
RPKPQOFF

1 AG0654 ck: 4974 len: 11 1 substance P - guinea pig
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLM

1 1:
RPKPQOFF

1 SZ0901 ck: 1434 len: 6,805 1 titin - rabbit (fragment)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
VMDGE

1 6,200: IPVIG
RPREDTW

1 JCL1409 ck: 3357 len: 471 1 glutamate--ammonia ligase (EC 6.3.1.2) - Ca
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(H)P-P-P(F)(F)
LYYDC

1 459: KOLOL
RPHPEFY

1 SA7038 ck: 219 len: 130 1 tachykinin 1 precursor - golden hamster
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 58: QRIAR
GLMGK

1 SA7038 ck: 844 len: 115 1 tachykinin 1 precursor - golden hamster
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 T52526 ck: 430 len: 130 1 neurokinin 1 precursor - mouse
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 T62742 ck: 3920 len: 72 1 tachykinin A gamma chain precursor - mou
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 23: QRIAR
RPKPQOFF

1 S12958 ck: 7129 len: 97 1 tachykinin delta precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 58: QRIAR
RPKPQOFF

1 JC2412 ck: 7417 len: 63 1 tachykinin gamma chain precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 11: QRIAR
RPKPQOFF

1 JC5455 ck: 4081 len: 72 1 preprotachykinin-A gamma precursor - bo
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK

1 23: QRIAR
RPKPQOFF

1 JND029 ck: 4995 len: 11 1 substance P - chicken
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
GLM

1 1:
RPKPQOFF

1 T408339 ck: 5542 len: 236 1 halosacid dehalogenase-1-like hydrolase - f
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(H)P-P-P(W)(F)
IALKM

1 148: PVGRG
KPHDIME

1 T13857 ck: 425 len: 3,828 1 trithorax protein - fruit fly (Drosophila)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(K)P-P-P(Y)(F)
GLATL

1 618: SDANG
KPKKNYF

1 E862849 ck: 4011 len: 290 1 hypothetical protein AAD39637.1 [Importe
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
RCFPD

1 123: KDANG
RPDPFW

1 E84421 ck: 2420 len: 302 1 probable phosphatidic acid phosphatase (

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1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
123: KVATG      (R)P(R)P-P-P(Y)(W)      RCFPD
      T3306 ck: 3281 len: 206 i hypothetical protein F56G3.9 - Caenorhabdit
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(R)P-P-P(F)(F)
108: RPYTE      KRPQMEF      DWDHT
      T09484 ck: 4681 len: 1,184 i cartilage intermediate layer protein precu
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(R)P-P-P(Y)(F)
335: CKATG      KRPDKYF      WYHND
      A84089 ck: 4652 len: 957 i hypothetical protein BH3513 [imported] - Ba
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (H)P(R)P-P-P(F)(W)
554: ELIRR      HPRPAIFW      EDLFG
      G96806 ck: 8387 len: 421 i unknown protein T5M16.25 [imported] - Arabi
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(K)P-P-P(W)(Y)
145: SRIKH      KRPVQWY      IGDSK
      S29344 ck: 2811 len: 800 i protein kinase KIN3 (EC 2.7.1.-) - yeast (S
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (R)P(R)P-P-P(Y)(Y)
503: HVPRS      RPRPTSYX      PGLSR
      S23308 ck: 4943 len: 11 i substance P - rainbow trout
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(R)P-P-P(F)(F)
1:      KRPHQGF      GLM
      F86524 ck: 9351 len: 286 i SuA5 type protein [imported] - Chlamydomoni
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (H)P(K)P-P-P(F)(Y)
241: GVCE      HPKPKNFY      TRLRE
      F85107 ck: 7623 len: 676 i hypothetical protein AT4G10370 [imported]
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (H)P(H)P-P-P(F)(F)
213: DPKS      HPHPLTF      PTOAS
      G84527 ck: 8684 len: 85 i hypothetical protein At2G15340 [imported]
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (R)P(H)P-P-P(Y)(F)
77: TALGA      RHPMLYF      F
      B44054 ck: 1211 len: 545 i orf2 protein - Junonia coenia densovirus
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(H)P-P-P(F)(F)

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528: KDVEL      KRPMTTF      LLLSK
      E70605 ck: 8381 len: 187 i hypothetical protein RV3567c - Mycobacte
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(R)P-P-P(F)(F)
146: EVPAV      KRPPLFY      RGDYT
      T36591 ck: 1196 len: 373 i hypothetical protein SCH24.26c - Strepto
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (R)P(R)P-P-P(Y)(F)
236: VRDHF      RRPPLSYF      QRMWA
      T04052 ck: 9930 len: 705 i hypothetical protein F24G24.170 - Arabid
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (H)P(H)P-P-P(F)(F)
244: DPKS      HPHPLTF      PTOAS
      T51199 ck: 9296 len: 422 i hypothetical protein B7M4.60 [imported]
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(K)P-P-P(Y)(Y)
239: KCQPP      KRPATY      PGLPP
      T18785 ck: 558 len: 912 i hypothetical protein B0564.7 - Caenorhab
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(R)P-P-P(F)(Y)
532: QWGSK      KRPPLFY      GMDQT
      T32912 ck: 8718 len: 173 i hypothetical protein C54G6.3 - Caenorhab
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (H)P(K)P-P-P(F)(W)
119: VTFIS      HPKPLFW      PLLFQ
      S33300 ck: 4938 len: 11 i probable substance P - smaller spotted c
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (K)P(R)P-P-P(F)(F)
1:      KRPQGF      GLM
      C72098 ck: 9351 len: 286 i SuA5/Yc10/YrDC family protein CP0489 [im
1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)      (H)P(K)P-P-P(F)(Y)
241: GVCE      HPKPKNFY      TRLRE

```

Databases searched: NBRL, Release 68.0, Released on 31Mar2001, Formatted on 26Jun2001

Total finds: 39
 Total length: 76,174,552
 Total sequences: 219,241
 CPU time: 06:44.26

!!AA_SEQUENCE 1.0
 P1:SPHUB - neurokinin 1 precursor, beta splice form [validated] - human
 N:Alternate names: neurokinin A; neurokinin alpha; neuromedin L; neuropeptide K; preprotachykinin; substance K; substance P; tachykinin A
 N:Contains: neurokinin 1; neurokinin 1 precursor; alpha splice form; neurokinin 1 precursor, delta splice form; neurokinin 1 precursor, gamma splice form; neurokinin 2
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1988 #sequence revision 26-May-1995 #text change 19-May-2000
 C:Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270; I62740; I84611
 R:Hammar, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Rosie, R.; Curtis, A.; Goigny, J.; Edwards, C.R.W.; Fink, G.
 FEBS Lett. 208, 67-72, 1986
 A:Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substance P and neurokinin A
 A:Reference number: A24805; MUID:87030957
 A:Accession: A24805
 A:Molecule type: mRNA
 A:Residues: 1-129 <HAR>
 A:Cross-references: GB:M28109; EMBL:X54469; NID:929482; PIDN:CAA38351.1; PID:929483
 R:McGregor, G.P.; Conlon, J.M.
 Peptides 11, 907-910, 1990
 A:Title: Characterization of the C-terminal flanking peptide of human beta-preprotachykinin
 A:Reference number: A60425; MUID:91133994
 A:Accession: A60425
 A:Molecule type: protein
 A:Residues: 111-126 <MG>
 A:Experimental source: neuroendocrine tumor of adrenal medulla
 R:Theodorsson-Morheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oberg, K.; Jacobsson, G.
 Eur. J. Biochem. 166, 693-697, 1987
 A:Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neurokinin A(4-10) from a neutral water extract of a metastatic ileal carcinoid tumor
 A:Reference number: S00069; MUID:87275962
 A:Accession: S00069
 A:Molecule type: protein
 A:Residues: 98-107 <THE>
 R:Age, R.; Thim, L.; Greutefeldt, W.; Conlon, J.M.
 Biochem. J. 253, 203-207, 1988
 A:Title: Post-translational processing of preprotachykinins. Isolation of preprotachykinin-(1-37)-peptide from human adrenal-medullary pheochromocytoma tissue
 A:Reference number: S03033; MUID:88339887
 A:Accession: S03033
 A:Molecule type: protein
 A:Residues: 20-30 <KAG>
 R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.
 Endocrinology 128, 2441-2448, 1991
 A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse testis
 A:Reference number: JC5450; MUID:91209287
 A:Accession: JC5450
 A:Molecule type: mRNA
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Residues: 36-73, 89-122 <CHI1>
 A:Cross-references: GB:M68907; NID:9190292; PIDN:AAA60160.1; PID:9553619
 A:Accession: JC5450
 A:Molecule type: mRNA
 A:Status: translation not shown
 A:Residues: 36-86, 'P', 88-122 <CHI2>
 A:Cross-references: GB:M68906; NID:9190290; PIDN:AAA60159.1; PID:9553618
 R:Tan, A.; Too, H.P.
 submitted to GenBank, October 1995
 A:Reference number: A59269
 A:Accession: A59269
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-129 <TAN>
 A:Cross-references: GB:U37529; NID:91017792; PIDN:AAA79195.1; PID:91017793

A:Experimental source: tissue brain cortex
 R:Lai, J.P.; Douglas, S.D.; Rappaport, E.; Wu, J.M.; Ho, W.Z.
 submitted to GenBank, February 1998
 A:Description: Identification of a delta isoform of preprotachykinin mRNA in human mononuclear phagocytes and lymphocytes.
 A:Reference number: A59270
 A:Accession: A59270
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 36-96, 'W', 116-118 <LAI1>
 A:Cross-references: GB:AF050656; NID:93098594; PIDN:AAC15702.1; PID:93098595
 A:Experimental source: delta splice form; tissue blood; tissue brain; cell type monocytes/macrophages; cell type lymphocytes
 A:Accession: B59270
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 36-73, 89-96, 'W', 116-122 <LAI2>
 A:Cross-references: GB:AF050658; NID:93098598; PIDN:AAC15704.1; PID:93098599
 A:Experimental source: delta splice form; tissue blood; tissue brain; cell type monocytes/macrophages; cell type lymphocytes
 C:Comment: This protein is processed to produce the tachykinin peptide hormones neurokinin 1 (substance P) a paracrine factor, and neurokinin 2 (neurokinin A, neurokinin alpha, neuromedin L or substance K).
 C:Genetics:
 A:Gene: GDB:TAC1; TAC2; NKNA; PPT-A
 A:Cross-references: GDB:119452; OMIM:162320
 A:Map position: 7q21-q22
 C:Superfamily: substance P precursor
 C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
 F:1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SP>
 F:1-96, 'W', 116-118/Product: neurokinin 1 precursor, alpha splice form #status predicted <SPA>
 F:1-73, 89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <SPG>
 F:1-73, 89-96, 'W', 116-122/Product: neurokinin 1 precursor, alpha splice form #status predicted <SPD>
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
 F:58-68/Product: neurokinin 1 #status experimental <NK1>
 F:72-107/Product: neuropeptide K #status predicted <NEK>
 F:98-107/Product: neurokinin 2 #status experimental <NK2>
 F:100-107/Product: neurokinin 2(3-10) #status experimental <NK23>
 F:101-107/Product: neurokinin 2(4-10) #status experimental <NK24>
 F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
 F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status experimental
 F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status experimental
 SPHUB Length: 129 April 1, 2002 16:31 Type: P Check: 9307 ..
 1 MKILVALAV FLYSTQLFAE EIGANDDLNY WSDWYDSQI KEELPEPFEH
 51 LIGRIARRPK PQDFGIMK RDADSIKQ VALLKALYGH GQSHRHKT
 101 DSFVGLMGKR ALNSVAYERS AMQYERRR
 !!AA_SEQUENCE 1.0
 P1:SPHUB - substance P beta precursor - rat
 N:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
 N:Contains: neurokinin A; substance P; substance P gamma precursor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence revision 26-May-1995 #text change 18-Jun-1999
 C:Accession: A37163; A26590; C26590; A25067; JC2411
 R:Carter, M.S.; Krause, J.E.
 J. Neurosci. 10, 2203-2214, 1990
 A:Title: Structure, expression, and some regulatory mechanisms of the rat preprotachykinin gene encoding substance P, neurokinin A, neuropeptide K, and neuropeptide gamma.
 A:Reference number: A37163; MUID:90331040
 A:Accession: A37163

A:Molecule type: DNA
A:Residues: 1-130 <CAR>
A:Cross-references: GB:M34159; GB:M34160; GB:M34162; NID:g206334;
PIDN:AAA1926.1; PID:g206336; GB:M34163
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A>Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P
and neurokinin A.
A:Reference number: A94187; MUID:87118268
A:Accession: A26590
A:Molecule type: mRNA
A:Residues: 1-130 <NRA>
A:Cross-references: GB:M15191; NID:g206341; PIDN:AAA1928.1; PID:g206342;
GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KR2>
A:Cross-references: GB:M34183; NID:g206343; PIDN:AAA1929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A>Title: Sequence analysis of cloned cDNA for rat substance P precursor:
existence of a third substance P precursor.
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KMA>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA1927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A>Title: Fourth isoform of preprotachykinin messenger RNA encoding for
substance P in the rat intestine.
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: Intestine
C:Comment: Alternative splicing of the mRNA for substance P precursor yields
the beta and gamma forms, presented in this entry, and the alpha form presented
in SPRTA (Bx6590).
C:Comment: The beta and gamma forms are processed to yield substance P and
neurokinin A (substance K).
C:Genetics: 41/3; 74/1; 89/1; 97/1; 115/1
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide;
tachykinin
F:1-130/Product: substance P beta precursor #status predicted <PREB>
F:1-73, 89-130/Product: substance P gamma precursor #status predicted <PREG>
F:1-130/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:98-107/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted

SPRTB Length: 130 April 1, 2002 16:31 Type: P Check: 239 ..

1 MKLIVAVAF FLVSTQLFAE EIGANDDLN WSDMSDDQI KEMPEFEH

51 LLIQRIARRR PQDFGLMGK RDADSSIEKQ VALIKALYGH GQISHRHKKT

101 DSFVGLMGKR ALNSVAYERS AMQNYERRRR

11AA_SEQUENCE 1.0

PI:SPDB - neurokinin 1 precursor, beta splice form [validated] - bovine

N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P

M:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin

1 precursor, gamma splice form; neurokinin 2

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Feb-1984 #sequence, revision 19-Feb-1984 #text, change 16-Jun-2000

C:Accession: A05093; A01557; B25067; A61460; JC3454; I45966

R:Nawa, H.; Kotani, H.; Nakanishi, S.

Nature 312, 729-734, 1984
A>Title: Tissue-specific generation of two preprotachykinin mRNAs from one gene
by alternative RNA splicing.
A:Reference number: A05093; MUID:85086245
A:Accession: A05093
A:Molecule type: DNA
A:Residues: 1-130 <NAM1>
A:Cross-references: GB:X02351; GB:M14786; NID:g655; PIDN:CAA26206.1;
PID:g1197197
R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A>Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain
substance P precursor.
A:Reference number: A9318; MUID:84039802
A:Accession: A01559
A:Molecule type: mRNA
A:Residues: 1-130 <NAM2>
A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A:Accession: A01557
A:Molecule type: mRNA
A:Residues: 1-96, 'M', 116-130 <NAM3>
A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A>Title: Sequence analysis of cloned cDNA for rat substance P precursor:
existence of a third substance P precursor.
A:Reference number: A25067; MUID:87025808
A:Accession: B25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KMA>
R:McGregor, G.P.; Kage, R.; Tilm, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A>Title: Quantitation and characterization of peptides from the C-terminal
flanking region of rat and bovine preprotachykinins.
A:Reference number: A61460; MUID:90039314
A:Accession: A61460
A:Molecule type: protein
A:Residues: 111-126 <MCG>
A:Experimental source: corpus striatum
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A>Title: Tachykinin (substance-P) gene expression in Leydig cells of the human
and mouse testis.
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5454
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-120, 'A', 122 <CHI>
A:Cross-references: GB:M68911; NID:g163591; PIDN:AAA30724.1; PID:g552335
C:Comment: The protein is processed to produce neurokinin 1 (substance P) and
neurokinin 2 (neurokinin A or substance K).
C:Genetics: 36-120; 122
A:Gene: PPT-A
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide;
tachykinin
F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted
<SPB>
F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status
predicted <SPA>
F:1-73, 89-130/Product: neurokinin 1 precursor, gamma splice form #status
predicted <SPG>
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-66/Product: neurokinin 1 #status experimental <SBP>
F:98-107/Product: neurokinin 2 #status predicted <NKA>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status experimental
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted

SPR08 Length: 130 April 1, 2002 16:31 Type: P Check: 421 ..

1 MKIIIVAAVFI FISTOLSAE EIGANDDNFY WSDWSDSDQI KEEMPEPEH

51 LLQRIARRPK PQOFFGLMGK RDADSTIEKO VALLKALYGH GOLSHKHKHT

101 DSFVGLMGKR ALNSVAVERS VMODYERRRR

!!AA_SEQUENCE 1.0

PI:SPR08 - substance P gamma precursor - rabbit

N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor;

N:Contans: neurokinin A; neuropeptide K; substance P

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C>Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999

C:Accession: JN0709; A60302; A60200; S18922

R:Megeert, H.J.; Helstrand, A.; Rose, M.; Forssmann, W.G.

Biochem. Biophys. Res. Commun. 195, 128-131, 1993

A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.

A:Reference number: JN0709; MUID:93371392

A:Accession: JN0709

A:Molecule type: mRNA

A:Residues: 1-115 <MA2>

A:Cross-references: EMBL:X62994; NID:91565; PIDN:CAA44728.1; PID:91566

R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.

Regul. Pept. 18, 346, 1987

A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from gamma-preprotachykinin.

A:Reference number: A60302

A:Accession: A60302

A:Molecule type: protein

A:Residues: 72-92 <KAG>

R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.

J. Neurochem. 50, 1412-1417, 1988

A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived from gamma-preprotachykinin.

A:Reference number: A60200; MUID:88199570

A:Accession: A60200

A:Molecule type: protein

A:Residues: 72-92 <KA2>

C:Comment: The gamma alternatively spliced form is processed to yield substance P and neurokinin A.

C:Superfamily: substance P precursor

C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:38-68/Product: substance P #status predicted <SBP>

F:72-92/Product: gamma-neuropeptide K #status experimental <NPK>

F:83-92/Product: neurokinin A #status predicted <NKA>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status predicted

F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status experimental

SPR08 Length: 115 April 1, 2002 16:31 Type: P Check: 1957 ..

1 MKIIIVAAVL ALVSTQLFAE DIRANDLNY WSDWSDSDQI KEEMPEPEH

51 LLQRIARRPK PQOFFGLMGK RDAGHGOISH KRHKTDSEVG LMGRALNSV

101 AYERSAMONY ERRRR

!!AA_SEQUENCE 1.0

PI:SPR08 - substance P alpha precursor - rat

N:Alternate names: preprotachykinin alpha

N:Contans: substance P

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999

C:Accession: B26590

R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987

A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neurokinin A.

A:Reference number: A94187; MUID:87118268

A:Accession: B26590

A:Molecule type: mRNA

A:Residues: 1-112 <KRA>

A:Cross-references: GB:M3184; NID:9206329; PIDN:AAA41925.1; PID:9206330

C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha form, presented in this entry, and the beta and gamma forms presented in SPR08 (A26590).

C:Comment: The alpha form is processed to yield substance P.

C:Superfamily: substance P precursor

C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin

F:1-112/Product: substance P alpha precursor #status predicted <PREA>

F:1-15/Domain: signal sequence #status predicted <SIG>

F:58-68/Product: substance P #status predicted <SBP>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status predicted

SPR08 Length: 112 April 1, 2002 16:31 Type: P Check: 2164 ..

SPR08 Length: 112 April 1, 2002 16:31 Type: P Check: 2164 ..

1 MKIIIVAAVFI FVSTQLFAE EIGANDLNY WSDWSDSDQI KEEMPEPEH

51 LLQRIARRPK PQOFFGLMGK RDADSTIEKO VALLKALYGH GOISHKMAVE

101 RSAMONYERR RK

!!AA_SEQUENCE 1.0

PI:SPR08 - substance P - horse

C:Species: *Equus caballus* (domestic horse)

C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C:Accession: A01558

R:Studer, R.O.; Tirciacik, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A:Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.

A:Reference number: A01558

A:Accession: A01558

A:Molecule type: protein

A:Residues: 1-11 <STU>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; hormone

F:11/Modified site: amidated carboxyl end (Met) #status experimental

SPR08 Length: 11 April 1, 2002 16:31 Type: P Check: 4974 ..

1 RRPQOFFGL M

!!AA_SEQUENCE 1.0

PI:A60654 - substance P - guinea pig

C:Species: *Cavia porcellus* (guinea pig)

C>Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C:Accession: A60654

R:Murphy, R.

Neuropeptides 14, 105-110, 1989

A:Title: Primary amino acid sequence of guinea-pig substance P.

A:Reference number: A60654; MUID:90044685

A:Accession: A60654

A:Molecule type: protein

A:Residues: 1-11 <MUR>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status experimental

A60654 Length: 11 April 1, 2002 16:31 Type: P Check: 4974 ..

1 RRPQOFFGL M

!!AA_SEQUENCE 1.0

PI:SPR08 - ttfm - rabbit (fragment)

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999

C:Accession: S20901; I46520

R:Labelf, S.; Gautei, M.; Lakey, A.; Trinick, J.

EMBO J. 11, 1711-1716, 1992

A:Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380
A:Accession: S20901
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-6805 <LAB>
A:Cross-references: EMBL:X64696
A:Note: the nucleotide sequence was submitted to the EMBL Data Library,
February 1992
R:Label: S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.;
Francke, U.; Leonard, K.; Wardale, J.; Whiting, A.; Trinick, J.
Mature 345, 273-276, 1990
A:Title: A regular pattern of two types of 100-residue motif in the sequence of
titin.
A:Reference number: I46520; MUID:90238553
A:Accession: I46520
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4235-5250 <LA2>
A:Cross-references: EMBL:X17329; NID:q1756; PIDN:CAA35207.1; PID:930251
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin
homology; protein kinase homology
C:Keywords: muscle

S20901 Length: 6805 April 1, 2002 16:31 Type: P Check: 1434 ..

```
1  RRLKSTDM RVHKSICK HYLVKCVEN QIEFRYQTK NEGESDWMK
51  TEEVYVKEKL QKPVLDKLS GVLTVKAGET IRLEAGYRCK PPEVYVWKD
101 KDAIDETRSP RAKIDTSADS SKFSLTRAKR SDGKYVYVTA TWTAGSFVAY
151 AYVNVLDKRG PVRNLIKIPDV SSDRCTIRMD PREDGGCEI QVYLIEKCS
201 KRWVSTYSA TVLTGTGTVT RLIEGNEXIF RYRAENKIGT GPPTSKPVI
251 AKTKYDRPCR PDPEVTVKS KEEMTVVWSP PEYDGGKSIY GYLLEKEKH
301 SVRWVPVNS AIPERLKVQ NLIPGHEYQF RYKAENIGV GPSPLSRPV
351 VAKDPIEPBG PPINKAVDT TKSSITLSWG KPYVDGAPV IGVYVVRPK
401 IADASPEDEG KRCNAAQOLV RTEFTVSLD ENQYEFRCV AQNOVGIGRP
451 AELKEAIKPK ELIPEPEIDL DASMRLVYV RACCPTRLFA IYRGPRPKV
501 TRKRGIDNV VRKGOVDLVD TMAFLVLPNS TRDDSGKYSL TLVNPAGEKA
551 VEVNVRVLDT PGVSDLKVS DVTKTSCHVS WAPPENDGGS QVTHYIVERR
601 DAEIKTWSIV NPEVKKTSQV VTNLVPGNEY YFRVTAVNEY GPGVPADVPK
651 PVLASDGLSE PDPPKKLEVY EMTKNSATLA WLPLRDGGA KIDGYIISYR
701 EBDQPADRMT EYSVVKDSL VITGLKEGKK YKFRVAARNA VGSVLPREAE
751 GYVEAKEQOLI PKILMPEQI TIKAGKKLR EAHVYGRPOP ICKMKKGEDD
801 VVTISHLAVH KAESSILITI KDVTTRKDSGY YSLTAENSSG TDTQIKIYIV
851 MDRPGPPPP FDISDIDADA CSLSMHIPLE DGGSNTINYI VEKCDVSRGD
901 WYTLALASVTK TSCRIGKLIIP GQEVYFVRVA ENRFGISEPL QSPKMLAQEP
951 FGVISEPKNA RVTKVKNDCI FVANDRPDSD GGSPTGYLI ERKGRNSLWM
1001 VRANDTAVNS TEYPCAGLVE GLEYSFRIVA LNKAGSSPPS KTEYVYFART
1051 PVDPGCKPEV IDVTKSTVSL IMARPKHDGG SKIIGYFVEA CLKLPDKNVR
1101 CNTTPHQIPH EBYVTGLEE NAOYQFRAIA KTAVNISQPS ELRTPVTHA
1151 ENVFPRIDS VAMKSLTVK AGTNVCDAT VEGKPMPTVS WKKEGTVLKP
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1201 AEGIKKAMQR NCTLELFSV NRKDSGDTI TAENSSGSKS ATIKLKVLDR
1251 PGPPASVKIN KMYSDRAMLS WEPPLEDGGS EITNYIYDKR EYSSRNMAOV
1301 SANVPITSCS VEKLIEGHEY QFRICAENKY GVDSDPVEFTEP AIAKNPYDPP
1351 GRCDPPIVSN VTKDMVTWSM KPPADDGSSP ITGYLLEKRE THAVNMTKYN
1401 RKVIERITIK ATGLOEGTEY EFRVTAINKA GPGKPSDASK AVYADPLYP
1451 PGPPAPPKVY DTRSSVSLS WKPAPYDGS PIIGYIVEYK RADTDNMYAC
1501 NLPOKLQKTR FEVTGLMENT EYQFRVAVN KVGYSPPSDV POKHCPKDL
1551 IPEGELDAD LRKTLILRAG VTMLLYPVK GRPPPKITWS KRNVLREAI
1601 GLDIKSTDFD TFLRCENYK YDAGKYLLTL ENSCGKKGYT IYKVLDPFG
1651 PPVNVTVKEI SRDSAYITWD PPIVDGSPV INYVEEKRA ERKSNSTVTT
1701 ECKTSPFRVS NLEEGKSYFF RYLAENEGI GDEGTRDAY KASETPGPVY
1751 DLKVLTVTKS SCNIGMKRPR SDGGSRTIGY VDFLTEENK WQVWKSLSL
1801 QYSTKDLNKG KQYTFRVSAE NENEGTPE ITVVAADVVY ABDLDLKLDP
1851 DICLYAKENS NFRKLIPIHOG KPAPSVYWK GEPLPLATDR VVESAVNT
1901 TLVVYDCQKS DAGKYITLK NVAGTKBGL SIRVGCKPGI PTGPIKFDEY
1951 TAEAITLKMG PKDDGSEI TNYLLEKRS VNNKWYTCAS AVQKTFRVT
2001 RLHEGMEYTF RYSAENKYG V GEGLSKPIV AKRPVDPDA PPPNIVDVR
2051 HDSVSLTWD PRKTGSPIT GYHIEFKERN SLLMKRANKT PIRMKDFKYT
2101 GLTEGLEVEF RVMAINLAGV GKPSLPSEPV VALDPIDPPG KEVINVTGN
2151 SVTLITEPK YDGHKILITGY IVEKRDLPK TMMKANHINV POCATVYDL
2201 VEGKYEYFRI RAKNTAGALS APSESTGTII CKDEYEAPTI VLDPTIKDGL
2251 TIKAGDTIVL NAISILGKPL PKSSMSKAG DIRPSDITQ TSTPSSMLT
2301 VKYASRKDAG EYTTATNPF GTKEEHYRVT VLDVPGPPGP IELSNVSAK
2351 ATLWTPLLE DGGSPDKSYV LEKRETSRL WTVVAEDIOS CRHVVTKLIQ
2401 GNEYLFRVSA VNHYGKEPV QSEPVKMYDR FGPPGPPGK EYSNVTKNTA
2451 TVSMKRPTDD GGSSETTYVY ERREKKGLRW VRATKTPVSD LACKYTGLOE
2501 GMYTEFRVSA ENRAGIGPPS DASNYVLMKD VAYAPGPPSN ARVTDTTKKS
2551 ASLAWGKPHY DGGLEITGY VEHQVGBET WVDJTGPAI RTEFVVPDL
2601 HTEKKNFRI SAINDAGVE PAVLPDVEIV ERMADPFEL DAELRRTLIV
2651 RAGLSIRIFV PIKGRPAEV TWTKDINLK TRANIENTES FYLLIIPEN
2701 RYDTGKFVMT IENPAGKKS FVNVRVLDTP GPVLNLRPD IYKDSVTLHM
2751 DLPLIDGSR ITNYIVERRE ATRKSYSTVT TKCHKCTYKV TGLSGCEYF
2801 FRVMAENEYG IGEPSETKEP VKASEAPSP DSLINDITK STVSLAMPKP
2851 KHDGSKITG YVIEQKRGKS DQWTHITTV GLECVARNLT BEEETTFQVM
2901 AVNSAGRSAP RESRPVYKE QTMLPELDR GIYQKVLIAK AGDNIKVEIP
2951 VLGRRKPTVT WKKGDVILQ TORVNVENTA TSTILNISBC VASDGGPYPL
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3001 TAKNIVEGV DVTIIOVHDI PGPGTGPIKF DEVSSDFVTF SWEPPENDGG
 3051 VPISNVIEIM RQFDSTWWE LATTVIRTTY KATRLTGV EYOFVKAQNR
 3101 YGVGGIISA SIVANYPEKV PGPGTPQVY AVTKDSMTIS WHEPLSDGGS
 3151 PILGVHERK ERNGILMOV SKALVPGNIF KSSGLTDGIA YEFRVAENM
 3201 AGSKRPSKPS EPVLALDPID PGKPIPLNI TRHTVTLKMA KREYTGGEKI
 3251 TSYIVEKROL PNGRWLKANF SNILENFYV SGLTEDAAYE FRVIAKNAG
 3301 AISPSEPSD AITCRDVEA PRILVDYREK DTVIILKAGEA FKLEADVSGR
 3351 PPPTMEWTKD GKELEGTKL EIKIADFSY LINKDSSRRD SGAYILTATD
 3401 PGGFAKHIFN KVVLDRGPP EGPLAVSEVT SEKCVLSMPL PLDDGAKIE
 3451 HIYOKRETS RLAMTNVASE VOYTKLKVTYK LKGNFYIFR VMAVNRKYGV
 3501 EPLESEPVLA VNPYGPDPDP KNEVTTITK DSMVVCWGHF DSDGSEIIN
 3551 YIVERRDKAG QRMVKCNKKT VTDLRFKVS LGTEGHEYFR IMAENAAGIS
 3601 ABSRTSPFYK ACDAVEKPPG PGNPRVLDTIS RSSISIAMNK PIYDGSSEIT
 3651 GYVMEIALPE EDEWKIVTPP AGLKATSYTI TNLVENOEYK IRIVAMNSBG
 3701 LGEPALVPOT PKAEDRMPLP EIELDADLRK LVYIRACCTL RLFVPIKGGP
 3751 DPEVKTREH GESLDKASIE STSSYILLIV GNVNRPDSGK YILTVENSSG
 3801 SKSAFVNVRV LDTPGPPQDL KVEEVTKTSV TLTWDPPLD GSKIKINYIV
 3851 EKRESTRKAY STVATNCHKT SMKYDQLOEG SSYFRVLAE NEXYGLGPAE
 3901 TAESYKASER PLPGKITLV DVTRNSVLS WEKPEHDGGS RILGYIVEMO
 3951 SKGSDKMATC ATVKYTEATI TGLIQGEYS FRVSAQNEKG ISDPROLSVP
 4001 VLAKLVLVPP AFKLEFNFT VLAGEDLKID VPRIGRPTT VYMHDDVPL
 4051 KOTTRVNAES TENSSLSLIK EACREDVGHY VVXLSNAGE ALETINAIL
 4101 DKRGPTGVV KMEVLTADSI TISWEPKYD GSSINNYIV EKROSTSTTW
 4151 QIVSATVAT TIKASRLKTG CEYOFRIAE NRYGKSTYLN SEPPIAOYVF
 4201 KVPGPPTPE VTLSSRDSME VOMNEPVNDG GSRVIGYHLE RKERSIILVY
 4251 KLNKPIPIQT KFKTTGLEEG IEVEFRVSAE NIVGIGKPSK VSECYVARDP
 4301 CDPGRPREI IVTRNSVTLQ WKKPTYDGS KITGYIVEKK ELPDGRMKA
 4351 SFTNIMDTQF EVTGLVEDHR YEFRVIAARNA AGVESSEPS TSALTARDEI
 4401 DEPRISMDBK YKDTIVHAG ESFRIDADIY GKPIPTQWI KGDQELSNYA
 4451 RLEISTDA TSLSKYKDAF VDSGNVYLKA QNVAGERSVT VAVKYLDRG
 4501 PPGPIVLSG VTAECTILAM KPPLDGGSD IINYIVERRE TSRLVWTVD
 4551 ANVQTLSCV TKLEGNFYI FRVAVVNRKYG VGEPLSEPY IAKNPFVVPD
 4601 ARKARECTIV TKDSMIYVWE RPASDGSSEI LGVLEKRXK BEIRTRCHK
 4651 RLIGELRLV TGLENNHYE FRVSAENAG LSEPPSPAY QKACDPIYK
 4701 GPPNPKVMD ITRSSVFLSM SKPIYDGCCE IOGYIVEKCD VSGEWMTCT
 4751 PPTGINKTNI EVEKLEKHE YNFRICAVNK AGVGDHADV GPVIVEKKE
 4801 ABDIDIDEL RKIINIRAG SLRLVPDKG RPTPEVKGWK VDGEIRDAAI

4851 IDSTSSTSL VLDNVRNRYDS GKYLTLLENS SGTKSAFVTV RYLDTPSPPV
 4901 NUKVTEITKD SVSITWEPPL LDGSGKIKNY IVEKROSTR SYAAVNTNCH
 4951 KSSWKIDQLO EGCSYFFRVT AENEXGICLP ARTADPIKVA EYDPPGKIT
 5001 VDDVTRNSVS LSWTRPEHDG GSKIIQYIVE MOAKHSEKMS ECARVKSLEA
 5051 VITNLPOGEE YLFRVAVNE KGRSDPRSLA VPIVAKLVI EPDVKRAFSS
 5101 YSVQVQDLK IEVPISGRPK PTTWTKDGL PLKQTRINV ADSLITLIS
 5151 IKETHKDDSG HYGITVANYV GOKTASIEII TLDPDPPKG PKFDEVSAB
 5201 SITLSMNPPL YTGGOQITNY IVHKRDITTT VMDVVSATVA RTTLKATKLK
 5251 TGTEYQFRIF PENRYQOSFA LDSEPIYAOY PYKEPGPGT PVTATSKDS
 5301 MVYQWHEPIN NGSPILIGYH LERKERNISIL WTKVDSIIH DTQFKALNE
 5351 EGIEYEFERY AENIVGVKA SKNSCYVAR DPCDPPGTE AIIVKNEIT
 5401 LQTKRPVYDG GMITGYIVE KRDLPEGRMM KASFTNVIET QFTVSGLTED
 5451 QRYEFRVIAK NAAGTMSKPS DSTGPITAKD EVELPRISM PYFRDITVYN
 5501 AGEFTFLEAD VAGKPLPTIE WLRODKVEE SARCEINTD FKALLVXKA
 5551 IRIDGQOYL RASNAGSKS FPVNVKVLDR PGPEGFVOY IGVTCCKCTL
 5601 TWSPPLDDG SDIPHYVER RETSLAMTV VASEVYNSL KITKLEONE
 5651 YIFRIAMVNK YGVGEPLSA PVMKNPFVY PGPKSLEVY NIAKDSMTVC
 5701 WNRPDGSGGS EITGYIVERK DRSGIRWIKC NKRRVYDLRF RYTGLEDHE
 5751 YEFRVSAENA AGVGEPPPAT VYKACDPVF KPGPTNAHV VDTKNSITL
 5801 AMGKPIYDGG SEVLGYIIEI CKADEEMOI VTPOGTGLKAN REISLIEH
 5851 QEYKIRVICAL NKVGLGEAAS VPGTVKPEBK LEABELDLS ELKGIIVRA
 5901 GGSARIIHP KGRPTPDITW SREEGEFTDK VOYEGKVNT QLSIDCDRN
 5951 DACKIYKLE NSSGKTAFV TVKVLDTGPP PONAIVAEV KDSAVLWEP
 6001 PIIDGAKVR NYVIDKREST RKAYANVSSK CNKTFEVEN LIEGAIYFR
 6051 VMAENERGVG VPETVDAVK AAEPSPPGK VTLTDVSGTS ASIMWEPKH
 6101 DGGSRVIGYV VEMOPKCTEK MSYVAESKVC NAVVTGLSSG HEQOFVKAY
 6151 NEKGKSDPRV LGVPVIAKDL TIOPSFKLP KRVSQAGED LKIEPIVIGR
 6201 PREPIFWKD GEPLRQTRV NVEETATSTI LHIKSSKDD FGKVTITATN
 6251 SACTATENLS VIVLEKPPG VGPVAFDEIS ADPVLSWEP PATGSGQIS
 6301 NYIVERKDDT TTTWHIVSAT VARTTIKVTK LKGSEYOFR IYAEINRYKS
 6351 TSIDSXRVIV QYFKEPGPP GTPVTSVSR DOMLVOMHEP VNDGSKVLG
 6401 YHLEQKEKNS IIMVKVKNKL IQDRFKYTG LDBGLELEPK VSAENIVGIA
 6451 SLAKCPNAFV ARDPCDPPGR PEALVITRNN VTLKMKRPAY DSGSKITGYI
 6501 VEKKDLPPDGR WMAKSEFNVL ETEFTVSGLV EDQRYEFRVI ARNAAGNLSE
 6551 PSSESGAITA RDEIDAPNAS LDPKYKDVIV VHAGETVYLE ADIRGAPID
 6601 VVWLKDGKEL EETTARMEIK STIOKTTLVV KDCIRTDGGO YVXLSNVGG

6651 TNSLPTTVK IDRPGPPEP LKVSQVTAEK CYLAMPNPLO DGASISHYI
6701 IEKRETSRLS WTVSTVEOVA LNYKVTLLP GNEYIFRVA VKYSGEPL
6751 ESEPVACNP YKPPPPPTP EASAITKDSM VITMARVVD GGAIEGYIL
6801 EKRDK

!!AA_SEQUENCE 1.0
P1:JC1403 - glutamate--ammonia ligase (EC 6.3.1.2) - Calothrix sp. (PCC 7601)
N:Alternate names: glutamine synthetase
C:Species: Calothrix sp.
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JC1403
R:Elmoujani, K.; Liotenberg, S.; Houmard, J.; de Marsac, N.T.
Biochem. Biophys. Res. Commun. 189, 1296-1302, 1992
A>Title: Molecular characterization of the gene encoding glutamine synthetase
in the cyanobacterium Calothrix sp. PCC 7601.
A:Reference number: JC1403; MOID:93129187
A:Accession: JC1403
A:Molecule type: DNA
A:Residues: 1-471 <EIM>
A:Cross-references: EMBL:L05609; NID:g144935; PIDN:AAA23288.1; PID:g144936
A:Gene: glna
C:Genetics:
C:Superfamily: glutamate--ammonia ligase
C:Keywords: ligase; phosphoprotein
F:399/Binding site: AMP (Tyr) (covalent) #status predicted

JC1403 Length: 471 April 1, 2002 16:31 Type: P Check: 3357 ..

1 MTPQEVKLK IQDKIQIMD LKFIIDPQTG QHLYVYNIQ DSSFTDGPV
51 FDCSSIRGKM GIEESDMTV LDPTAWIDP FMKEPTLSTI CSIKERTGE
101 WYHRCPRVIA OKADYLVST GLGDTAFEGP EAEFFIFDDA RPDQANSGY
151 YVDSYEGRW NSGKDEGPNL AYKPRFKEGY FVPAPTDTFQ DMRTMLTLM
201 AACGVPIEKQ HHEVATGOC ELGFRFGKLI EAADWMTYK YYIKNNAKY
251 GRVITMPKP IFGDNGSMH CHOSIWKDK PLEGGDKYAG LSDMALYYIG
301 GILKHPALL GITNPTNSY KRLVGYEAR VNLAYSOGN SASVRIPLSG
351 TNEKARLER RCPDATSNPY LAFAMLCAG IDGIKNKIHP GEPLDNIIE
401 LSEELAKVP STPGSLEIAL EALENDNAFL TEGVFTEDF IONWIEYKLV
451 NEVQQLQLRP HPEFYLYYD C

!!AA_SEQUENCE 1.0
P1:S47038 - tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47038
R:Helldand, A.; Krühoffer, M.; Juergen Maegerl, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47038
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <HEI>
A:Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C:Superfamily: substance P precursor

S47038 Length: 130 April 1, 2002 16:31 Type: P Check: 219 ..

1 MKLIVAAVF FLVSTQLSAE EIGANDDLNY WSDWSDSDQI KEALPEPFH
51 ILQRIARRPK PQQFGLMGK RDADSSIEKQ VALLKALYGH GQISHRHHT
101 DSFVGLMGKR ALNSVAVERS AMQYERRRK

!!AA_SEQUENCE 1.0
P1:S47039 - tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47039
R:Helldand, A.; Krühoffer, M.; Juergen Maegerl, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47039
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <HEI>
A:Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
C:Superfamily: substance P precursor

S47039 Length: 115 April 1, 2002 16:31 Type: P Check: 844 ..

1 MKLIVAAVF FLVSTQLSAE EIGANDDLNY WSDWSDSDQI KEALPEPFH
51 ILQRIARRPK PQQFGLMGK RDAGHGQISH KRHTDSFVG LMGKRRLNSV
101 APEFSAMQNT ERRRK

!!AA_SEQUENCE 1.0
P1:I52526 - neurokinin 1 precursor - mouse
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 2
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C:Accession: I52526; JC5452; I62741
R:Kako, K.; Munekata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A>Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin
A and B.
A:Reference number: I52526
A:Accession: I52526
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <KAK>
A:Cross-references: GB:D17584; NID:g407345; PIDN:BA04508.1; PID:g435121
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.
Endocrinology 128, 2441-2448, 1991
A>Title: Tachykinin (substance-P) gene expression in Leydig cells of the human
and mouse testis.
A:Reference number: JC5450; MOID:91209287
A:Accession: JC5452
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 36-122 <CHT>
A:Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status predicted <NK1>
F:98-107/Product: neurokinin 2 #status predicted <NK2>
F:111-126/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted

I52526 Length: 130 April 1, 2002 16:31 Type: P Check: 430 ..

1 MKLIVAAVF FLVSTQLFAE EIDANDDLNY WSDWSDSDQI KEALPEPFH
51 LLQRIARRPK PQQFGLMGK RDADSSVEKQ VALLKALYGH GQISHRHHT
101 DSFVGLMGKR ALNSVAVERS AMQYERRRK

11AA_SEQUENCE 1.0
 FI:162742 tachykinin A gamma chain precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 C:Accession: J03453
 R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
 Endocrinology 128, 2441-2448, 1991
 A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse testis.
 A:Reference number: JC5450; MUID:91209287
 A:Accession: 162742
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-72 <RES>
 A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:9554261
 C:Comment: This protein contains two tachykinin peptide hormone substance-P and neurokinin-A (substance-K).
 C:Genetics:
 A:Gene: gamma-PPT-A
 C:Superfamily: substance P precursor
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-33/Product: substance-P #status predicted <STP>
 F:48-57/Product: neurokinin-A #status predicted <NKA>
 162742 Length: 72 April 1, 2002 16:31 Type: P Check: 3920 ..

1 DSDQIKEMP EPFHLQRI ARRPQOFF GLMKRDAGH GQISHKRRKT
 51 DSFVGLMGKR ALNSVAYERS AM

11AA_SEQUENCE 1.0
 FI:152958 tachykinin delta precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S12958; JC2413
 R:Harmer, A.J.; Hyde, V.; Chapman, K.
 FEBS Lett. 275, 22-24, 1990
 A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing variant of the rat substance P precursor.
 A:Reference number: S12958; MUID:91085565
 A:Accession: S12958
 A:Molecule type: mRNA
 A:Residues: 1-97 <HAR>
 A:Cross-references: GB:X56306; NID:956067; PIDN:CAA39752.1; PID:956068
 R:Khan, I.; Collins, S.M.
 Biochem. Biophys. Res. Commun. 202, 796-802, 1994
 A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat intestine.
 A:Reference number: JC2411; MUID:94324969
 A:Accession: JC2413
 A:Molecule type: mRNA
 A:Residues: 48-92 <KHA>
 A:Cross-references: GB:S72369; NID:9632805; PIDN:AAE31499.1; PID:9632806
 C:Superfamily: substance P precursor
 C:Keywords: amidated carboxyl end
 F:59-68/Product: substance P #status predicted <SUP>
 F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status predicted
 S12958 Length: 97 April 1, 2002 16:31 Type: P Check: 7129 ..

1 MKIIIVAVVF FIVSTQFAE EIGANDLIN WSDWMSDOI KEAMPEPEH
 51 LLQRIARRPK PQOFFGLMGK RDAGHGOISH KMAVERSAMQ NYERRRK

11AA_SEQUENCE 1.0
 FI:JC2412 tachykinin gamma chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: JC2412
 R:Khan, I.; Collins, S.M.
 Biochem. Biophys. Res. Commun. 202, 796-802, 1994

A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat intestine.
 A:Reference number: JC2411; MUID:94324969
 A:Accession: JC2412
 A:Molecule type: mRNA
 A:Residues: 1-63 <KHA>
 C:Superfamily: substance P precursor
 C:Keywords: amidated carboxyl end
 F:12-21/Product: substance P #status predicted <SUP>
 F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status predicted
 JC2412 Length: 63 April 1, 2002 16:31 Type: P Check: 7417 ..

1 FEHLQRIARRPK PQOFFGL MGKRDAGHGO ISHKRRKTDS FVGLMGKRAL
 51 NSVAYERSAM ONY

11AA_SEQUENCE 1.0
 FI:JC5455 preprotachykinin-A gamma precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
 C:Accession: JC5455; I45967
 R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
 Endocrinology 128, 2441-2448, 1991
 A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse testis.
 A:Reference number: JC5450; MUID:91209287
 A:Accession: JC5455
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-72 <CHI>
 A:Cross-references: GB:M68912; NID:9163593; PIDN:AAA30725.1; PID:9552336
 C:Comment: This protein contains two tachykinin peptide hormone substance-P which is involved in a local feedback reaction and acts as a paracrine factor, and neurokinin-A (substance-K).
 C:Genetics:
 A:Gene: PPT-A
 C:Superfamily: substance P precursor
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-33/Product: substance-P #status predicted <STP>
 F:48-57/Product: neurokinin-A #status predicted <NKA>
 JC5455 Length: 72 April 1, 2002 16:31 Type: P Check: 4081 ..

1 DSDQIKEMP EPFHLQRI ARRPQOFF GLMKRDAGH GOLSHKRRKT
 51 DSFVGLMGKR ALNSVAYERS AM

11AA_SEQUENCE 1.0
 FI:JN0023 substance P - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
 C:Accession: JN0023
 R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
 Regul. Pept. 20, 171-180, 1988
 A:Title: [arg3]substance P and neurokinin A from chicken small intestine.
 A:Reference number: JN0023; MUID:88204263
 A:Accession: JN0023
 A:Molecule type: protein
 A:Residues: 1-11 <CON>
 C:Superfamily: substance P precursor
 C:Keywords: amidated carboxyl end; tachykinin
 F:11/Modified site: amidated carboxyl end (Met) #status predicted
 JN0023 Length: 11 April 1, 2002 16:31 Type: P Check: 4995 ..

1 RRPQOFFGL M

11AA_SEQUENCE 1.0
 FI:TA0833 haloacid dehalogenase-like hydrolase - fission yeast
 (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: t140833
R:Oliver, K.; Harris, D.; Wood, V.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, May 1998
A:Reference number: 221950
A:Accession: t140833
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-236
A:Cross-references: EMBL:AL023518; PIDN:CAA18995.1; GSPDB:GN00068;
SPDB:SPCC1023.07
A:Experimental source: strain 972h-; cosmid c1020
C:Genetics:
A:Gene: SPDB:SPCC1020.07
A:Map position: 3
A:Introns: 11/3; 26/1; 47/1
C:Superfamily: hypothetical protein b2690

T140833 Length: 236 April 1, 2002 16:31 Type: P Check: 5542 ..

1 MIPKACLFDM DGLVDTESI YTKSTNIILK RYKGFESME VKAKMGRTS
51 KEASHIFIDW SGIDTCEBY IALQRETQAE LMRHTKPLFG VMNLISKLKS
101 LNIPIALATS SDTHNFEKKS AHLSHLFDFH DGNIIITGDDP RLPGVRGKPH
151 PDINFIALKM INDKRKAQOQ AEILPENCIV FEDSITGVOS GRAGMKVVM
201 VPDVNIILFF SLSPQAAADK HITKVLSEIN PDVTKY
11AA_SEQUENCE 1.0
P1:t13857 - t13857 protein - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: t13857
R:Mazo, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: 217801
A:Accession: t13857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3828 <MAZ>
A:Cross-references: EMBL:Z50038; MID:q899253; PID:q899254; PIDN:CAA90349.1
C:Genetics:
A:Cross-references: FLYBase:FBgn0014844
A:Introns: 337/3; 529/1; 721/1; 791/1; 3668/2; 3713/1; 3771/3
C:Superfamily: Drosophila trithorax protein
C:Keywords: DNA binding; transcription regulation; zinc finger

T13857 Length: 3828 April 1, 2002 16:31 Type: P Check: 425 ..

1 MGRSFFPQNP SKSINRRKIS VLOLEDEAAS AAAAAAATA ATTEDHOOSE
51 QSAGSSASRE KGNCCDDDD DNAPSGAITS GNRGASSGAS DAAPEGNSY
101 GNGSSTGSKT TNGGNVNGS HHKSATAPAE LKECKNQNO IEPNXCIAE
151 PGGTEDTND DDDSSNDKK PTAATAAAA AAFVGPSSL QRAKRGKK
201 FKNILNARPE VMLPSTSKLQ QQQQQOQLN CPSASASIS SSAAAAAAA
251 APTTTTTSAS ATATTATAT STSTSSLPCT PLSTIAGGG GAAAAALLA
301 NPFLSVETKV VEVAATAATA ATAAATAAG AGEDVGMLKA STEMANEGL
351 EAPVAVAKSS GSSPNNHNP NAVAGSTSA ACPATATQ KKYTFKNIL
401 ETSDDKSVK RYFNDNRVP LVSIMKDSL NRPLNYCRGS EPIVPSILS
451 KILKNSMID KLSLKRFSV HASSNSIOES SSTTNLES GLSRFGAPI
501 DDERAVSGV TFRKQEPQHK TPEDNDDGS ASSDAIEDDE DIDDAAEEN

551 EBAASEKSAE TTASVDEKEA DDROLVMDKH FVLPKRSTRS SRIIPKRL
601 LEVGIGCSKR SPSPANGKPK PKNYFGLATL PAKCTPRRRR SAATLSSOKL
651 GKETEASEFT AKVNSSFYLR QPRLQFQTDK SRSEVSAKPT LPTTVLPAS
701 SSAITSANVL SFGALNNANS AVAAASTCAV CSAPVNNKDA PLARKYGVIA
751 CEVCKRFNRN MTKISKSTP MHSNPSTSTA QSQOQLKCD GNCCLISLK
801 SOLKNEKLY KERCKACWLK KCLATLQIPA GHRSLSAIL PASMREAVP
851 KDKCPBELLS PTASLFTAP TSSASGTTI KMKSAETAV NSIKSNPLAE
901 NNVTGCTPL LRPALLEPL FLKIGSDNK AKSKEALGL SVVPSSEAA
951 VAPGKTTTRA KODEKAREL EAEPPLSPNA KTTTEANTPE TOKDQOPAST
1001 TTTSNASSS TSHSSAATN SSOLETEEA NASAVPDNLK RQRIDLKPR
1051 VHHVCRSASI VLQGPLATFG DEBELAAE AGPAPTTTT TTSPEVILIK
1101 PKSPQPMQMI IDENDNCASC ILPTEATAE AQPAVKSYLE SRSKSNQT
1151 EAKKTPATG SSKGVTTN ATAVTSVAS SLVATKKORN IEVSSISS
1201 QAAATQSRRA LAKEVNRLLA LISTDFWENY DPAEVCOTGE GLIVETVAAQ
1251 RALCFLGST GLDPLIFCAG CCEPYHOYV LDEYNLKHSS FEDTLMTSL
1301 ETSNNACATS AATNTALNQL TORLNLCPR CTVCYTCNNS SSKVKQKOC
1351 QKNYHSTGIC TSKRLGADR PLICVNCLKC KSCATTKVKS FGNLPMCTA
1401 CFKLRKKGNF CPICQCTYD NDFDLKMEC GDCNQVHSH CEGLSDEQTN
1451 LLSLPESE FICKKCARC DVSRRKADW RQAVMEFKS SLYSVLKLS
1501 KSRQACALLK LSPRKNMRC SAGAOPAKAH SQGLQPKAL QTYNGLGSD
1551 GESQNSDDLY EFKEDHSTNR KPSTPVPCSC LQPLSOPSP SLVDIKOKIA
1601 SNAVYSLAEF NYDMSQVIOQ SNCELDIAY KELLSEQFPM FQNETKACTD
1651 ALEEDMFESC GYEELKESPT TYAEHHTASQ APRTGLLDIP LDDVDLGGC
1701 AKTRLDTNV CLFCRKSCEG LSGEERLLY CGHDCVNHIN CAMSAEVE
1751 EIDGSLQNVH SAVARGMIK CTVCNNGAT VGCNVKSGE HYHYPCARTI
1801 DCAFLTDKSM YCPAHARNAL KANGSPSVTY ESNFEVSRPV YVELBRKRRK
1851 LIIPAKVOFH IGSVAVRQLG SIYPRFSDSF EALVPLNPLC SKLYSSKEP
1901 WKIVETVART TIONSYSTLT TLDAGNFTV DHTNPNCSLV QGLAQIARW
1951 HSLARSDLL DTDMAEPNS YVPADENTEE EPQOMADLIP PEIKDAIFED
2001 LPHELLDGIS MLDIFMYEDL GDKTELFAMS EDSKDGTTAT SOAGASAYII
2051 CDEDTRNNS LNKHLVLSNC CTASNPDVA MLCAARSSQ EKECDVLKK
2101 TDTAPTBSWP KLDDGSVAAF KRRRLSNIA EGYLLSLNR SKKEAATVAG
2151 ITRROSVGCS SELPAEGSAT MTKSFTWSA AKCLEFKNS REEPKLTIM
2201 QMDGVDDSIY EYRIIGSDN LSTAQFTGOV KERCOCOTYR NYDSQRHLG
2251 SCEPMSTSES ESEIATGTAQ LSAESLNELO KQALAATIS NNGCLNYLOT
2301 SFPQVONLAT LGQFGVOGLQ GLQTLQLOP SLGNGFFLSO PNAOATNSG
2351 NDVLQLYANS LQNLANLGG GFTLTQPTMS TQAPOLIAL STNPDTQOF

2401 IQLPSNGAT TQLLTATAPL RCNATYOTLQ ATNSDKIVL LFLAGDPLQ
 2451 EYVTAQQA TAAHQKOLK SGHGVKICA KLQGGQOQOR HQHQHQHCH
 2501 QQQQQQQQQQ QQQQQPTIV AQHGTTQLL GQNLQPOLL PQSNAPOQO
 2551 QLLLPOTQAO NISFVTGDS SQNQPLQYIS IPTTDFKPK QTSPTFELT
 2601 AFGGATFLQ TDASGNMLT TAPANSGLQ LMGLOLTOQ VIGTLIQPT
 2651 LQLTGADGT QTATAQPLI LGATGGGTT GLEFATAPV ILATPMYTG
 2701 LETIVQNTVM SSQGFVSTAM PGYLSNSSF SATTTQVQA SKIEPIVDLP
 2751 AGYVLLNAV DASGNTSLQ QSQTQATDDA TALLQNAQF QPQTPTTST
 2801 QQTMTSTDPV PLVVTAKVP VQMKRNTNA NNSPIVLSK VOPQPOQSOV
 2851 VAKVLPNTVI QQQQQQQQQQ QQQQQQMPK QQLAGNALK LTSQFORQO
 2901 ANELKNKQAA GQGTGTCGA PPSIAKPLQ KTNILRPH KVEVPKIMK
 2951 QAPKLATSAA SMOHQOQOS PAALNQAVY ALLQQLABA PQPQOQEPQ
 3001 EQQLHQOQO QQQQQQHQO QHQQQQQQLS MPQLRAQOP IISIVTAEF
 3051 QAAQFVIRP ALQQAQPIQ LQEQSQOQO QQPAEQLNG KAARQRYAS
 3101 NSLPTNVNP LQOQRCASAN NSSNSNTQO NSTIINSRP TNRVLPMDOR
 3151 QPPTLSNDV VQSPPTPKP IEEVPAGAS TQKPIKCYA QLEKSPGYE
 3201 TELKTNITLD NLEQTNSTTT MQLQPPQGP IYGEQIFPKO SQAQVQLEK
 3251 KHNMLLEA TSCQOQOQO QHMEMVNDG FOLTSNECL LEKHGENEA
 3301 VMDTEDEHYA SMKNGSGGA AEGIGYDDA EDEDDDDDE SLKMATSAQN
 3351 DHEMDSEEP AVKEKISKIL DNLTNDCSD STATATVEA SAGYQOMVD
 3401 VLATTAAGSV STDEFTTAT AEAVEAASY INEMAHLE QLKQQAQVE
 3451 IDLKRPKLDV PQOPDTPVP NVVPTAAPQ QPPMRDPK ISGPHLYEI
 3501 QSEDEFTYS SSIAETWEKV PEAVQVARRA HGLTPLEPB LADMGVQMI
 3551 GLKTNALKYL IEQLPGVEKC VKYTPKYHRK NGNVSTAAG GHARTAGSNP
 3601 AALAGAEEL IDYGSQDEL QENAYECAR EPVVSSEVD MFSMLASRR
 3651 KQPIQFVOP SDNELVPRRG TGSMLPAMK YRLKETKD YGVFRSHIH
 3701 GRGLYCTKDI EAGENVIEYA GELIRSTLTD KRERYVDSRG IGCYMFKIDD
 3751 NLVVDATMG NAARINHC EPNCYSKVD ILGKHIIIF ALRRIYQGE
 3801 LTYDKFFPE DEKIPSCGS KRCKRYLN

!!AA_SEQUENCE 1.0
 P1:E86284 -hyothetical protein AAD39637.1 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E86284
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Egu, P.; Felblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.E.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.;

Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Millscher, J.; Miranda, M.; Nguyen, M.; Niemman, W.C.; Osborne, B.L.; Pal, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzman, S.L.; Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: E86284
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <STO>
 A:Cross-references: GB:AE005172; NID:g5103807; PIDN:AAD39637.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

E86284 Length: 290 April 1, 2002 16:31 Type: P Check: 4011 ..
 1 MPEIHGAHT ISHGVTAR FHMMDWLL LLIYIEVLN VIEPFRFVG
 51 EDMVLDLRP LQDNTIPMA VPLIAVLPF AVICVYFIR NDVYDLHNAI
 101 LGLFSLVLT GVITDAIKDA VGRPRDFEW RCPFDGIGIF HNTKKNVLT
 151 GAKDVKEGH KSPFGHTSM SFAGIGFLSL YLSKIRVDF QKRVAKLCI
 201 VILPLVAAL VGSVRVDYW HHMDVFEQA IIGLTVATFC YLQFPFPPYD
 251 PDGMGPAYF QMLADSRNDV QDSAGMHLIS VRQTELESVR

!!AA_SEQUENCE 1.0
 P1:E84421 -probable phosphatidic acid phosphatase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84421
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Felblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: E84421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <STO>
 A:Cross-references: GB:AE002093; NID:g4262225; PIDN:AAD14518.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g01180
 A:Map position: 2

E84421 Length: 302 April 1, 2002 16:31 Type: P Check: 2420 ..
 1 MQEIDLSVHT IKSHGRVAS KHKHDMILV ILIAIEGLN LISPFYRVG
 51 KDMNTDLKTP FKDNVYPTMS VPYAVLLPI IVEYCFYLRK TCYYDDHHSI
 101 LGLFAVLIT GVITDSIKVA TGRPRNFW RCPFDGKELY DALGVVCHG
 151 KAEVVEGHK SPFGHTSMS FAGLFLSLY LSKIKAFNN EGHVAKLCV
 201 IFPLAACLV GISRDVDYH HMQVFAFAL IGLTVAFYCY RQYPPYHE
 251 EGMGPAYFK AAOERGVPV TSQNGDALRA MSLQMDSTSL ENNESGTSFA
 301 PR

!!AA_SEQUENCE 1.0
 PI:T33064 - Hypothetical protein F56C3.9 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T33064
 R:Stonking, T.
 submitted to the EMBL Data Library, May 1998
 A:Description: The sequence of *C. elegans* cosmid F56C3.
 A:Reference number: 221276
 A:Accession: T33064
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-206 <STO>
 A:Cross-references: EMBL:AF067214; PIDN:AC17009.1; GSPDB:GN00028; CESP:F56C3.9
 A:Experimental source: strain Bristol N2; clone F56C3
 C:Genetics:
 A:Gene: CESP:F56C3.9
 A:Map position: X
 A:Introns: 43/2; 87/1; 116/1; 141/2; 184/3

T33064 Length: 206 April 1, 2002 16:31 Type: P Check: 3281 ..

1 MTQOKMHMFSTETALKKFOI NTQSDTIYV LNTLAELESEY FHILRTGFS
 51 EMTAEKYNLN DYFAEDLYVF LSYVCPDGE FDRITNOHNI TPLVPSDRLL
 101 VEFWVKEVH KYLNSEAFON EIYDELLVQ LCYLHSONY SELDVVFKKI
 151 ALIDNPLVD RLVOEITDSD VQSEFTKKIL QYRPYTEKPR PQMFEDMDHT
 201 PYSAVY

!!AA_SEQUENCE 1.0
 PI:T09484 - Cartilage intermediate layer protein precursor - human
 C:Species: *Homo sapiens* (man)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09484
 R:Lorenz, P.; Neame, P.; Sommarin, Y.; Heinegard, D.
 J. Biol. Chem. 273, 23469-23475, 1998
 A>Title: Cloning and deduced amino acid sequence of a novel cartilage protein (CILP) identifies a proteom including a nucleotide pyrophosphorylase.
 A:Reference number: Z16689; MUID:98389785
 A:Accession: T09484
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1184 <LOR>
 A:Cross-references: EMBL:AF035408; NID:93513502; PIDN:AC33838.1; PID:93513503
 A:Experimental source: tissue type articular cartilage
 C:Genetics:
 A:Note: CILP
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-1184/Product: cartilage intermediate layer protein #status predicted <MAT>

T09484 Length: 1184 April 1, 2002 16:31 Type: P Check: 4681 ..

1 MVGTKAVES FLVLETVSVL GRQFWLTQSV RRVQPKKNP SIFAKPADTL
 51 ESEGEWTTLF NIDYPGKGD YERLDARFY YGDRVCARPL RLEARTDWT
 101 PAGSTQVVH GSPREGFWCL NREORPGNC SNVTVRFLCP PGSLRDRTER
 151 IWSWSPWSK CSAAGQITGV QTRTRICLAE MSLCSEASE EGOHCWGDC
 201 TACDLCPMG QVNADOCACM CODEMLHGV SLFGAPASG AAIYLLTKRP
 251 KLITQDSOG RFRIGLCPD GKSLIKITKV KFAPIVLMP KTSLKAAITK
 301 AEFVRAETPY MYMNPETKAR RAGOSVSLCC KATGKPRDK YFWYHNDTLL
 351 DPLUYHESK LVLRKLQOHQ AGEYFCKAOS DAGAVKSKVA QLIYASDET
 401 PCNPVPESTY IRLPHDCFON ATNSFYVDG RCPYKTCAGQ ODNGIRCDA

451 VONCGISKT EEREIQCSGY TLPTKAKKC SCQCTETRS IYGRVSAAD
 501 NGEMRFGHV YMGNSRYMT GYKGTFTLHV PODERLVLV FVRLQKFN
 551 TTKVLPPNKK GSAVFHEIKM LRKEPTILE AMETNIPLG EYGEDPMAE
 601 LEIRSRSFYR QNGEPIGVK KASVTFIDPR NISTATAQT DLNFINDEGD
 651 TFLRTYGMF SVDFREVTIS EPLNAGKYV HLDSTQKMP EHIYSTKIMS
 701 LNPDTGLME EGDKEFNOR RNKREDRTFL VGNLEIRRR LFNLDVPESR
 751 RCFVKAAYR SERFLPSEOI QGVVISYVNL EPTGFLSNP RAMGRDSVI
 801 TGPAGACVPA FCDQSPDAY SAYVLASLAG EELDAVESP KFPNMAIGV
 851 QPYLNKLNYR RTDHEDPYK KTAFOISMAR PRPSAEBEN GPITYAFENLR
 901 ACEAPPSAA HFRFYQIEGD RYDYNTPFEN EDDPMSTED YLAWMPKPMK
 951 FRACIYVKI VGPLEYNVS RNMGTHTRT VGKLYGIRDV RSTRDRQPN
 1001 VSAACLEFKC SGMLYDQDRV DTLVKVLPQ GSCRRASVNP MLHELYVNLH
 1051 PLAVNNDTSE YTMALPLDPL GHNYGITYVT DQDRTAKEI ALGRCPDGT
 1101 DGSSRIKSN VGVALTFNCV EROVGRQSAF QYLOSTPAQS PAAGTQGRV
 1151 PSRRQRAER GGORQSGVVA SLRFPRAAQ PLIN

!!AA_SEQUENCE 1.0
 PI:A84089 - Hypothetical protein BH3513 [imported] - *Bacillus halodurans*
 (strain C-125)
 C:Species: *Bacillus halodurans*
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: A84089
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirama, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.
 A:Reference number: A83650; MUID:20263314
 A:Accession: A84089
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-957 <STO>
 A:Cross-references: GB:AP001519; GB:BA000004; NID:910176109; PIDN:BA07232.1; GSPDB:GN00137
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3513

A84089 Length: 957 April 1, 2002 16:31 Type: P Check: 4652 ..

1 MKFISWTLNE PSNAQFAEYA TEVSPGEWRI LNPDAKRMWG GNQKNFMLAF
 51 MNHHDKIYGV GLHDEGVNAD GTIYSYKAGE GYPLNDEET AIRMMNRDSL
 101 RFLVDHYRNI KWSLQWCFD PSRVEPIIDN VNGAQDTFVR QLKKAIELYL
 151 NRPFGRIKGI EMDFEKTSR PRSAQPEPKY RDLRLRYKDE VCAPLGLAIR
 201 VNLHAMTGEY NPSWYMTNV STIAADIDE YQIUSYPSFA GNAAPPSRP
 251 VMNLLEVLDH VRNVLPPEKT FIGNAAYGR WSLNRDRIGT AIAYWQLLOW
 301 QNGLFKHNAG ORNDQSEFTM FDQSFIPYCG FHDESGEY TELHCYDRFQ
 351 ARFARLLPYN NSQVYRGTY RNAEYTSYS KHQAKFTGI QRVLTEATST
 401 SGHISDAHSV WEKDDLPY TFGYNTLPQ QYLYDEATNS CVASAGAIGQ

451 DGRVYSPSL STPTGYRLIA TVEFPYLNCR IPINWGVYD VIGEDIDPMW
501 PEFVNPSPHF FDCGTFSFST SMITIVGVQD DSAQIMGFVI CRDEHNGSG
551 GEVEYNVLQ VPKKRGSVLD GAVTKVDADM PDEVTLIEL IRRIHPRAIF
601 WEDLEFPAD QEVENLTETN YVORAITGFR APNGPYVDG ACRGPLONIG
651 YSNGTMRVA ASGDEAHVY COARNSAQL VLNREFSFA HIEDIRALD
701 SNAIYGFYF ARNDGVYNG YIAQLNRYNR TVRLYESGG SSQVLAITAM
751 SETLANGIS RHLLTIRVN GRIKILYCAV EYINYSGLP GSLRGAHGV
801 YANCRIRCY RHIAITNDY EPEKYSALV DGREVALAE DRPSYDELG
851 YLYVSGENPD EGLDIDIDND YDNFPIVNI SVWGEKNIRI RLVDAGWLR
901 NFVYDGEY SIAMNSDLEG FITTLGFIKN YGCKGVGMWT IGEDPRVFT
951 YLPPEND

!!AA_SEQUENCE 1.0
PI:G96806 ? unknown protein T5M16.25 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96806
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
O.; Alonso, J.; Altif, H.; Arujo, R.; Bowman, C.L.; Brooks, S.Y.; Bueller, E.;
Chen, A.; Cho, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.;
Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.;
Feldblum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.;
Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.;
Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.;
Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Miltischer, J.;
Miranda, M.; Nguyen, M.; Nieman, W.C.; Osborne, B.I.; Pal, G.; Peterson, J.;
Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
Tallon, L.J.; Tambunga, G.; Tortum, M.J.; Town, C.D.; Utechtack, T.; van Aken,
S.; Vaysberg, M.; Vysotskaya, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.;
Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <STO>
A:Cross-references: GB:AE05173; NID:96382510; PID:AAF07796.1; GSPDB:GN00141
C:Genetics:
A:Gene: T5M16.25
A:Map position: 1

G96806 length: 421 April 1, 2002 16:31 Type: P Check: 8387

1 MSQKLTITQ SSLRSPSTI RSSIQSLSTI TECDDFNETS HHRRODLEA
51 GEKEKORRR KPVKSGSMN RIKPGIAFTL ACLSPSLSS FLFFVDEIF
101 TSENLLGLI FVALALFPAS RNMAVINQTV IAIKOIRVRS RIKHKRPVQ
151 WYIGSKREP IKEETRLVY KEGVQFFSNG DYEGEFNG KCNGSVYYY
201 YVNGRYESDW INGRYDGYI ECWSKSGSKYX GOYKQGLRHG FGYYWYTGCD
251 SYSGEMFNQ SHRGVOTCA DGSSFVGEFK FGVIKHGLASY HFRNDKYAG
301 EYFGKINGF GVIYFANGHY YEGAMHGRK OGQYTYRFT GDINSGEMD
351 GNLVNHFLD SDPVRAVQS ARERAKNGV ORRIDEQVIR AVAANKAAT

401 AARVAARAV ONOMDKICD N

!!AA_SEQUENCE 1.0
PI:S29344 ? protein kinase KIN3 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O5220; protein YOR233w
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C:Accession: S29344; S67126; S24707
R:Kambouris, N.G.; Burke, D.J.; Creutz, C.E.
Yeast 9, 141-150, 1993
A:Title: Cloning and genetic analysis of the gene encoding a new protein kinase
in Saccharomyces cerevisiae.
A:Reference number: S29344; MUID:93220392
A:Accession: S29344
A:Molecule type: DNA
A:Residues: 1-800 <KAM>
A:Cross-references: EMBL:X67916; NID:95514; PID:CAA48115.1; PID:95515
R:Boyer, J.; Fairhead, C.; Gallion, L.; Gallison, F.; Michaux, G.; Thierry, A.;
Dujon, B.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67104
A:Accession: S67126
A:Molecule type: DNA
A:Residues: 1-800 <BOY>
A:Cross-references: EMBL:Z75141; NID:91420534; PID:CAA99453.1; PID:e252094;
PID:91420535; MIPS:YOR233w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:KIN4; KIN3; KIN31
A:Cross-references: SGD:S0005759; MIPS:YOR233w
A:Map position: 15R
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
E:44-313/Domain: protein kinase homology <KIN>
E:52-60/Region: protein kinase ATP-binding motif

S29344 length: 800 April 1, 2002 16:31 Type: P Check: 2811

1 MASVRRKHTY GGNVYTDNR HSLDRNNEIL HPHKQRKH ATFGYITGS
51 TLGESEFGKV KLGWTKASS NEVPKQYAK LIRDTIKRD ADKEIKIYRE
101 INALKHLTHP NIYLEEVLQ NSKYIGIVLE FVSGGEFYK IQKRRLKES
151 SKCRLEAQLI SGVNMHTKG LVHRDLKEN LLLDKHENLV ITDFGFVNEF
201 FEDNELMKTG CGSPCYAPE LVVSTKAYEA RKADVWSCGV ILYAMLAGYL
251 PWDDHENTP GDGLARLKY ITOTPLKFFE YITPIPRDL RLILVNPFR
301 RINLOTIKRH VWLKPHEAFL SIQPNYDEH LQKRRKPPN KQDVGRHSY
351 SSSASSYSKS RDRNSLIES TLBOHRMSPQ LATSRPASPT FSTGSKVVLN
401 DTKNDKEEN INERTSASC RYTRDSKNG QNQIEGVARS HSSRGNKHTS
451 VAGLVITPS PTAARTNAP SKKITEHYKD SSTSTSTQEE FRIKGNHYV
501 RSRPRETSY PGLSRNTADN SLADIPVNL GSGRLTDAK DVPPLAITHD
551 TKATISNNS IMLSECPAA KTSFVDHYA IGDNLHGDKP ITEVIDKINK
601 DLTHRAENG FPRESIDPS TSTILYKPE TNSDDEHYE SOLENGHSS
651 NKSDASSDKD SKKIYKRRF SFMSLYSSLN GSRSTVESRT SKGNAPVSS
701 RMPGSGSNS NIKITQOOPR NLSDRVNPD KKINDRIRD NAPSVAESEN
751 PGRSVASVY VSTLREKRS ELSNEGNVVE AQTSTARKVL NFKRSMRY

!!AA_SEQUENCE 1.0
PI:S23308 ? substance P - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S23308
 R:Jensen, J.; Conlon, J. M.
 Eur. J. Biochem. 206, 659-664, 1992
 A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.
 A:Reference number: S23308; MUID:92298992
 A:Accession: S23308
 A:Molecule type: protein
 A:Residues: 1-11 <LEN>
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
 A>Note: substance P is derived by post-translational processing of preprotachykinin A
 C:Superfamily: unassigned animal peptides
 C:Keywords: neuropeptide; amidated carboxyl end (Met) #status predicted
 F:11/Modified site: amidated carboxyl end (Met) #status predicted

S23308 Length: 11 April 1, 2002 16:31 Type: P Check: 4943 ..

1 KRPHQFGL M

!!AA_SEQUENCE 1.0
 P1:F65524 } sub5 type protein [imported] - Chlamydomonas pneumoniae (strain J138)
 C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: F65524
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T.
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A66491; MUID:20330349
 A:Accession: F65524
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <STO>
 A:Cross-references: GB:BA000008; NID:98978644; PIDN:BA98460.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: ywlc

F65524 Length: 286 April 1, 2002 16:31 Type: P Check: 9351 ..

1 MPKKAQITF SLPEYMAIH QGKIVALPTD TYGFLVLSLY ASEAEERLYA

51 LKDRPSKAF ALVYNSIEDI ENISGYPLSP TAKKLAQLFP GAITLVVNR

101 NRPFKETLA FRIYDHSVYR EIVDHGCTLI GTSANLSEFP SALTNOELFA

151 DFADHDLCTF DGPCSHGLES TVVASDPLYI YREGLISRSV IENIAGTEAK

201 IFHRTSHAFS KHIIYTVKN QEDLVSPFSG SLDFKGVCE HPRKNEFYTR

251 LREALKKKTP SIVFIYDINT SDPELEPFL SPYIIE

!!AA_SEQUENCE 1.0
 P1:F85107 } hypothetical protein At4g10370 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: F85107
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor, Washington University in St Louis and PE Biosystems
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488
 A:Accession: F85107
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-676 <STO>
 A:Cross-references: GB:NC_001268; NID:97267734; PIDN:CA878160.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4g10370
 A:Map position: 4

F85107 Length: 676 April 1, 2002 16:31 Type: P Check: 7623 ..

1 MDENLFFVK LQNDYPTSS GEVLAMSTG DDQPLDQPLE LCPDARIKH

51 KKIQRDGD IFDYDFKHP YISSPHFPPK RSGDQGGESI LDCDEGDIK

101 LPVPLFWCN NKESDSREFQ CGGCRDSMLS ASYVACLOE KKFHRECVES

151 PLEIKHPTHL FHSRLYYHP APEFCIOCKT EYVMIFYHCL TONLSMHPVC

201 AMKRVPEFLD HPSKHPHPLT FEPTQASLVC HFCALIKKLD PLYCTKCVF

251 VHKGCIGFP HVIRISRTH RISFTSLPC GKLSGVCVHQ QVNDYGAVS

301 CKKDAVEFH SKCALQRHNV DGNLEAVE EDDMIDGER FKRIDGILL

351 HPHSHNLHL QTRAYDENT YCRGALPIY EGOFYSCIES DFLHEHCAN

401 APRMKRHPH PHLPLLVAT RGPENEGTF QCDACHRKGT GFYEHHTDQ

451 ENIFMDIHC ASIFEPFOYQ GHEHPLFLPS EPRKMKRCQM CYEYVNNLT

501 NCLECDYILC FHCATLPYKV RYKHDSHFLK ICKGRANDQ SYWCEICECK

551 IEEGTERAFY NTPKKDTSFY KGNACCTTIL QRCLLGIDRY MKPGETVDY

601 LSIKXASBG QSKESITDVO ILNNSPTR ICRCRCRCRC PFIFKGNHT

651 IFCSWDCVED SAMRSYORLL YSLWLG

!!AA_SEQUENCE 1.0
 P1:G84527 } hypothetical protein At2g15340 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84527
 R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Crozin, L.A.; Shen, M.; Vanden, S.E.; Umayan, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Coppenhaver, G.P.; Preuss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-85 <STO>
 A:Cross-references: GB:AE002093; NID:94544379; PIDN:AA022290.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g15340
 A:Map position: 2

G84527 Length: 85 April 1, 2002 16:31 Type: P Check: 8684 ..

1 MALSGQKKR RGAGVLYTAT AGDGDLMALA PLPOAOVOLL VIQTLAVOTL

51 EVRIIVVLAP LGDLGGVGD PTALGARPHR MLTYEF

!!AA_SEQUENCE 1.0
 P1:B4054 } orf2 protein - Junonia coenia densovirus
 C:Species: Junonia coenia densovirus
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
 C:Accession: B4054

R.Dumas, B.; Jourdan, M.; Pascaud, A.M.; Bergoin, M.
 Virology 191, 202-222, 1992
 A:Title: Complete nucleotide sequence of the cloned infectious genome of
 Junonia coenia densovirus reveals an organization unique among parvoviruses.
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36591
 A:Reference number: A44054; MUID:93033112
 A:Accession: B44054
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <DUM>
 A:Cross-references: GB:S47266; MID:9257675; PIDN:AB23699.1; PID:9257677

B44054 Length: 545 April 1, 2002 16:31 Type: P Check: 1211 ..

1 MANGDTNRET DSTTRPNQDI IRESSGRTSP SECCSVVAMT SKRRMSHG
 51 RCTMASIAKE SOENFOYAE ELEKMGSEFF GYTGOSIIP SSAYISDYII
 101 LRDIDLQDC LDVLEYGERS RRNLGFGSE EGDHIVIH D CSYTRNSGRD
 151 IMISQVKKPG SVQTKGKPVK FIMEFKRTDW YDFEIEFVR KRGEAIIYR
 201 GSGKIPSD ECVNTRTEFK EREWVSSDC TDYEECOE HKISRRSDAG
 251 SNGRLYEKK AYSAGKEFAYI RKTAKALLRK YVSPVSAIC DYPERRDDL
 301 LCDPKRDYI QAACDDFGKD LNMALREIY NLITEDYNT DEQELNPYAL
 351 FISSMKYDNL ENSLNIITEL LKFOCNDDED LIVEFLTNLY NVLDRIIPKL
 401 NAFLLISPPS AGKNFFPDM FGLLSYGOL GQANRHLLFA EQEAPNRYL
 451 LNNEPVESS LDTIKMEG GDPYTVAVKN RMDAHYKRP VILLNNYVP
 501 EMETAFSDR IIOYKMNAP FLKDYELKPH PMTFILLK YNITF

!!AA_SEQUENCE 1.0
 PIR:ET0605 hypothetical protein RV3567c - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: E70605
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
 Gordon, S.V.; Eigmeier, K.; Gao, S.; Barry III, C.E.; Tekala, F.; Badcock, K.;
 Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
 Felkell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.;
 Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail,
 M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.;
 Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70605
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-187 <COI>
 A:Cross-references: GB:Z92774; GB:AL123456; MID:93261729; PIDN:CAB07141.1;
 PID:E306707; PID:91877298
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: RV3567c

E70605 Length: 187 April 1, 2002 16:31 Type: P Check: 8381 ..

1 MSAQIDPRTF RSVLQFCGTG ITVITTVHDD VPVGFAQSP AALSLPEPLY
 51 LRCPTKVSRS MQAIEASGRF CVNVLTERRK DVSAREGSKE PKKPGIDMR
 101 PSLGSPITE GSLAIIDCTV ASVHDGDHF VVFGAVESLS EYPAVKRPPL
 151 LFYRGDYGTGI EPEKTPAHM RDLLEAFLLT TTQDTWL

!!AA_SEQUENCE 1.0
 PIR:T36591 - hypothetical protein SCH24.26c - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36591
 A:Reference number: T36591
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-373 <OLI>
 A:Cross-references: EMBL:AL049826; PIDN:CAB42732.1; GSPDB:GN00070;
 SCOEDB:SCH24.26c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SCH24.26c

T36591 Length: 373 April 1, 2002 16:31 Type: P Check: 1196 ..

1 MSLLTFTSR EOHLYIOSL PAASHMOVPA WADYKAEWRS ENLGWPDRT
 51 GELVAGALVL YROLPKIRRY LAYLPEGPVI NMFAPNLODM MBPMLAHLKQ
 101 QGAFSVKMP PYIIRMDAT SIKKGIODPD VKRLRIEAD HIEPRAFEVA
 151 DKIRRMGOO GEDGAGFGD VQPRYFQVP LANRSLEEVH KNFNOLMRRN
 201 IKKAERAGVE VVOGGYHLE EMQRLYEITA VRDHFPRPRL SYFQMMAL
 251 NNEDPRMRL YFARHNGVNL SAATMLVVG HWVYSYGASD NIGREVRPSN
 301 ANQMAMLRDS YALGATVYDL RGISDSIDES DMLFGLIQK VETGGOAAEY
 351 LGEMDFPLNK LHKALDIYM SRR

!!AA_SEQUENCE 1.0

PIR:T04052 hypothetical protein F24G24.170 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 C:Accession: T04052
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.;
 Mayer, K.F.X.; Scheller, C.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: T25184
 A:Accession: T04052
 A:Molecule type: DNA
 A:Residues: 1-705 <BEV>
 A:Cross-references: EMBL:AL049488
 A:Experimental source: cultivar Columbia; BAC clone F24G24
 C:Genetics:
 A:Map position: 4
 A:Note: F24G24.170

T04052 Length: 705 April 1, 2002 16:31 Type: P Check: 9930 ..

1 GEKERNTIK IQIPIVAMS SVGVFHKVEM DENLYRVYKL TOTDYPTSSG
 51 EYLANDSTGD DQPLDPLFL CPDARIKFKH LKIQREDDGI FQYDEKFNHY
 101 ISSPHFPSKR SGDQGESIL DCDDEGICKL PVPPLFCMNN KESDSREPC
 151 GGCDSMLSA STYACLOCEK KFKECVESP LEIKHPTHLF HSLRLYHDA
 201 PERFCIOCKTE VMIFVHCLT CNLSMHPVCA MRKVPEFIDH PRSHPHPLTF
 251 FPLQASLVCH FCALLKKIDP TYICTKCVF IHKGCIGFPH VIRISRHTHR
 301 ISFTSSLPCG KUSCGVCHQO VNDYGAVSC KRCDAVFVHS KCALORHWD
 351 GKDLSEVPPEE DDMIDGEPF KRIADGIIH PFRSHNLHIQ TRAYDENTY

401 CRGALPIYE GQFYSCIESD FILHEHCANA PRMKRHLPHR HPLTLVATR
 451 GPENEGSTQ CDACHRKGTG FEYEHHTDOE NIFMLDICA SIFEPFOQOG
 501 HEHPLFLPSE PNKMGRCOMG TYETVNLNLN CLECDYILCE HCATLPIYKVR
 551 YKDSHFELKI CNKREANDOS YWCEICECKI EESTERAFYN TPKKDTSFYK
 601 CNACCTLIHQ RCLIGIDITYM KPGETVADYL SSIKVASEGO SKESITDVQI
 651 LNSSSTRPI CTRCICRCPP PIFKGHNTI FCSMDCVEDS AMRSTQRLLY
 701 SFLMG

11AA_SEQUENCE 1.0
 PI:T51199 hypothetical protein B7N4.60 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
 C:Accession: T51199
 R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.;
 Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.
 submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225286
 A:Accession: T51199
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-422 <SCH>
 A:Cross-references: EMBL:AL390218; GSPDB:GN00116; NCSP:B7N4.60
 A:Experimental source: BAC clone B7N4; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B7N4.60
 A:Map position: 6

T51199 Length: 422 April 1, 2002 16:31 Type: P Check: 9296

1 MDNLNRMGAR GGEGLLPCHL DRLFPFEMD TAMEARVRA LMAEFGTPG
 51 RYGRSDSLE RLREERAQRQ ROANDRYRE RRAEYQGYR LRGGSDDDA
 101 DAERGSMEER RSSSRVEIQS TSQASPCIQ RYTTVARSQS RSRSSRRRR
 151 RPSDNDQTS SSQDRKPPDL HVFTSGTKH PKRRSSAVL SCKRPAYVK
 201 CHTKFEDYSC LEPPHPIPTS CHSRPRPKTP VVAKCOPPKR KPAYVPCILP
 251 PGHPTSPFS PYPARAOTCH PRASSQVCH SSKPRKATY RRRPRPRPC
 301 GPYKSRPERI YREVPYIHEI PVREIREYEV EYVRYVEVY EYVRYVPEV
 351 PVRYNVPARY PVHVPVHVYV PQPYVYHGG GGGGGYGYG GYGHGGRYG
 401 ARADEGPWYR FKAVTWQSGP PF

11AA_SEQUENCE 1.0
 PI:T18785 hypothetical protein B0564.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18785
 R:Lightning, J.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: Z19021
 A:Accession: T18785
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-912 <MIU>
 A:Cross-references: EMBL:Z73422; PIDN:CAA97769.1; GSPDB:GN00022; CESP:B0564.7
 A:Experimental source: Clone B0564
 C:Genetics:
 A:Gene: CESP:B0564.7
 A:Map position: 4
 A:Introns: 33/1; 61/3; 144/1; 187/2; 415/2; 517/3; 546/3; 591/3; 639/3; 675/2;
 712/2; 747/3; 818/1; 852/2

T18785 Length: 912 April 1, 2002 16:31 Type: P Check: 558

1 MMSRGLPTLC RTIPORQFSV AAQAGAPAE IDDFLSHIAA APQGLVKNR
 51 TYLESTEFF KMLEONPIKS IDOFITAAQM AITVKSTEON KAFSIIDIA
 101 KVLKPEYEN FGPKETVDAL REVLOLNSKG KYSTDIQNLF LEKISQSDL
 151 QTVPFDTLV IIRYKSSID QNVIESIATS LISRIKEIA NPADLLAIIA
 201 GDGYEKSKAF HNEAFLEKAE RLVAVMGMAE KCALLKHMAY NKORRQILG
 251 AINNAISSSS QVLTVSQIVS VTGSCALTY YPPKIAKIS NDLEKNSVL
 301 AQMDVLSIA DSFIRMGD QKSNLLVRY AIEVNAQAP ARLSKFSGL
 351 ARGPSSGKP LAKALKPFLV KERASTNNW LNIVFSLAF QELEAVHDS
 401 VLKSEFVDQI MNSTWEIHDR LKRAMTLMT SSAKAVDMOG KYEGPTVKE
 451 TFARFGIND AKTIRNARQL KYSSNHSEC RYFLKSLFKL APQDTHCOLP
 501 NWEDGAFVD AYVMDPNSN LLVNTSOMGS KKRPLFFYG WLQTONET
 551 SGEINTVGOE QLGRLMBSA GFDPVVEKT ELDYCSIED QOKFQNMVI
 601 TFPFADGVDP KPVCIYADI FETWTARAKI HFSIYVIFRK NVELAEPFL
 651 LYTTEKKNAV HLDGVAODF GLPMTKDDG QRAPDISROK NDYILDFET
 701 NINNPEDGFS YCWDICISTK NTTWVPRQLM PPSKRSKMLY LLLPEESNI
 751 MYLSEKAYS LQLMKKHRKM GQPPQVGCY INENCOTSKY MEGCHVYCE
 801 QCLNSWNDKP CSVCLKPYTS EPTQKLROG PCFPDLCSPR SSTMTIVLIP
 851 CGCHVACQNL EDAYERNKHH LEPLIEKIKY CPPEPCRIYV RKLKRFWHQ
 901 QDKHTLEMN SA

11AA_SEQUENCE 1.0
 PI:T32912 hypothetical protein C54G6.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32912
 R:Tin-Wollam, A.; Graves, T.; Ozeraky, P.
 submitted to the EMBL Data Library, January 1998
 A:Description: The sequence of C. elegans cosmid C54G6.
 A:Reference number: Z21245
 A:Accession: T32912
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-173 <TIN>
 A:Cross-references: EMBL:AF043698; PIDN:AA097561.1; GSPDB:GN00019; CESP:C54G6.3
 A:Experimental source: strain Bristol N2; clone C54G6
 C:Genetics:
 A:Gene: CESP:C54G6.3
 A:Map position: 1
 A:Introns: 17/2; 51/3; 94/1; 169/2

T32912 Length: 173 April 1, 2002 16:31 Type: P Check: 8718

1 MALLKVRDEC TKLVGYQFLN SHICLSISLI QLLVCCMAVA QHVNYSYTHS
 51 KILKDFLEG SLPLEAVDAV IFDRLRHYL WGRGCAVEE LDGGRGLLM
 101 CVSHCLTVF SIPVTFISHP KPCLFWPLLF QVSWLKKFGK KLFNPFKA
 151 QMDPRLPLT TAWFESAVVL EKF

11AA_SEQUENCE 1.0
 PI:S33300 probable substance P - smaller spotted catshark
 C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted

dogfish)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C:Accession: S33300
R:Maugh, D.; Wang, Y.; Hazou, N.; Balment, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A:Title: Primary structures and biological activities of substance-P-related
peptides from the brain of the dogfish, *Scyliorhinus canicula*.
A:Reference number: S33300; MUID:93292508
A:Accession: S33300
A:Molecule type: protein
A:Residues: 1-11 <MAU>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of
cardiovascular and gastrointestinal functions
A>Note: substance P is derived by post-translational processing of
preprotachykinin A
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

S33300 length: 11 April 1, 2002 16:31 Type: P Check: 4938 ..

1 KPRPGCFGL M

!!AA_SEQUENCE 1.0
P1:C72098 -Sua5/Yc10/Yrc family protein CP0489 [imported] - Chlamydomophila
pneumoniae (strains CML029 and AR39)
C:Species: Chlamydomophila pneumoniae; Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: C72098; B81572
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lamell, C.; Fan, J.; Olinger, L.;
Grimwood, J.; Davis, R.W.; Stephens, R.S.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: C72098
A:Molecule type: DNA
A:Residues: 1-286 <ARN>
A:Cross-references: GB:AE001612; GB:AE001363; NID:g4376541; PIDN:AAD18419.1;
PID:g4376543
A:Experimental source: strain CML029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
Hickey, E.R.; Peterson, J.; Uterback, T.; Berry, K.; Bass, S.; Liner, K.;
Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwin, M.; Nelson,
W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
C.M.
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia
pneumoniae AR39.
A:Reference number: A81500; MUID:20150255
A:Accession: B81572
A:Molecule type: DNA
A:Residues: 1-286 <REA>
A:Cross-references: GB:AE002210; GB:AE002161; NID:g7189400; PIDN:AAF38319.1;
PID:g7189407; GSPDB:GN00122; TIGR:CP0489
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: yw1C; CP0489

C72098 length: 286 April 1, 2002 16:31 Type: P Check: 9351 ..

1 MPDKKAQITE SLPEYMSAIH QGKIVALPTD TYVGFVLSLY ASEAEERLYA

51 LQDREPSKAF ALVYNSIEDI ENISGYPLSP TAKKLAQLFP GAITLVKHR

101 NRPFKETLA FRIVDSYVR EIVDHCCTLI GTSANLSEFP SALTAQELIPA

151 DFADHDLCTF DQPCSHLES TVVADPLYI YREGLSRSY IENAGTEAK

201 IFHRTSHAS KHIKIYTVN QEQLVSLSG SLDFKGVCE HPPKNEYTR

251 LREALKKTP SIVFIYDINT SDYPELFPFL SPYIE

1	18: RFRPH	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W)	HPRPQSEFW	EARAK	
1	Q9K760	ck: 4652 len: 957	1 Q9K760 bacillus halodurans. bh3513 protein.		
1	594: ELIRR	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W)	HPRAIFW	EDLFG	
1	Q59760	ck: 5542 len: 236	1 Q59760 schizosaccharomyces pombe (fission y		
1	148: PVGRG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(W)(F)	KHPDIFW	IALKM	
1	Q9P3B8	ck: 9296 len: 422	1 Q9P3B8 neurospora crassa. conserved hypoch		
1	339: KCOFP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(Y)	KPKPTTY	PGLRP	
1	Q13512	ck: 4657 len: 551	1 Q13512 homo sapiens (human). protein b. 6/2		
1	251: DHEPV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(W)	KPKPLTYW	KDVL	
1	Q15410	ck: 7370 len: 652	1 Q15410 homo sapiens (human). cagha45. 11/199		
1	203: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	RPRPRXY	LEPLP	
1	Q75557	ck: 6311 len: 2,023	1 Q75557 homo sapiens (human). opa-containing		
1	1,578: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	RPRPRXY	LEPLP	
1	Q9Y6V5	ck: 8014 len: 128	1 Q9Y6V5 homo sapiens (human). wugsc:h_dj0841		
1	58: QRIAR	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	RPKPQGF	GLMGK	
1	Q15740	ck: 4695 len: 551	1 Q15740 homo sapiens (human). b protein. 6/2		
1	251: DHEPV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(W)	KPKPLTYW	KDVL	
1	Q75339	ck: 4681 len: 1,184	1 Q75339 homo sapiens (human). cartilage inte		
1	335: CKATG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(F)	KRPDKYF	WYHND	
1	Q9UND7	ck: 7074 len: 2,023	1 Q9UND7 homo sapiens (human). opa-containing		
1	1,578: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	RPRPRXY	LEPLP	
1	Q9UND6	ck: 8071 len: 2,212	1 Q9UND6 homo sapiens (human). thyroid hor		
1	1,766: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	RPRPRXY	LEPLP	
1	Q9Y494	ck: 3943 len: 72	1 Q9Y494 homo sapiens (human). gamma prepr		
1	23: QRIAR	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	RPKPQGF	GLMGK	
1	Q9H6A8	ck: 4809 len: 566	1 Q9H6A8 homo sapiens (human). cdna: flj22		
1	551: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	RPRPRTF	SMLAS	
1	Q9HB06	ck: 4523 len: 159	1 Q9HB06 homo sapiens (human). hypotheticala		
1	144: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	RPRPRTF	SMLAS	
1	Q9BY45	ck: 3438 len: 175	1 Q9BY45 homo sapiens (human). htpap. 6/20		
1	72: KLIVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	RPRDFTY	RCPDP	
1	Q9BT44	ck: 1992 len: 649	1 Q9BT44 homo sapiens (human). trinulecti		
1	203: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	RPRPRXY	LEPLP	
1	Q9BSU8	ck: 5292 len: 433	1 Q9BSU8 homo sapiens (human). unknown (pr		
1	418: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	RPRPRTF	SMLAS	
1	Q44981	ck: 8718 len: 173	1 Q44981 caenorhabditis elegans. c5496.3 p		
1	119: VTEIS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W)	HPKCLFW	PLLFQ	
1	Q61761	ck: 3281 len: 206	1 Q61761 caenorhabditis elegans. f56c3.9 p		
1	188: RPYTE	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F)	KPRQMF	DMDHT	
1	P91767	ck: 6396 len: 1,264	1 P91767 manduca sexta (tobacco hawkmoth)		
1	157: EPPDG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(Y)(W)	HPKRVYW	MLQGD	

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1 Q17532 ck: 558 len: 912 i Q17532 caenorhabditis elegans. b0564.7 prot
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(Y)
GMLQT

1 532: QMGSK
(K)P(R)P-P-P(F)(Y)
GMLQT

1 Q9VQ10 ck: 4431 len: 823 i Q9VQ10 drosophila melanogaster (fruit fly)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(R)P-P-P(Y)(W)
SVEGN

1 302: QOANG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
KPKPGYF
TITST

1 Q9VKA3 ck: 6286 len: 1,677 i Q9VKA3 drosophila melanogaster (fruit fly)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
KPKPGYF
TITST

1,429: NNRHL
(K)P(R)P-P-P(Y)(F)
KPKPGYF
TITST

1 Q9WA61 ck: 4133 len: 355 i Q9WA61 drosophila melanogaster (fruit fly)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(H)P-P-P(F)(Y)
KHPDEIFY
AACNF

1 180: DLPWE
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(H)P-P-P(F)(Y)
KHPDEIFY
AACNF

1 Q9VND5 ck: 2785 len: 412 i Q9VND5 drosophila melanogaster (fruit fly)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(Y)
RCPDYEY
RCEPD

1 221: KITVG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(Y)
RCPDYEY
RCEPD

1 Q9GPP7 ck: 6657 len: 1,406 i Q9GPP7 drosophila melanogaster (fruit fly)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(R)P-P-P(Y)(W)
HPRPLTW
SVEGN

1 343: QOANG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(R)P-P-P(Y)(W)
HPRPLTW
SVEGN

1 Q28733 ck: 9453 len: 6,875 i Q28733 oryctolagus cuniculus (rabbit). titl
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
KRPDEIFW
VKDGE

1 6,270: IPVIG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
KRPDEIFW
VKDGE

1 Q97947 ck: 870 len: 114 i Q97947 tupia belangeri (northern tree shrew)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
RKPQOQF
GLMGK

1 58: QRIAR
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
RKPQOQF
GLMGK

1 Q97948 ck: 8952 len: 129 i Q97948 tupia belangeri (northern tree shrew)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
RKPQOQF
GLMGK

1 58: QRIAR
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
RKPQOQF
GLMGK

1 Q9M181 ck: 5275 len: 355 i Q9M181 physarum polycephalum (slime mold).
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F)
KRPDNEF
SLSEE

1 207: DKRPH
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F)
KRPDNEF
SLSEE

1 Q9ZU49 ck: 2420 len: 302 i Q9ZU49 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
KRPLOYF
THGL

1 123: KVANG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(Y)
KRPVAXY
KPKPV

1 Q9ZSD3 ck: 6830 len: 182 i Q9ZSD3 ceratopteris richardii. gametophy
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(Y)
KRPVAXY
KPKPV

1 115: TVVY
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(Y)
KRPVAXY
KPKPV

1 Q9X160 ck: 4011 len: 290 i Q9X160 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
RPRPDFW
RCEPD

1 123: KDANG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
RPRPDFW
RCEPD

1 Q9SV85 ck: 9930 len: 705 i Q9SV85 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAS

1 244: DHPKS
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAS

1 Q9SJP7 ck: 8684 len: 85 i Q9SJP7 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(H)P-P-P(Y)(F)
RPHPLTF
F

1 77: TALGA
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(H)P-P-P(Y)(F)
RPHPLTF
F

1 Q9MAG7 ck: 2190 len: 667 i Q9MAG7 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PKQSF

1 222: DHPKR
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PKQSF

1 Q9M882 ck: 6307 len: 314 i Q9M882 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
RPRPDFW
RCEPD

1 123: KNAVG
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
RPRPDFW
RCEPD

1 Q9M0N5 ck: 7623 len: 676 i Q9M0N5 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAS

1 215: DHPKS
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAS

1 Q9LTV1 ck: 6135 len: 681 i Q9LTV1 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAT

1 219: DHPKS
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAT

1 Q9LN20 ck: 5875 len: 734 i Q9LN20 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAS

1 294: DHPKS
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
HPHPLTF
PTQAS

1 Q9LIS2 ck: 2503 len: 90 i Q9LIS2 prunus dulcis (almond) (prunus am
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
KRPLOYF
THGL

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1 Q9LQ7 ck: 92 len: 374 i Q9LQ7 vigna unguiculata (cowpea). phosphat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(Y)
178: KNGVG RRPDPFW RCFPD
1 Q9LQ8 ck: 3777 len: 307 i Q9LQ8 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(Y)
123: KDAVG RRPDPFW RCFPD
1 Q9LQ4 ck: 4935 len: 221 i Q9LQ4 prunus dulcis (almond) (prunus amygd)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
30: RTKCS KRPPLQYF TINGL
1 Q9FV1 ck: 8335 len: 322 i Q9FV1 vigna unguiculata (cowpea). phosphat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
123: KDGVC RRPDPFW RCFPD
1 Q9FV1 ck: 7946 len: 162 i Q9FV1 prunus dulcis (almond) (prunus amygd)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
19: RTKCS KRPPLQYF TINGL
1 Q9FV0 ck: 5836 len: 172 i Q9FV0 prunus dulcis (almond) (prunus amygd)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(Y)(F)
21: KRPCS KRPPLQYF TINGL
1 Q9FM6 ck: 7091 len: 685 i Q9FM6 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(H)P-P-P(F)(F)
230: DHKCS HPHPLSF PTQAS
1 Q9CAP2 ck: 8387 len: 421 i Q9CAP2 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(K)P-P-P(W)(Y)
145: SRIRH KRPVQWY IGDSK
1 Q9AWT8 ck: 2435 len: 362 i Q9AWT8 oryza sativa (rice). putative phosphat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(W)
126: KNAVG RRPDPFW RCFPD
1 Q88542 ck: 415 len: 2,074 i Q88542 mus musculus (mouse). opa-containing
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(Y)(Y)
1,638: YHTHL RRPRAVY LEPLP
1 Q9D788 ck: 7438 len: 158 i Q9D788 mus musculus (mouse). 2310022a04rik

```

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1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(Y)
109: KLIVG RRPDPFW RCFPD
Database searched:
SWISS-PROT Release 39.2, Released on 24Aug2001, Formatted on 27Aug2001
SPRINTBL, Release 17.0, Released on 1Jun2001, Formatted on 26Jun2001
Total finds: 73
Total length: 182,937,156
Total sequences: 573,564
CPU time: 16:28.16

```

11AA_SEQUENCE 1.0 STANDARD: PRT: 470 AA.
 ID GLNA_FREDI...3
 AC P33035;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
 GN GLNA.
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella.
 OX NCBI_TaxId=1197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93129187; PubMed=1362348;
 RA Elmorjani K., Liotenberg S., Houmad J., de Marsac N.T.;
 RT "Molecular characterization of the gene encoding glutamine synthetase
 in the cyanobacterium Calothrix sp. PCC 7601.";
 RL Biochem. Biophys. Res. Commun. 189:1296-1302(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 ORTHOPHOSPHATE.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 HEXAGON.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L05609; AAA3288.1; -
 CC PIR: JCI403; JCI403.
 CC DR HSSP: P06201; 2LGS.
 CC DR InterPro: IPR001691; GLN_synth.
 CC DR InterPro: IPR001637; GLNA_adenyltn.
 CC DR Pfam: PF00120; gln-synt; 1.
 CC DR ProDom: PD001057; GLNA_adenyltn; 1.
 CC DR PROSITE: PS00180; GLNA_1; 1.
 CC DR PROSITE: PS00181; GLNA_ATP; 1.
 CC DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 CC KW Ligase.
 CC FT INIT MET 0 0 BY SIMILARITY.
 CC SQ SEQUENCE 470 AA; 52919 MW; ADD7B49A7789E832 CRC64;
 GLNA_FREDI Length: 470 April 1, 2002 16:32 Type: P Check: 2021 ..

01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SERINE/THREONINE-PROTEIN KINASE KIN4 (EC 2.7.1.1).
 GN KIN4 OR KIN31 OR KIN3 OR YOR233W OR O5220.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93220392; PubMed=8465601;
 RA Kambouris N.G., Burke D.J., Creutz C.E.;
 RT "Cloning and genetic analysis of the gene encoding a new protein
 kinase in Saccharomyces cerevisiae.";
 RL Yeast 9:141-150(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / FY1679;
 RX MEDLINE=97127829; PubMed=8972580;
 RA Boyer J., Michaux G., Fairhead C., Gallion L., Dujon B.;
 RT "Sequence and analysis of a 26.9 kb fragment from chromosome XV of
 the yeast Saccharomyces cerevisiae.";
 RL Yeast 12:1575-1586(1996).
 CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN
 KINASE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
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 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X67916; CAA4815.1; -
 CC DR EMBL: 275141; CAA39453.1; -
 CC DR PIR: S29344; S29344.
 CC DR HSSP: O63450; 1A06.
 CC DR SGD: S0005759; KIN4.
 CC DR InterPro: IPR000719; Euk_pkinase.
 CC DR InterPro: IPR002290; Ser_thr_kin_actsite.
 CC DR Pfam: PF00069; pkinase; 1.
 CC DR SMART: SM00220; S_TKc; 1.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW transferase; Serine/threonine-protein kinase; ATP-binding.
 CC FT DOMAIN 46 313
 CC FT NP_BIND 52 60 ATP (BY SIMILARITY).
 CC FT BINDING 80 80 ATP (BY SIMILARITY).
 CC FT ACT_SITE 175 175 BY SIMILARITY.
 CC SQ SEQUENCE 800 AA; 90087 MW; 655B5B5EB0AC65 CRC64;
 KIN4_YEAST Length: 800 April 1, 2002 16:32 Type: P Check: 2811 ..

451 VAGLVTPGS PTTARTRNAP SSKLTHVAD SSQTSFQEE FHRIGNVHV
 501 KSRRPRTSY PGLSRNTADN SLADIPVKNL GSNGLRLDAK DPLPLAIHD
 551 TNKATISNNS IMLESGPAA KTSPPDYHYA IGDINHDKP ITEVIDKINK
 601 LETHKAENG FPRESIDPES TSTILVTEKP TNSDEDEHVE SOLENYGHSS
 651 NKSDASSDKD SKKIYEKKRF SPMSLXSSLN GSRSTVESRT SKKNAPPVSS
 701 RNPSGQSNRS NIKITQOOPR NISDRVPND KKIINDRIKD NADVAESEN
 751 PGRSVRASVM VSTLREENRS ELSNEGNNVE AQTSTARKVL NFKRRSMRV

IIA SEQUENCE 1.0
 ID SERO_GALME 3 STANDARD; PRT: 167 AA.
 AC 076192;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE SEROIN PRECURSOR (SILK 23 KDA GLYCOPROTEIN).
 OS Galleria mellonella (wax moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pelegrypota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Pyralidae; Pyralidae; Galleriinae; Galleria.
 OX NCBI_TaxID=7137;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-31.
 RC TISSUE-Silk gland;
 RX MEDLINE=98288272; PubMed=9624126;
 RA Zurovec M., Yang C., Kodrik D., Sehna F.;
 RT "Identification of a novel type of silk protein and regulation of its
 expression.";
 RL J. Biol. Chem. 273:15423-15428(1998).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY BOTH THE POSTERIOR (PSC) AND
 CC MIDDLE (MSG) SECTIONS OF SILK GLANDS.
 CC -1- DEVELOPMENTAL STAGE: SEROIN MRNA IS HIGH IN THE SILK GLANDS OF
 CC FEEDING LARVAE, DECLINES AT ECDYSIS, REACHES A MAXIMUM DURING
 CC COCOON SPINNING, AND THEREAFTER RAPIDLY DROPS TO AN UNDETECTABLE
 CC LEVEL.
 CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF009828; AAC25171.1;
 KW Silk; Glycoprotein; Signal; Repeat.
 FT CHAIN 1 17
 FT SIGNAL 1 17
 FT REPEAT 18 167 SEROIN.
 FT REPEAT 38 46 1-1.
 FT REPEAT 56 64 1-2.
 FT REPEAT 76 78 2-1.
 FT REPEAT 79 81 2-2.
 FT REPEAT 82 84 2-3.
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 167 AA; 18088 MW; 27A6ABEB62774EB9 CRC64;

SENO_GALME Length: 167 April 1, 2002 16:32 Type: P Check: 3636

1 MATKILFILS FVALSSAGFV WYDDNNNSFP KLRQLYVPL POPPLPLNIP
 51 GLQGPPLPQ PPLPLGFDFS PILPLPPIP IPPLPLPPF INIPAPEDIK
 101 NIKPKPGQFF NGISVSRSG YALDKGNRV KTGSTAVLIN DNGEVNETIV
 151 GDNPKPFES RKSSSN

IIA SEQUENCE 1.0
 ID TKNL_BOVIN 0 STANDARD; PRT: 130 AA.
 AC P01289; P01291; P04091; P20773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ I PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TACT OR NKA OR TAC2 OR NKA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=85086245; PubMed=6083453;
 RA Nawa H., Kotani H., Nakanishi S.;
 RT "Tissue-specific generation of two preprotachykinin mRNAs from one
 RT gene by alternative RNA splicing.";
 RL Nature 312:729-734(1984).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=84039802; PubMed=6195531;
 RA Nawa H., Hirose T., Takashima H., Inayama S., Nakanishi S.;
 RT "Nucleotide sequences of cloned cDNAs for two types of bovine brain
 RT substance P precursor.";
 RL Nature 306:32-36(1983).
 RN [3]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE-Hypothalamus;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chivakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOK BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X00075; CAA24939.1;
 DR EMBL: X00075; CAA24940.1;
 DR EMBL: X00075; CAA24941.1;
 DR EMBL: X00076; CAA24942.1;
 DR EMBL: X00076; CAA24943.1; ALT_SEQ.
 DR EMBL: X00351; CAA26206.1;
 DR EMBL: X01396; CAA26206.1; JOINED.
 DR EMBL: X01397; CAA26206.1; JOINED.
 DR EMBL: X01398; CAA26206.1; JOINED.
 DR EMBL: X01399; CAA26206.1; JOINED.
 DR EMBL: X01400; CAA26206.1; JOINED.
 DR EMBL: M68911; AAA30724.1;
 DR EMBL: M68912; AAA30725.1;
 DR PIR: A01557; SPBOA.
 DR PIR: A01559; SPBOB.
 DR PIR: A05093; A05093.
 DR PIR: B25067; B25067.
 DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR Prodom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 RW Amidation; Alternative splicing; Signal; Neurotransmitter.
 KW SIGNAL
 FT PROPEP 1 19
 FT PEPTIDE 20 56
 FT PEPTIDE 58 68
 FT PEPTIDE 72 107
 FT PEPTIDE 72 107
 FT PEPTIDE 72 107
 FT PEPTIDE 89 107
 FT PEPTIDE 98 107
 FT PEPTIDE 111 126
 FT MOD_RES 68 68
 FT MOD_RES 107 107
 FT VARSPLIC 74 88
 FT VARSPLIC 97 114
 FT VARSPLIC 115 115
 FT CONFLICT 121 121
 FT SEQUENCE 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;
 TKNL_BOVIN Length: 130 April 1, 2002 16:32 Type: P Check: 421 ..

1 MKILVAVAVI FFISTQLSAE EIGANDDENY WSDMSDSDOI KEENPEPEH
 51 ILQRIARRRK PQOFFGLMGR RDADSSIEKQ VALLKALYGH GOLSHRRKKT
 101 DSFVGIMGR ALNSVAYERS VMQDYERRK

11AA:SEQUENCE 1.0 STANDARD; PRT; 129 AA.
 AC -P20366; Q00072; O60601;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTAHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 (NKA) (SUBSTANCE K) (NEUROMEDIN 1); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKRA OR TAC2 OR NKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 OX 11
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=87030957; PubMed=3770210;
 RA Hartman A.J., Armstrong A., Pascual J.C., Chapman K., Rosie R.,
 RT Curtis A., Goling J., Edwards C.R.W., Fink G.;
 RT "cDNA sequence of human beta-preprotachykinin, the common precursor
 RT to substance P and neurokinin A.";
 RL FEBS Lett. 208:67-72(1986).
 RN 12
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC TISSUE=Brain;
 RA Tan A., Too H.P.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN 13
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Testis;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chivakata C., Breckmann B., Hunt N., Davidoff M., Schlize W.,
 RA Iveli R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 RN 14
 RP SEQUENCE OF 98-107.
 RX MEDLINE=87275962; PubMed=3038549;

RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
 RA Oeberg K., Jacobsson G.;
 RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
 RT and neurokinin A(4-10) from a neutral water extract of a metastatic
 RT ileal carcinoid tumour.";
 RL Eur. J. Biochem. 166:693-697(1987).
 RN 15
 RP SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Blood, and Brain;
 RA Lal J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
 RT "Identification of a delta isoform of preprotachykinin mRNA in human
 RT mononuclear phagocytes and lymphocytes.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN 16
 RP SEQUENCE OF 111-126.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=9113394; PubMed=2284201;
 RA McGregor G.P., Conlon J.M.;
 RT "Characterization of the C-terminal flanking peptide of human
 RT beta-preprotachykinin.";
 RL Peptides 11:907-910(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: X54469; CAA8351.1; -;
 DR EMBL: U37529; AAA79195.1; -;
 DR EMBL: M68906; AAA60159.1; -;
 DR EMBL: M68907; AAA60160.1; -;
 DR EMBL: AF050656; AAC15702.1; -;
 DR EMBL: AF050658; AAC15704.1; -;
 DR PIR: A24805; A24805.
 DR PIR: S00069; S00069.
 DR MIM: 162320; -;
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR Prodom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 KW SIGNAL
 FT PROPEP 1 19
 FT PEPTIDE 20 56
 FT PEPTIDE 58 68
 FT PEPTIDE 72 107
 FT PEPTIDE 72 107
 FT PEPTIDE 72 107
 FT PEPTIDE 89 107
 FT PEPTIDE 98 107
 FT PEPTIDE 111 126
 FT MOD_RES 68 68
 FT MOD_RES 107 107
 FT VARSPLIC 74 88
 FT VARSPLIC 97 114
 FT VARSPLIC 115 115
 FT CONFLICT 87 87
 FT SEQUENCE 129 AA; 15003 MW; 51412C1692368DE4 CRC64;

TKNL_HUMAN Length: 129 April 1, 2002 16:32 Type: P Check: 9307 ..

1 MKILVALAV FLYSTQLFAE EIGANDDLNY WSDWYSDQI KEELPEPFEH

51 ILORIARRPK POOFGLMKR RDADSIKQ VALLKALYGH GOISHRHKT

101 DSFVGLMKR ALNSVAFERS AMONYERRR

11AA-SEQUENCE 1.0 STANDARD; PRT; 130 AA.

ID TKNL_MESAU 060541; P49110;

AC 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTECHININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE GAMMA; C-TERMINAL FLANKING PEPTIDE)].

GN TAC1 OR NKMA OR TAC2 OR NKA.

OS Mesocricetus auratus (Golden hamster);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.

OC NCBI_TaxID=10036;

OX [1]

RN SEQUENCE FROM N.A. (ISOFORMS BETA AND GAMMA).

RP STRAIN-AURA; TISSUE-Brain;

RA Heiland A., Kruehoffer M., Juegen Maegert H.J., Forssmann W.G.;

RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE), GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

CC -----

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CC -----

CC EMBL: X30662; CAAS6691.1; -

DR EMBL: X30663; CAAS6692.1; -

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR ProDom: PD005598; Protachykinin; 1.

DR SMART: SM00203; TK; 2.

DR PROSITE: PS00267; TACHYKININ; 2.

KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Alternative splicing; Signal; Neurotransmitter.

KM SIGNAL 1 19

FT PROPEP 20 56

FT PEPTIDE 58 68

FT PEPTIDE 72 107

FT PEPTIDE 72 107

FT PEPTIDE 72 107

FT PEPTIDE 89 107

FT PEPTIDE 89 107

FT PEPTIDE 111 126

FT MOD.RES 68 68

FT MOD.RES 107 107

FT VARSPLIC 74 88

SEQUENCE 130 AA; 14907 MW; CC92E9371A64F2E CRC64;

TKNL_MESAU Length: 130 April 1, 2002 16:32 Type: P Check: 219 ..

1 MKILVALAV FLYSTQLFAE EIGANDDLNY WSDWYSDQI KEELPEPFEH

51 ILORIARRPK POOFGLMKR RDADSIKQ VALLKALYGH GOISHRHKT

101 DSFVGLMKR ALNSVAFERS AMONYERRR

11AA-SEQUENCE 1.0 STANDARD; PRT; 130 AA.

ID TKNL_MOUSE P41539; Q00073;

AC 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTECHININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE GAMMA; C-TERMINAL FLANKING PEPTIDE)].

GN TAC1 OR NKMA OR TAC2 OR NKA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A. (ISOFORM BETA).

RP STRAIN-ICR; TISSUE-Brain;

RA Kato K., Muneoka E., Hosaka M., Murakami K., Nakayama K.;

RL Cloning and sequence analysis of mouse CDNA's encoding preprotachykinin A and B.

RL Biomed. Res. 14:253-259(1993).

RN [2]

RN SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).

RP TISSUE-Brain;

RC MEDLINE=91209287; PubMed=1708336;

RX Chivakata C., Brackmann B., Hunt N., Davidoff M., Schulze W., Ivell R.;

RA Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse testis.

RL Endocrinology 128:2441-2448(1991).

CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE), GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

CC -----

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CC -----

CC EMBL: D17584; BAA04508.1; -

DR EMBL: M68908; AAA39969.1; -

DR EMBL: M68909; AAA39970.1; -

DR MGD: MGI:98474; Tactl.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR ProDom: PD005598; Protachykinin; 1.

DR SMART: SM00203; TK; 2.

DR PROSITE: PS00267; TACHYKININ; 2.

KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Alternative splicing; Signal; Neurotransmitter.

KM SIGNAL 1 19

FT PROPEP 20 56

FT PEPTIDE 58 68

FT PEPTIDE 72 107

FT PEPTIDE 72 107

FT PEPTIDE 72 107

FT PEPTIDE 89 107

FT PEPTIDE 89 107

FT PEPTIDE 111 126

FT MOD.RES 68 68

FT MOD.RES 107 107

FT VARSPLIC 74 88

SEQUENCE 130 AA; 15045 MW; 7BE8DA15FE272F8 CRC64;

TKN1_MOUSE Length: 130 April 1, 2002 16:32 Type: P Check: 430 ..

1 MKILVAVAVF ELVSTQLFAE EIDANDLNV WSDMSDSDOI KEAPPEPEH

51 LLQRIARRPK PQPFGLMGK RQADSSVERQ VALLKALYGH GOISHKRHKT

101 DSFVGLMGKR ALNSVAYERS AMONYERRRR

11AA_SEQUENCE 1.0 STANDARD: PRT: 115 AA.

1D_TKN1_RABIT 4 STANDARD: PRT: 115 AA.

AC_P41540: 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTAACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL FLANKING PEPTIDE].

GN TACT OR NKNA OR TAC2 OR NKA.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1] SEQUENCE FROM N.A.

RP TISSUE=Brain;

RX MEDLINE=93371392; PubMed=8363593;

RA Maegret H.J., Heltland A., Rose M., Forssmann W.G.;

RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.";

RL Biochem. Biophys. Res. Commun. 195:128-131(1993).

RN [2] SEQUENCE OF 72-92.

RP Kage R., McGregor G.P., Thim L., Conlon J.M.;

RX "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is

RT derived from gamma-preprotachykinin.";

RL Regul. Pept. 18:346-346(1987).

RN [3] FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

RP EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

RX SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

RL MUSCLES.

RN [4] ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),

RP GAMMA AND DELTA, ARE PRODUCED BY ALTERNATIVE SPLICING.

RX -1 SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

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RP between the Swiss Institute of Bioinformatics and the EMBL outstation -

RX the European Bioinformatics Institute. There are no restrictions on its

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RP entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X62994; CAA44728.1; -

DR PIR; S18922; S18922.

DR InterPro; IPR003580; Protachykinin.

DR InterPro; IPR002040; Tachykinin.

DR Pfam; PF02202; Tachykinin.1.

DR ProDom; PD005598; Protachykinin.1.

DR SMART; SM00203; TK.2.

DR PROSITE; PS00267; TACHYKININ.2.

RW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;

KW Amidation; Alternative splicing; Signal; Neurotransmitter.

FT SIGNAL 1 19 POTENTIAL.

FT PEPTIDE 20 56 SUBSTANCE P.

FT PEPTIDE 58 68 NEUROPEPTIDE GAMMA.

FT PEPTIDE 72 92 NEUROPEPTIDE GAMMA.

FT PEPTIDE 83 92 NEUROKININ A.

FT PEPTIDE 96 111 C-TERMINAL FLANKING PEPTIDE.

FT MOD RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).

FT MOD RES 92 92 AMIDATION (G-93 PROVIDE AMIDE GROUP).

SO SEQUENCE 115 AA; 13370 MW; 5EC76F7C9B10E1C6 CRC64;

TKN1_RABIT Length: 115 April 1, 2002 16:32 Type: P Check: 1957 ..

1 MKILVALAVL ALVSTQLFAE DIRANDLNV WSDMSDSDOI KEELPEPEH

51 LLQRIARRPK PQPFGLMGK RQAGHGQISH KKHKIDSFVG LMGKRALNSV

101 AYERSAMONY ERRRR

11AA_SEQUENCE 1.0 STANDARD: PRT: 130 AA.

1D_TKN1_RAT 4 STANDARD: PRT: 130 AA.

AC_P06767; P08856; P08857; P22356;

DT 01-JAN-1988 (Rel. 06, Created)

DE 01-NOV-1988 (Rel. 09, Last sequence update)

DE 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTAACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE GAMMA; C-TERMINAL FLANKING PEPTIDE].

GN TACT OR NKNA OR TAC2 OR NKA.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1] SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).

RP MEDLINE=90331040; PubMed=1695945;

RA Carter M.S., Krause J.E.;

RT "Structure, expression, and some regulatory mechanisms of the rat

RL preprotachykinin gene encoding substance P, neurokinin A,

RP neuropeptide K, and neuropeptide gamma.";

RL J. Neurosci. 10:2203-2214(1990).

RN [2] SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).

RP MEDLINE=87118268; PubMed=2433692;

RX Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;

RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance

RL P and neurokinin A.";

RX Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).

RN [3] SEQUENCE FROM N.A. (ISOFORM GAMMA).

RP MEDLINE=87025808; PubMed=2429656;

RX Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;

RT "Sequence analysis of cloned cDNA for rat substance P precursor:

RL existence of a third substance P precursor.";

RX Biochem. Biophys. Res. Commun. 139:1040-1046(1986).

RN [4] SEQUENCE FROM N.A. (ISOFORM DELTA).

RP TISSUE=Dorsal root ganglion;

RL MEDLINE=91085565; PubMed=1702066;

RX Hartmar A.J., Hyde V., Chapman K.E.;

RT "Identification and cDNA sequence of delta-preprotachykinin, a fourth

RL splicing variant of the rat substance P precursor.";

CC FERS Lett. 275:22-24(1990).

CC [5] SEQUENCE OF 1-41 FROM N.A.

CC MEDLINE=93192337; PubMed=8448217;

CC Chapman K.E., Lyons V., Hartmar A.J.;

CC "The sequence of 5' flanking DNA from the rat preprotachykinin gene;

CC analysis of putative transcription factor binding sites.";

CC Biochim. Biophys. Acta 1172:361-363(1993).

CC [6] FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

CC MUSCLES.

CC [7] ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),

CC GAMMA AND DELTA, ARE PRODUCED BY ALTERNATIVE SPLICING.

CC [8] SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

RP SEQUENCE.
RC TISSUE-Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance P-related and neurokinin A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC CC
CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: S23307; S23307.
DR PIR: S23308; S23308.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

TKNA_ONCMY Length: 11 April 1, 2002 16:32 Type: P Check: 4943 ..

1 KRPFGQFGL M

11AA_SEQUENCE 1.0
ID TKNA_SCYCA 1 STANDARD; PRT; 11 AA.
AC P41333;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carchariaformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_Taxid=7830;
RN [1]
RP SEQUENCE.

RC TISSUE-Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance P-related
peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC CC
CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR: S33300; S33300.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

TKNA_SCYCA Length: 11 April 1, 2002 16:32 Type: P Check: 4938 ..

1 KRPFGQFGL M

11AA_SEQUENCE 1.0
ID TRX_DROVI 1 STANDARD; PRT; 3828 AA.
AC Q24742;

DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRITHORAX PROTEIN.

GN TRX.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7244;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=96100387; PubMed=8555104;
RA Tillib S., Sedkov Y., Mizrokh L., Mazo A.;
RT "Conservation of structure and expression of the trithorax gene
between Drosophila virilis and Drosophila melanogaster.";
RL Mech. Dev. 53:113-122(1995).
CC -I- FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION
WITH GENES OF BITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES.
IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.

CC -I- SUBCELLULAR LOCATION: NUCLEAR.
CC -I- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
FACTORS.

CC -I- SIMILARITY: CONTAINS 1 'SET' DOMAIN.
CC -I- SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS.

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or send an email to license@sib-sib.ch).

CC EMBL: Z50038; CAA90349.1; -.
CC HSSP: P04002; IMFA.
DR FlyBase: FBgn0014844; Dvir\trx.

DR InterPro: IPR003889; Fyricl_C.
DR InterPro: IPR003888; Fyricl_N.
DR InterPro: IPR001965; PHD.
DR InterPro: IPR003616; PostSET.
DR InterPro: IPR001214; SET.
DR InterPro: IPR001841; ZnF_ring.

DR InterPro: IPR001628; Zf-C4.
DR Pfam: PF00628; PHD; 2.
DR Pfam: PF00856; SET; 1.
DR SMART: SM00542; FYRC; 1.
DR SMART: SM00541; FYRC; 1.
DR SMART: SM00249; PHD; 4.
DR SMART: SM00508; PostSET; 1.
DR SMART: SM00184; RING; 2.
DR SMART: SM00317; SET; 1.
DR SMART: SM00399; ZNF_C4; 1.
DR PROSITE: PS0280; SET; 1.

KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
KW Nuclear protein; Developmental protein; Activator.

FT ZN_FING 1251 1334
FT ZN_FING 1335 1380
FT ZN_FING 1408 1469
FT ZN_FING 1708 1767
FT ZN_FING 1768 1818
FT ZN_FING 3701 3810
FT DOMAIN 28 41
FT DOMAIN 66 71
FT DOMAIN 160 164
FT DOMAIN 173 182
FT DOMAIN 221 228
FT DOMAIN 243 251
FT DOMAIN 253 258
FT DOMAIN 292 296
FT DOMAIN 538 546
FT DOMAIN 1072 1075
FT DOMAIN 2483 3271
FT DOMAIN 3333 3339
SQ SEQUENCE 3828 AA; 413721 MW; 32059CF303A3C504 CRC64;

TRX_DROVI Length: 3828 April 1, 2002 16:32 Type: P Check: 425 ..

1 MGRSKPEGNP SKSINKKRIS VLOLEDEAS AAAAAAATA ATTEHQOSE
 51 QSAGSSASRE KGNCDNDD DNAPSGATS GNRGASSGAS DAAPEGNNY
 101 GNGSSGSKT TNGGVNNGS HHKSATPAE LKECKNOGQ IEPNNCIAE
 151 PGTEEDTND DDDSSNDKK PTAASAAAAA AAFVPGSAL ORARKGNRK
 201 FKNLNLARPE VMLPSTSKL QQQQQOOLN CPASASLS SAAAAAANA
 251 APTTTTAS ASATLTATAT STSTSLPDT PLSYIAGGG GAAAAALLA
 301 NPASVETKV VEYNAATATA ATAAATAAG AGEDVGLKA SIEMANEGL
 351 EAVAVANKSS GSSPNHNHP NAVAGSTAA APGAPTATQ KKTVTKNLL
 401 ETSDDKSVM RPYNDNRVP LVSIMKDSL NRPLNYCRGS EPIVRPSILS
 451 KLINKNSNID KLSLKFERSV HASSNSIOES SSTTNLFCS GLSRAGAPI
 501 DDDAVSGV TERKQEPQHK TPEDNDDGS ASSDAIEDDE DDDDDAEEN
 551 ELAASEKSAE TTAASDEKA DDROLVMDKH FVLPRKSTRS SRIKPNKRL
 601 LEVGLICSKR SPSDANGKPK PKNYFGLATL PAKCTPRRR SATALSOKL
 651 GKEFPASFAT AKVNSFVL RPRLOFOTDK SRSFVSAKPT LPTTYLPLRS
 701 S&AITSANVL SFQALNNANS AVAAASTCAV CSAPVNNKA PLARKGVIA
 751 CEVCRKENSR MTKISKLSLP MHSNPFSTTA QSGOQLKCTD GGNCSILSEK
 801 SCLNFKKLY KERCKACWLK KCLATLOLPA GHRSRLSAIL PASMREVP
 851 KDKCPPLLS PTASLFTAP TSSASSGTTI KMKSSAETAV NSTKSNPLAE
 901 NNVTFGTPL LRPAILKPL FLKIGSDNKK AKESKEALGL SPVSTSEAA
 951 VAPGKTRKA KODKEKAREL EAKRPLSPNA KKTTEANTPE TOKDEGPST
 1001 TTVYSAASSS TSHTSSAATN SSOLETTAA NASAVPDNLK RORIDLKPR
 1051 VKHVCRSASI VLGOPLATFG DEEBELAAE AGPAPTTTTT TSPEVIIRK
 1101 PKSPQPMQMI IDENDCASC ILTPEATAE AQPAVKSVLE SRSKSNTOGT
 1151 EAKKTPTSG SSKGVYTRN ATATVTVAS SLVATKKORN IEVSSISSS
 1201 QAAATOSRRA LAKEVNRLKA LISIDFEMNY DPAEVCOTGF GLIVETVAQ
 1251 RALCFLOGST GUDPLIFCAG COEPYHOYCV LDEVNLKHSS FEDTLMTSLL
 1301 ETSNNACAIS AATNTALNOL TORLWMLCPR CTVCYTCNMS SSGKVCQKC
 1351 QKHVSTCLG TSKRLIGADR PLICVNCCLK KSCATTKVSK FVGNLPMCTA
 1401 CFI LRKKNF CPIOCKCYDD NDFDKMMEC GDCNOMWHSK CEBLSDEQIN
 1451 LLSLTPESIE FTCKKCARRC DVSRNKADEW ROAVMEEFKS SLYSVLKLS
 1501 KSHOACALIK LSPRKNMRC SAGAOPAKAH SOGLQPKAL QFYNYGLSGD
 1551 GEFQNSDIY EFKEQHSNTR KPSPTVPCSC LQPLSQSPSF SLVDIOKTA
 1601 SNPYVSLAEF NYDMQVIOQ SNCELDIAY KELLSQFPW FONEACTAD
 1651 ALIEMFESC GYEELKESPT TYAEHHTASQ APRTGLDIP LDDVDLGGC
 1701 AVETRLDTRV CLFCRKSGBG LSGEARLLY CGHDCWYHIN CAMMSAEVE
 1751 EIDGSLONVH SAVARGMITK CTVCNGRAT VGCNVKSGE HHYPCARTI

1801 DCAFLTDSM YCPAHARNAL KANGSPSVTY ESNEFVSRPV YVELERKKK
 1851 LIVPAKVOFH IGSVAVRQLG SIVPRFSDSF EALVPINFLC SRLYSSKEP
 1901 WKIVETVKT TIONSYSTL TLDAGRNFTV DHTNPMSLV QUGLOIARW
 1951 HSSLARSDDL DTDMAEFPNS YVPADENTEE EPOONADLPE PEIKDAIFED
 2001 LPHELLDGIS MDIFWEDL GDKTELFAMS EQSKDGTAT SQAGASVLI
 2051 CDEDTNMSNS LNKHLVLSNC CTASNVPDDA MLCANSSSO EKECGDYLK
 2101 TDTAPTRSWP KLDGGSVAAF KRRRLSKNIA EGVLLSNOR SKEMATVAG
 2151 ITRQSVCS SELPAGSAT MTKSFMTSA AKCLFENES REPAKLTIM
 2201 QMDGVDDST EYRTIGSDN LSTAOFTGOV KCERCCTTR NYDSFORILG
 2251 SCEPMSTSES ESETATGTAQ LSAESLNELO KOALAAATLS NTGLNYLOT
 2301 SFPQVQNLAT LGQFGVGLQ GLQTLQLOPQ SLNGFFLSQ PMAAQATSNQ
 2351 NDVLOLYANS LONLANLGG GFITLTOPMS TOAOPOLIAL STNPGTOQF
 2401 IOLPQNGAT TOLLQTAAPL RCNATYOTIQ ATNSDKKIYL LELEAGDPLQ
 2451 EYVTOAAQA TAAHQOKLK SGHGVKPIQA KLGQOQOQOR HQHQHQHQH
 2501 QOQOQOQOQO QOQOQOQOQO QOQOQOQOQO QOQOQOQOQO QOQOQOQOQO
 2551 OLLPOTOAQ NIISFVTDG SQNOPLOYIS IPTTDFKPO QTTSTPFTLT
 2601 APGGATFLQ TDASGNLMLT TAPANSGLQW LTGOLQTOPO VIGTLIOPOT
 2651 LOITGADGI QTATNOQPLI LGGATGGGT GLEFATAPOV ILATQPMYIG
 2701 LETIVONTVA SSQOFVSTAM PGVLSONSSF SATTTVOFQA SKIEPIVDLP
 2751 AGYVLNNAV DASGNTSWLO QSOTQATDDA TAOULLNAGF QOTPTPTST
 2801 QOTMSTDIAP PLYVTAKVP VAQMKRNTNA NKSPISVLSK VOPQOQOSV
 2851 VNKVLEPTNYI QOQOQOQOQO QOQOQOQOQO QOLAGNANLK LISOFOROQO
 2901 ANELKNKQAA GOQTGSTGA PPSIASKPLQ KTNLIRPIH KYEVPKIMK
 2951 QAPKLATSA SMQHQQOQS PALINQYAKV ALLQORLAPA PPOQOQEP
 3001 EQOHLHQOQO QOQOQOQOQO QHQOQOQOQS MPOLLRAQOP IISIVNTAEP
 3051 QAATQFVIRP ALQAQAPIO LQEQOSQOQO QQPAEOLING KAARLORYAS
 3101 NSLPTNVVP LQOQRCASAN NSSNSNTYQO NSTITINSRP TNRVLPQOOR
 3151 QEPTPLSNDV VVQSPTPPKP IEEPVPAQAS TOKPIYKVA QLEOKSPGE
 3201 TELKTNTITD NLEQINSITT MLOQPOQGP IYGEQJFEKQ SEAOQVLEKP
 3251 KHMDLMLLEA TSCQOQOQOQ QHMEMVYDNG FOLTSNESC LKHGFNVEA
 3301 VPMDETDHYA SMKNSGGGA AEGIGQYDDA EDEDEDDDD SLKMATSAON
 3351 DHEMSDEEP AVKEKISKIL DNLINDCSD SIATATVVA SAGYOQWED
 3401 VLAITTAAGV STDDFTTAT AEAVEAASY INEMAEHEL QLOLOAGYE
 3451 LDLKKPKLDV POQOPDTVP NVVPTAAAPQ QPPPMRPPK ISGPHLYEI
 3501 QSEDFITYKS SSIAIEMKV FEAVQVARA HGLTLPLEGP LADMGSYQMI
 3551 GLKTNALKYL IEQDPGEVC VKYTPKXHKR NGNVSTAAG GHARTAGSNP
 3601 AALAGAESL IDYGSDOEEL QENAVECARC EPVYSRSEYD MFSWLASRRH

3651 KQIQLVFPV SDNELVPRRG TGSNLPMAK YRTLKETYAD YVGVERSHIH
3701 GRGLYCTDI EAGMVIETEA GELIRSTLND KRERYDSNG IGCIMFKIDD
3751 NLVVDATMRG NAAEFINHSC EPNCYSKAYD ILGKHIIIF ALRRIYOGEE
3801 LTYDKFPFE DEKIPSCSGS KRCRKYLN

11AA_SEQUENCE 1.0 STANDARD; PRT; 545 AA.
ID VNCSDSDNV
AC -071153;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1).
GN NS1.
OS Diatraea saccharalis densovirus (DsdNV).
OC Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
OX NCBI_TaxID=72003;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobblik Y., Kouassi K.N., Cavallaro C., Bergoin M.;
RT "Complete nucleotide sequence and genome organization of an infectious clone of Diatraea saccharalis densovirus (DsdNV).";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL; AF036333; AAC1999.1; "
DR InterPro: IPR001257; Parvo_NSI.
DR Pfam: PF01057; Parvo_NSI; 1.
KW Nonstructural protein.
SQ SEQUENCE 545 AA; 63475 MW; 810A0E440432E2B1 CRC64;

VNCSDSDNV Length: 545 April 1, 2002 16:32 Type: P Check: 3506 ..

1 MNNGDSNET DSTSRDQSN LRESPTSPS SEQCSMVATT SRKREMAWG
51 RGTMASIAKE SQENFOYMAE ELEKMGNOFP GYVTGOSVAP SSAYISDVII
101 LRDIDLROQC LDVLEYGERS RRNGLFGFSE EGDHIVHND CSYTRNSCRD
151 IWLGVKPPFG TVOKTGKPVK YIMEFKRTDW YDVFIFYFVR KRGERAIYVR
201 GESGKIPSD ECVWAREEFK EREMVSDDC TDIYECEOE HKISRSDAG
251 STNGRLYEKK TYSAKFAYI ROKTKALLRK YVSPISAIC DYPEPRDDL
301 LCDPRNRDYI QAACDFGKD LNAMSUREIY NLTEDEYNT DDKELNPAQ
351 FISSKKYDNL EGSILVNEL LKQCNDDED LIVEFLTNLV NVLDRIRKL
401 NAFLLISPPS GKNFFEDMI FGLLSYGOL GOANRHNLFA FOEAPNKRVL
451 LMNEPNEYSS LDTIKMFG GDEYTVRVKN RMDAHKRRP VILTNNTVP
501 FWEYAFSDR ITYKWNAP FLKDYELKPH PMTFILLSK YNITF

11AA_SEQUENCE 1.0 STANDARD; PRT; 545 AA.
ID VNCSDSDNV
AC 090054;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1).

GN NS1.
OS Junonia coenia densovirus (JcdNV).
OC Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
OX NCBI_TaxID=12524;
RN [1]
RP SEQUENCE FROM N.A.
RA Medina J., Jourdan M., Pascud A.M., Bergoin M.;
RT "Complete nucleotide sequence of the cloned infectious genome of Junonia coenia densovirus reveals an organization unique among parvoviruses.";
RL Virology 191:202-222(1992).
CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL; S47266; AAB23699.1; "
DR InterPro: IPR001257; Parvo_NSI.
DR Pfam: PF01057; Parvo_NSI; 1.
KW Nonstructural protein.
SQ SEQUENCE 545 AA; 63461 MW; 97CD825268ABC6AE CRC64;

VNCSDSDNV Length: 545 April 1, 2002 16:32 Type: P Check: 1211 ..

1 MNNGDTRRET DSTRPNDI IRESSGRTSP SEQCSMVANT SRKREWSHG
51 RGTMASIAKE SQENFOYMAE ELEKMGSEFF GYVTGOSVAP SSAYISDVII
101 LRDIDLROQC LDVLEYGERS RRNGLFGFSE EGDHIVHND CSYTRNSCRD
151 IWLGVKPPFG TVOKTGKPVK YIMEFKRTDW YDVFIFYFVR KRGERAIYVR
201 GESGKIPSD ECVWRTREK EREMVSDDC TDIYECEOE HKISRSDAG
251 SSNGRLYEKK AYSAGKFAYI RKTTKALLRK YVSPISAIC DYPEPRDDL
301 LCDPRNRDYI QAACDFGKD LNAMSUREIY NLTEDEYNT DEQELNPAAL
351 FISSKKYDNL ENSLIIITL LKQCNDDED LIVEFLTNLV NVLDRIRKL
401 NAFLLISPPS AGKNFFEDMI FGLLSYGOL GOANRHNLFA FOEAPNKRVL
451 LMNEPNEYSS LDTIKMFG GDEYTVRVKN RMDAHKRRP VILTNNTVP
501 FWEYAFSDR ITYKWNAP FLKDYELKPH PMTFILLSK YNITF

11AA_SEQUENCE 1.0 STANDARD; PRT; 2124 AA.
ID Y192_HUMAN
AC 093074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).
GN KIAA0192.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96281124; PubMed=8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 3:17-24(1996).

CC -1- TISSUE SPECIFICITY: UBICUITOUS.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D83783; BAI2112.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 FT DOMAIN 599 602 POLY-SER.
 FT DOMAIN 1201 1207 POLY-GLY.
 FT DOMAIN 1998 2124 GLN-RICH.
 FT DOMAIN 1998 2023 POLY-GLN.
 FT DOMAIN 2028 2033 POLY-GLN.
 FT DOMAIN 2037 2070 POLY-GLN.
 FT DOMAIN 2090 2097 POLY-GLN.
 SQ SEQUENCE 2124 AA; 237207 MW; 255FB9419EC39F42 CRC64;

Y192_HUMAN Length: 2124 April 1, 2002 16:32 Type: P Check: 6689

1 DHGSAKNVS FNPAKISNF SSIAEKLRG NTLPTGRRK POYNOKDNFM
 51 LVTARQSAL NTWETDLACT KPLTQLAKV PIFSKEEVF GYLAKTVAV
 101 MFAAMLIKMT CAYIAAIST KVKRRHDPF MENTQITTKY LMEQLAKAE
 151 YRRPGASG GCGSTIGPLP HDVEVAIRQW DYTEKLAMFM FODGMIDRHE
 201 FLTWVLECFE KIRPGEDELL KLLPLLLRY SGEFVSAYL SRLAVFCIR
 251 RLALQDQVS SHSHVISAQ STSLPTTPA PDPPTSTPS TPESDLKMP
 301 QHRPLVEGLS CILQITLLCC PSALWHSYL TDSRIKTGSP LDHLPAPSN
 351 LPRPEGNSAF TQOVRKLRRE IEQIKERQO AVEYRMSFDK COEATGFTI
 401 GRVLTLEVL DSHSPERSDF SNSLSDLCNR IFGLGPKDG HEISSDDAV
 451 VSLCEMAVS CRRGRHRAM VVAKLLEKRO AEIEAERCGE SEAADEKGI
 501 ASSSLAPSA PLEQVYLQF LDTQAPMLTD PRSESEVEF FNVLFCFL
 551 IRIDVSHNM YTCTLSRCD LAFGAPGRP PSPDPDAD PPKKEGESS
 601 SSKLEDPGLS ESMIDPSSS VLFEDMEKPD FSLFSPTPMC EGKSPSPER
 651 PDVEKEVKPP PREKIEGTG VLYDQPRHVQ YATHFPIPOE ESOSEHCNR
 701 LVTLFGVGKQ RDDARHAIRK ITKDLIKLYN RKGTAEITDOL APIVLPINPD
 751 LTVLGEDGQ KRRRNPEAF PTADIDFAK QHLSHYDQO VTAOVSRLVL
 801 EQTSPALGM SYHLPVQHV QEIFDLMEYS LSTISGLDFA IQLNELSVY
 851 EAILLLKSSD LVGYTTSLC LCYIAVLRHY HACLIINQOQ MAOVEGLCG
 901 VVHGNRRSD GSAERCILA YLYDLYTSCS HLNRKEGELF SDPSCVKNKT
 951 IYCNVPSSES NMRWAPPEMI DTLENPAHT FTYTGIGKSL SENPARYSF
 1001 VCAALMHVCY GHDDPRVND IAILCAELTG YCKSLSEWL GYLKALCSS
 1051 NNCTGFNDL ICNVVSDLS FHDLSATFVA ILIARQCLL EDLIRCAIP
 1101 SLTNACSEQ DSEPARLTC RILHLFRT QLNPCQSDN KPTVGIRSSC
 1151 DRLLLAASON RIVDGAIVAV LKAVFVLGDA ELKSGGTTV GGTIELPEEE
 1201 GGGSGSGRRQ GGRNISVETA SLDVAKYVL RSICQDEWVG ERLKSLCED

1251 SNDLQPVLS SAQAORLMQL ICYPHRLDN EDGENPQOR IKRILQNLDO
 1301 WMRQSSLEL QUMIKOTENN EMNLLLENIA KATIEVPQNS AETGSSGST
 1351 ASNMPPSSKT KPVLSLERS GWWLVAPLIA KLPTSVQGVH LKAAGELEK
 1401 GQHLGSSSRK ERDRQKQSM SLISQPFLS LVLTCLKGD EQREGLLNSL
 1451 YSVQHVIVNN WRDDOYLDDC KPKOLMHEAL KLRNLVGM EPTVQRSTQ
 1501 TTEWAMALLE IISGVDMQ SNNELFTTVL DMLSVLNGT LAADSSISQ
 1551 GSMEENKRAY NMLAKLOKE LGEROSDLE KVRQLPLPK QTRDVITCEP
 1601 QGSLDITKGN KIAGFDSIFK KEGLOVSTQK KISPMPLFEB LKPSAPLSMG
 1651 WFGTVAVDRR VARGEEOQL LLYHTHLRPR PRAVYLEPLP LPPEDEEPPA
 1701 PTLLEPEKKA PEPPYDPRG AAPSTEERK KSTKGKRS QPATKTEDYG
 1751 MGRGRSGPYG VTPPDLHLN PNRGSIHLN YRGSGIGLT QNQLPAGP
 1801 RVDYRPRVRL PMOKLPTAPT YPGVLPPTMT GVGLEPSSY KTSVYRQOP
 1851 AVPOGQRLHQ QLOQSQMLG QSSVHQMTPS SSYGLQTSQ YTPVYSHGL
 1901 QQHTGPRAGTM VPPSYSSQPY QSTHPSTNPT LVDPTHLQD RSGGVHQA
 1951 PYYHGLTST QFESHQTLQD TPMISTMTPM SAQVQAGVA STALLPEQOQ
 2001 QQQQQQQQQQQ QQQQQQQQQQQ QQQYHQQQ QQQILRQQQ QQQQQQQQQQ
 2051 QQQQQQQQQQQ QQQQQQQQQQQ AAPQOPQOS QPQOPQGLD Q7QQQQQ7RA
 2101 LVRLQLOQLS NTQOPQSTNI FGAY
 !!AA SEQUENCE 1.0
 ID Q9X8U0 } PRELIMINARY; PRT: 373 AA.
 AC Q9X8U0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HYPOTHEICAL 42.9 KDA PROTEIN.
 GN SCH24.26C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=843436;
 RA Redenbach M., Kleser H.M., Denaparte D., Elchner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL049826; CAB42732.1; -
 DR InterPro: IPR003447; FemAB.
 DR Pfam: PF02388; FemAB; 1.

KW Hypothetical protein.
SQ SEQUENCE 373 AA; 42910 MW; 7EFD1F982299DC6A CRC64;
O9X800 Length: 373 April 1, 2002 16:32 Type: P Check: 1196 ..

1 MSLLRTISR EQLHAYIOSL PAASHQVPA MADVKAEMWS ENLGFEDRT
51 GELVAGLVL YRQLPKIKRY LAYLPGSPVI NMFAPNLQDM MEPMALHKQ
101 OGAFSVKMGK PVITRRMDAT SIKKGIQDDP VKRLDIEAD HIEPRAFEVA
151 DKLRMGMOQ GEDGAGFGD VQPRVYQVY LANRSLEEVH KNFQOLWERN
201 IKKAERKAGVE VQGGYHDL EMOQLVEYTA VRDHFRPRPL SYFGOMMAL
251 NNEDNRRRL YFARHNGVNL SAATMLVYG HWYYSYGASD NIGREVRPSN
301 AMQWMLRDS YALGATVYDL RGISDSLDES DHLFGLIOEK VTGGQAAEY
351 LGEMDFPLNK LHKALDIYM SRR

11AA SEQUENCE 1.0
ID P96849.9 PRELIMINARY; PRT; 187 AA.
AC P96849;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHEITICAL 20.5 KDA PROTEIN.
GN RV3567C OR MTCY06G11.14C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL: Z92774; CAB07141.1; -;
DR Tuberculist; RV3567C; -;
DR InterPro: IPR002563; Flavin_Reduct.
DR Pfam: PF01613; Flavin_Reduct; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 187 AA; 20539 MW; 4FF7CCE26F797BD1 CRC64;
P96849 Length: 187 April 1, 2002 16:32 Type: P Check: 8381 ..

1 MSAQIDPRTF RSVLQFCTG ITVITYTHD VPGVFCQSF AALSLEPLY
51 LECPTKVSRS WQAIASGRF CWNVLEKOK DVSARPSKE PDKFAGIDMR
101 PSELSPITE GSLAYIDCTV ASVHDGDHF VVGAVESLS EYPAVKPRPL
151 LFYRGDYICI EPEKTPAHM RDLEAFLLIT TTQDTWL

11AA SEQUENCE 1.0
ID Q928R8.9 PRELIMINARY; PRT; 286 AA.
AC Q928R8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SUAS SUPERFAMILY-RELATED PROTEIN.
GN TWLC OR CPN0270 OR CP0489.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S., Trachomatis.",
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.",
RL Nat. Genet. 21:385-389(1999).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
[3]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.R., Peterson J., Umayam L.A., Utterback T.,
RA Berry K., Bass S., Linher K., Weidman J., Khouli H., Craven B.,
RA Bowman C., Dodson R., Gwin M., Nelson M., Deboy R., Kolonay J.,
RA McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL: AE001612; AAD18419.1; -;
DR EMBL: AP002546; BA98480.1; -;
DR EMBL: AE002210; AAF38319.1; -;
DR TIGR: CP0489; -;
DR InterPro: IPR000666; Sna5_yjc10.yrDC.
DR Pfam: PF01300; Sna5_yjc10.yrDC; 1.
KW Complete proteome.
SQ SEQUENCE 286 AA; 32082 MW; E8C1DBCD4A0223 CRC64;
Q928R8 Length: 286 April 1, 2002 16:32 Type: P Check: 9351 ..

1 MDKKAQITF SLPEWSAII QGKIVLPTD TYGFGFLSYL ASEAERLYA
51 LKDRPSKAF ALVNSIEDI ENISGYPLSP TACKKAQLFP GATLVYKHR
101 NRPFKETIA FRIYDHSYVR EIVDHGCTLI GTSANLSEPP SALTAQOEIFA
151 DFADHDICF DGPCSHGLES TVVADPLVI YREGLSRSV IENIAGTEAK
201 IHRHSHAFS KHIIYTVKN QEOIVSFLSG SLDFKGVCE HPKPKNYTR
251 LREALKKTP SIVFIYDINT SDYPELEPFL SPYIIE

11AA SEQUENCE 1.0
ID Q91541.3 PRELIMINARY; PRT; 214 AA.
AC Q91541;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NITRILE HYDRATASE ALPHA SUBUNIT.
OS Bacillus sp. BR449.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=123759;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=BR499;
RA Kim S.-H., Ortel P.;
RT "Cloning and Expression of the Nitrile Hydratase and Amidase Genes
RT from Bacillus sp. BR449 into Escherichia coli.";
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF257489; AAF69002.1; -
 DR InterPro: IPR002114; PTS_HPr_ser.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN.1.
 SO SEQUENCE 214 AA; 24572 MW; C31F78365CE54726 CRC64;

09J541 Length: 214 April 1, 2002 16:32 Type: P Check: 2826 ..

1 MTIDQKNTNI DPREPHNHR POSFEARAK ALESLLIEKG HISSDAIERV
 51 IKHHEHLGR MNGAKYVAKA WTDPAFKORL LEDEPYLRE LGYGGQGEH
 101 IRVVENTDV HNVYCTICS CYWPLDGLP PSWYKEPAYR ARVYKEPROV
 151 LKEFGDLDP SVEIRWDS SREIRFVLPQ RPECTEGMTE EELAKLVTRD
 201 SMIGVAKIEP LKLR

11AA_SEQUENCE 1.0

ID 09K760 J PRELIMINARY; PRT; 957 AA.

AC 09K760;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE BH3513 PROTEIN.

GN BH3513.

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=86665;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;

RX MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kubota S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus

RT halodurans and genomic sequence comparison with Bacillus subtilis."

RL Nucleic Acids Res. 28.4317-4331(2000).

DR EMBL: AP001519; BAB07232.1; -

DR InterPro: IPR000209; Peptidase_S8.

DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN.1.

DR Complete proteome.

KW SEQUENCE 957 AA; 108853 MW; DC6AANA50F6342B8 CRC64;

09K760 Length: 957 April 1, 2002 16:32 Type: P Check: 4652 ..

1 MKFTSWTLANE PSNAQFAEYA TEVSGEWR I LNPDAKRWG GNOKNFWLAF
 51 MNHDKIYGV GLHDFGVNAD GTIYSYKAGE GYPVLNDEDT AIRMMNRDSL
 101 RFLVDHPNI KMSLQWCFD PSRVEPILDN VNGAQDFVR QLKIAELYL
 151 NREGRKIGI EMDFEKTSR PRSAQPEPKY RDLIRAKDE YCPRLGLEIR
 201 VNJHMTGEY NPSWAMTNY STIADADIE YQIMSYDFA GNTAPSPSP
 251 VMNLLEVLIDH VRNVLPPEKT FIGNAAYGR WSLNRDRIGT ALAYWQLLQW
 301 QNLFKINAG QNRDQGEFTW FDQSTIPYCG FHDESGEY TFLHCYDRQ
 351 ARPARLLPYN NSQVYRGTY RNAEYITSY KHORAKFTGI ORVLTREATST
 401 SGHISDAHV WEPKDLPQY TFGYNTLPG QYLDATNS CVRASAIAIQ
 451 DGIYTSFSL STPGYRLIA TYFPYLCR IPIVNGVDY VIGEDIPDW
 501 PFLVPSNHF FDCGFSEST SNTITVGTYQ DSAQIMFVI CRDFEHGMSG
 551 GEVEYVNNLQ VPKKRGSLD GVTFKVDADM PDEVTLFAEL IRNHRPAIF
 601 WEDLFGEFAD QEYENLTETN YTORAITGR APNGPYVDG ACRPLQNIIG

651 YSNGWRPVA ASGDEAHV CDARNSAOL VLNRESFNA HTEADRALD
 701 SNAIYGRF ARNPCTVNG YIAQLNRYNR TYRLVYESG SSQVATIAM
 751 SETLANGLS RHTLTIRVHN GRIKILGAV EYINYSGLP GLSRQAMCV
 801 YANGTRIRCY RLHIATNDY EPMKVSAY DGREYALAE DRPYSDLG
 851 YLVSGFNPD EGLDDIDND YDNFPYVNP SWGKNIRI RLVDAGVWL
 901 NRYVGGGEY STAMNSLEG FITLGFIGN YGCKGVGMT IQEDPRVFT
 951 YLPPND

11AA_SEQUENCE 1.0

ID 059760 J PRELIMINARY; PRT; 236 AA.

AC 059760;

DT 01-AUG-1998 (Tremblrel. 07, Created)

DT 01-AUG-1998 (Tremblrel. 07, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE HYPOTHETICAL 26.5 KDA PROTEIN.

GN SPC1020.07.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972H-;

RA Oliver K., Harris D., Wood V., Lyne M., Rajandream M.A., Barrell B.G.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL023518; CAI18995.1; -

DR InterPro: IPR000531; TonB_box.

DR Pfam: PF00702; Hydrolase_1.

DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN.1.

KW Hypothetical protein.

SO SEQUENCE 236 AA; 26496 MW; 51EAC546F81A037B CRC64;

059760 Length: 236 April 1, 2002 16:32 Type: P Check: 5542 ..

1 MPEACLFDM DGLVDTESI YTKSTNIIK RYKNGPMSV VAKKMGRTS
 51 KEASRIFLDM SGIDLCEHY IALQRETOAE LMRHTRPLG VMNLSKLS
 101 LNIPIALAT SPTNFEKKS AHSILFDHF DGNIIIGDDP RLPVGRGKH
 151 PDIMFIALKM INDKRKAQOQ AEILPENCLV FEDSTIGVQS GRAAGKVVW
 201 VPDVNILPFF SLSPQADK HITKVLSEN FDTVTV
 11AA_SEQUENCE 1.0
 ID 09P388 J PRELIMINARY; PRT; 422 AA.
 AC 09P388;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN B7N4.60.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL390218; CAB99237.1; .
 DR InterPro: IPR002965; P-rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENS.
 SQ SEQUENCE 422 AA; 47111 MW; DEB1307CE33E1AD CRC64;

G9P3B8 Length: 422 April 1, 2002 16:32 Type: P Check: 9296 ..

1 MDNLNRCAR GGEGLPGHL DRLFPFMD TAMEARVRA IMAAFGTG
 51 RYTGSDSLE RLREARORQ RQANODRVRE RRAEVOGR LRGGSDDDA
 101 DAERGSMER RSSRVEIQS TSGASPGIQ RVTTVRSOS RSRSRRRR
 151 RSDNPFQSS SSODRKPDL HVFTSGTKH PKRRSSAVL SCKRPVATK
 201 CHTKPEDYSC LPPHPIPTS CHSRPRKTP VVAKCPKRP KPATYPCLP
 251 PCHPISFSPS PYPAPAOQCH PPAASSQVCH SSKPKPKATY RPRPRPQC
 301 GPVKSHPRI YREVPYHEI PVREIREVEV EYVAVPEVY EYVAVPEV
 351 PVRVNPARY PVHVPVHPV PÖPVPYHGG GGGGGYGGIG GYGGHGRYG
 401 ARADEGPWYP FKAVTWOSGP PF

11AA-SEQUENCE 1.0

ID 013512 PRELIMINARY: PRT: 551 AA.

AC 013512; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PROTEIN B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PIBROSARCOMA;
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
 RA Malley T., Gibbs R.A.;
 RA "A gene-rich cluster between the CD4 and triosephosphate isomerase
 RT genes at human chromosome 12p13."
 RT Genome Res. 6:314-326(1996).
 RL EMBL: U47926; AAC50464.1; .
 DR InterPro: IPR000886; ER_target.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 551 AA; 62264 MW; F16E4048C0664F58 CRC64;

Q13512 Length: 551 April 1, 2002 16:32 Type: P Check: 4657 ..

1 MHLQMEDMA KYRMSGVAP QSFRLDLETPP HMAAYDTGLE LIGROEAGIA
 51 LPLLEBALOG SLAQMESCRD DCEGPEEQG AEEEDGQAS OGGLYEALNG
 101 HMLQVLOCRQ KCVGEAATRP GRSPVPDFL PNQLRLHEA HMQVNLISA
 151 IENVLSVLE YPEDEAARKA LNOYQALGE PRPGLPREP IORFLIRSIG
 201 EKRLQYAME HLGTSFKDPD PWTPALIPE ALREKLREDQ EKRPMDHEPV
 251 KKPLTYMKD VLLGCVILT QDSROLNGSE RAVLDGLTP AACGVILQIA
 301 KDAAGAGANS GYGRRSRPH PHERFEGITV LKAQILARAG TVSGQAKIL
 351 LEYSEVRATL TOAYFSPERP LHLSTHLVC RSAIEGBOQ RMDLSHPVHA
 401 DNGVLDPDG ECGREPPATY YRDYSGILYL NDDPQSGDL FTEPNALTYT
 451 ARVPRCGRL VAFSSGVENP HGVAWVTRGR RCALAIWHTV ADHREQEMI
 501 EAKELQESQ EEEEEEEEM PSKDPSPERP SRHRQVQDK TGRAPVREE

551 L

11AA-SEQUENCE 1.0
 ID 015410 PRELIMINARY: PRT: 652 AA.

AC 015410; 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE CAGH45.
 GN CAGH45.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=97369492; PubMed=9225980;
 RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
 RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
 RT "CDNs with long CAG trinucleotide repeats from human brain."
 RL Hum. Genet. 100:114-122(1997).
 DR EMBL: U80742; AAB91440.1; .
 SQ SEQUENCE 652 AA; 73626 MW; 7A72D515989C546B CRC64;

Q15410 Length: 652 April 1, 2002 16:32 Type: P Check: 7370 ..

1 MHEALKRLN LVGMEDTVQ RSTQOTTEWA MLLEITISG TVDMQNNEL
 51 FTVLDMLSV LINGTLADM SSISQGSME NKRANVNLAK KLQKEIGERO
 101 SDSLKVRQL LPLPKOTRDV ITCPOGSLI DTKGNKIAG DSIFKKEGQ
 151 VSTQKISPW DFEGLKPSA PLSWGFVY RVDRAVARG EQORLLLYHT
 201 HLRRPRAYV LEPLRPEDD EEPAPTLLE PEKKAPERP TDKPAAPPS
 251 TERKKKSTK GKRSQAPTK TEDIQMGPR SGYGYTVPR DLLHPNPS
 301 ITHLNRQGS IGLYQNOPL PAGSPRVDPY RPYRLPMQKL PRRPYPGVL
 351 PTTMGVMGL EPPSYKTSYV RQQPAPVPOG QRLRQQLQAK IQSGMLGQS
 401 SVHQMPSSS YGLQTSQGYT PYSHVGLQ HTBPAGTWAP PYSQPYQS
 451 THSTNPPLV DPTRLQORP SGVYHQAPY YGHGLSTOR FSHQTLQOTP
 501 MSTWPMQA QGVQGVNST ALPEQDQDQ QDQDQDQDQ QDQDQDQDQ
 551 QYHRRQDQD QILRQDQDQ QDQDQDQDQ QDQDQDQDQ HQQDQDQDQA
 601 PPOPOPOPO OFORQLOOT QDQDQDTALV ROLQDQLSNT QDOPSTNIFG
 651 RV
 11AA-SEQUENCE 1.0
 ID 075557 PRELIMINARY: PRT: 2023 AA.
 AC 075557; 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OPA-CONTAINING PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Philibert R.A., King B.H., Cook E.H., Lee Y.-H., Stubblefield B.,
 RA Damschroder-Williams P., Dea C., Palotie A., Tengstrom C.,
 RA Martin B.M., Gins E.I.;
 RT "The association of a dodecamer insertional variant with mental

RT retardation.";
 RL MOL. PSYCH. 0:0-0(1998).
 DR EMBL: AF071309; AAC83163.1; -
 DR InterPro: IPR001241; DNA_TopoISOM.
 DR PROSITE: PS00177; TOPOISOMERASE_II; UNKNOWN_1.
 SQ SEQUENCE 2023 AA; 225881 MW; 1263335676047484 CRC64;
 075557 Length: 2023 April 1, 2002 16:32 Type: P Check: 6311

1 MRAAMLIKMT CAYVAAISET KYKKRHNDP MENTOITTKY LMEQLQKMAE
 51 YRRPGASG GCGSTIGPLP HDVEVAIRQW DYTEKLMFM FODGMIDRHE
 101 FJTWLECFE KIRGEDELL KLLPLLLRY SGEFVQAYL SRIAYFCTR
 151 RLALQDQVS SHSHVYSNO STSLPTTPA POPPTSTPS TFPDILMKP
 201 QHRPLVFGLS CILQITLLCC PSALVMHYSL TDSRIKIGSP LDHLPAPSN
 251 LPMPEGNSAF TQVRAKIRE IEQOIKERQ AVEVMSFDK COEATAGFTI
 301 GIVLHLEVL DSHSPERSDF SNSLDSLCNR IFGLGPKDG HEISSDDAV
 351 VSLCEMAVS CKRSGRRHAM VVAKLLEKQ AEIEAERCGE SEADEKSGSI
 401 ASGSLAPSA PIFQVLLQF LDTQAPMLTD PRSESEVEF FNLVLLFCFL
 451 IHHVDSHNM YTCILSRGD LAFGAPGRP PSPPDADD PEKKEGSS
 501 SKLEDPGLS ESMIDPSSS VLFEDMEKPD FSLESPMPK EKGSPSPK
 551 PVEKEVKPP PEKIEGTIG VLYDQPRHQ YATHFPIPO ESCSHCNQR
 601 LVVLFQGGKQ RDDARHAIK ITKOLKVLN RKGAEIDQL APYVIRPBD
 651 LTFVGEGDQ KRRNRPEAF PTAEDIFAK QHLSHYDQH VTAQVSRNVL
 701 EQITSEFALM SYHPLVQHV QFIEDLMEYS LSISGLIDFA IQLNELSVY
 751 EAELLKSSD LVGSYTSLC LCIVAVLRHY HACILNQDQ MAQVEFGLCG
 801 VVKHGMNRSD GSSAERCILA YLYDLYTSCS HLKNGGELF SPFCSKVNT
 851 IYCNVERSES NMRWAPEFMI DTLENPAHT FTYTGKLSL SENPARYSF
 901 VCAALMHVCV GHHDPRVND IAILCAELTG YCKSLSEML GYLKALCCS
 951 NNSTCGFNDL LCNVDVSDLS FHDSLATFVA ILIARQCLL EDLIRCAIP
 1001 SLZNAACSEQ DSEPGARLTC RILLHLEKTP QLNPCQSDGN KPTVGRSSC
 1051 DRHLLAASQ RIVDGAFFAV LKAVFVLGA ELKSGFTTV GGEEELPEBE
 1101 GGGSGGGRQ GGRNISVETA SLDVYAKYVL RSICQGEWVG ERLKSLCED
 1151 SNLDOPVLS SAQORLMQL ICYPHRLDN EDGENPORQR IKRIQNLDO
 1201 WTRQSSLEL QLMIKOTPNM EMNSILEMIA KATIEVQOS AETGSSSGT
 1251 ASIMPSSSKT KPYLSLERS GVMVLAPLIA KLPTSVQGVH LKAAGELEK
 1301 GQHLGSSSRK ERDROKQSM SLSQOPFLS LVLTCLKGQD EQREGLLTSL
 1351 YSVQHVQVNN WRDDOYLDC KPKQLMHAL KLRLNLVGM FDTVQASTQ
 1401 TTEMAMILLE IISGTVDQ SNNELETTVL DMLSVLLNGT LAADMSISQ
 1451 GSKENKRAY MNLAKLQKE LGEROSDLE KVRQLPLPK QTRDVITCP
 1501 QGLIDTKGN KIAGFDSIK KEGLOVSTKQ KISPMDFEG LKPSAPLSMG
 1551 WFGTVRDRR VARGEQORL LLYHTHLRPR PRAYYLEPLP LPPEDEEPPA

1601 PTLLEPEKKA PEPPKTDKPG AAPSTEERK KSTKGKRS QPATKEDYG
 1651 MGPRSGRPG VTPPDLHLH PNEGSIHLN YROGSIGLT QNOPLPAGP
 1701 RUDYPRVRL PMOKLPTPT YPGVLPPTMT GVGLEPSSY KTSVYRQOP
 1751 AVPGQRLRQ QLOSGMLGQ SSVHQMTSS SYGLQTSQGY TPVSHVGLQ
 1801 QHTGPAGTAV PPSYSSQRYQ STHPSTNPTL VDPTRHLQOR PSQVHQAP
 1851 TYGHGLTSTQ RESHOTLOOT PMISTMTMS AQGVQAGVS TAILPEQOQ
 1901 QOQOQOQOQOQ QOQOQOQOQOQ QQYHIRQOQ QQLIRQOQOQ QOQOQOQOQOQ
 1951 QOQOQOQOQOQ QHQQOQOQOQ AAPQOPQSQ PQFRQGLQQ TQQOQQTAL
 2001 VROLQOQLSN TOPDPSTNIF GRY

11AA-SEQUENCE 1.0
 ID 09Y6V5 PRELIMINARY: PRT: 128 AA.
 AC 09Y6V5

DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE WUGSC:H_DJ0841B21.1 PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kalicki J., Angell S.;
 RT "The sequence of Homo sapiens PAC clone DJ0841B21.";
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC004140; AAC02754.1; -
 DR InterPro: IPR002040; Tachykinin.
 DR InterPro: IPR003580; Protachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
 DR SMART: SM00203; TK; 1.
 SQ SEQUENCE 128 AA; 14770 MW; 0F8D61774FECICA CRC64;
 09Y6V5 Length: 128 April 1, 2002 16:32 Type: P Check: 8014

1 MKILVALAV FLVSTQLFAE EIGANDDLNY WSDWYSDQI KEELPEPEH
 51 LQRIARRPK PQQFGLMGK RDADSIKQ VALLKALYGH KTDSPVGLMG
 101 KRALNSGMYE IMTENROYLK SISIFSRT

11AA-SEQUENCE 1.0
 ID 015740 PRELIMINARY: PRT: 551 AA.
 AC 015740

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE B PROTEIN.
 GN B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
 RA Malley T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 genes at human chromosome 12p13.";

RL Genome Res. 6:314-326(1996).
 DR EMBL; U47924; AAB51312.1; -;
 DR InterPro; IPR000886; ER_target.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SO SEQUENCE 551 AA; 62294 MW; 1CAA483E15659886 CRC64;

015740 Length: 551 April 1, 2002 16:32 Type: P Check: 4695

1 MHLQREDMA KYRMMSGVPR QSFRLDETPP HMAAYDTGLE LLGRQEGALA
 51 LPRLEALQGS SLAOMESCRA DCEGPEEQG AEEEDGAAS QGGLYEALAG
 101 HMIOVLQCRQ RCVGETATRP GRSPFVDPFL PMQLRLRHEA HAQVGNLSQA
 151 IENVLSVLEF YPEDEAKRA LNQYQALGE PRPGIGPRHD IQRTILSLGS
 201 EKROLTYAME HLGTSFKDDP PWTPLALPE ALREKLREDO EKRPMDHEPV
 251 KRPPLTYWKD VLLLEGVLT ODSROLNGSB RAVLDGLLTP AECGVLLQLA
 301 KDAAGAGARS GYRGRRSPHT PHERFEGLYV LKAQLARAG TVGSQAKLL
 351 LEVSERVTL TQAVFSPEPP LHLSTHLYC NSAIQGEBOQ RMDLSHPVHA
 401 DNCVLDPDTG ECWREPPAYT YRDYSGLLYL NDDFGGDLF FTEPNALTVT
 451 ARVRRCGRLL VAPSSGVENP HGWMATVTRG RCALALMHTW APREHDEMI
 501 EAKELLQESQ EEEEEEEEM PSKDPSPPEP SRHQRVODK TGRAPVREE
 551 L

11AA-SEQUENCE 1.0
 ID -075339 PRELIMINARY; PRT; 1184 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CARTILAGE INTERMEDIATE LAYER PROTEIN.
 GN CLIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ARTICULAR CARTILAGE;
 RA MEDLINE=98389785; PubMed=9722584;
 RX Lorenzo P., Neame P., Sommarin Y., Heinegard D.;
 RT "Cloning and deduced amino acid sequence of a novel cartilage protein
 (CLIP) identifies a proform including a nucleotide
 RT pyrophosphohydrolase.";
 RL J. Biol. Chem. 273:23469-23475(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nakamura I., Okawa A., Ikegawa S., Takaoka K., Nakamura Y.;
 RT "Genomic organization, mapping, and polymorphisms of the gene encoding
 RT human cartilage intermediate layer protein (CLIP).";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lorenzo P., Aman P., Sommarin Y., Heinegard D.;
 RT "Pro-CLIP: Gene structure and chromosomal localization.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- STIMULATORY TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL; AF035408; AAC33838.1; -;
 DR EMBL; AB022430; BAA76692.1; -;
 DR EMBL; AF035455; AAF14689.1; -;
 DR EMBL; AF035448; AAF14689.1; JOINED.
 DR EMBL; AF035449; AAF14689.1; JOINED.
 DR EMBL; AF035451; AAF14689.1; JOINED.
 DR EMBL; AF035453; AAF14689.1; JOINED.

DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR001451; Hexapep_transf.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00090; TSP_1; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 DR PROSITE; PS50092; TSP1; 1.
 SO SEQUENCE 1184 AA; 132538 MW; 4449F05537CC99C3 CRC64;

075339 Length: 1184 April 1, 2002 16:32 Type: P Check: 4681

1 MYTKAWFS FLVLEVTSVL GRQTMLTQSV RRVQPKKNP SIFAKPADTL
 51 ESPGEWTLTF NIDYPGGKD YERLDAIRFY YGDRVCARPL RLEARTTDMT
 101 PAGSTGQVNH GSPREGFWCL NREQRPQNC SMYTVRFCLP PGLRRODTER
 151 IWSFWSFWSK CSAAGQGTQV QTRTRICLAE MVSLSSEASE EGQHCWGQDC
 201 TACDLTCEPMG QVNADCDACM CODFMLHGAV SLPGAPASG AAIYLLTKTP
 251 KLTLQTDSDG RFRIPGLCPD GKSLIKTKV KRAPVLTMP KTSLKAAITK
 301 AEFVRAETPY MYMNPETKAR RAGQSVSLCC KATGRPRPK YFWYHNDTLL
 351 DPLYKHESK LVLRKLOHQ AGEYFCKAOS DAGAVSKVA QLIYASDET
 401 PCNPPESTL IRLRHDFON ATNSFYTDVG RCPVATCAQ QDNGTRCDA
 451 VONCGGISKT EEREIOCSGY TLPTVAKEC SCQRCETRS IVGRFVSAD
 501 NEPMRFQHV YMGNSRVSMT GYKGTFLHV PDTERLVLT FVDRLOKRVN
 551 TTKVLPFNKK GSAVFHEIKM LRKEPTTLE AMETNIPIPG EYVGDDPAE
 601 LEIPSRSFYR QNGEPTIGKV KASYTFLLPR NISTATAQT DLNFINDEGD
 651 TPELRTYGMF SVDRDEYTS EPLNAGKVY HLDSTQKMP EHISTVKLMS
 701 LNPDTGIMEE EGDFEFENOR RNRKREDTFL VGNLEIRERK LENLDVPSR
 751 RCFVVRAYR SERELPSEOI QGVVIVYINL EPRTGFLSNP RAMGRFDSVI
 801 TGPNGACVPA FCDQSPDAY SAYVLASLAG EELQAVESSP KFNPAIGVP
 851 QPYLNKLNR RTDIEDPRVK KTAFOISMAL PRPNSAEESN GPITYAFENLR
 901 ACEEAPPSAA HFRFYQIEGD RYDNTVPFN EDDPMSTED YLAMPKPRME
 951 FRACYITKVI VGPLEVNVRS RNMGTGTRRT VGKLYGIRDV RSTRDDQPN
 1001 VSAACLEFEC SGMLYDQDRV DRLLVYIPIQ GSCRASVNP MIHELIVNHL
 1051 PLAVNNDTSE YTMCLAPDPL GHNYGIYTVT DDDPRTAKEL ALGRCFDSTS
 1101 DSSSRIMKSN VGVALTFNCY EROVGROSAL QYLOSTPAOS PAAGTVQGRV
 1151 PSRRQORASR GGQROSSGVA SLRPRVAQO PLIN
 11AA-SEQUENCE 1.0
 ID -090ND7 PRELIMINARY; PRT; 2023 AA.
 AC 090ND7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OPA-CONTAINING PROTEIN.
 GN HOPA.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Philibert R.A., Winfield S., Damschoeder-Williams P., Martin B.M.,
 RA Glins E.;
 RT "The genomic structure and developmental expression patterns of the
 RT Human CPA Containing Gene (HCPA)";
 RL Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF132033; AAD4162.1; -;
 DR InterPro; IPR001241; DNA_topoisomII;
 DR PROSITE; PS00177; TOPOISOMERASE_II; UNKNOWN_1.
 SQ SEQUENCE 2023 AA; 225874 MW; C5746B9ACA25DBC2 CRC64;

Q9UWD7 Length: 2023 April 1, 2002 16:32 Type: P Check: 7074

1 MFAAMLIKMT CAYYAISET KVKRRHVPF MENTQITTKY LMEOLQKMAE
 51 YRPGPAGSG GCGSTIGPLP HDVEVALROW DYTEKLAMFW FODGMLDRHE
 101 FLTWLECE KIRGEDELL KLLPLLRV SGFVOSATL SRRLVFCR
 151 RLALQDGV SSSHVISAQ STSTLPTTPA POPPTSTPS TPFSDLMCP
 201 QHRPLVGLS CILQITLLCC PSALVMHYSL TDSRIKTSF IDHLPIAPS
 251 LPRPENSAPF TQVRAKURE IEQIKERQO AVEKRSFQK COEATAGFI
 301 GRVLTLEVL DSHFSERDF SNSLDSLCNR IFGLGFSKDG HEISSDDAV
 351 VSLCEMAVS CKRSGRHRAM VVAKLEKRO AEIEARCGE SEADEKESI
 401 ASSSLAPSA PIFQVILLQF LDTPAPMLTD PRESEKVER FVLVLLFCFL
 451 IRHDFSHNM YTCILISRGD LAFGAPGPRP PSFPDPPAD PPKKAEGSS
 501 SSXLEDPGLS ESMIDPSSS VLFEDMEKRP FSLFSEPTMC EKGSGSPSEK
 551 PDVEKEVPR PREKIEGTLG VLYDQPRHVQ YATHFPIPOE EECSEHCNR
 601 LVYLFVGVQ RDDARNAIK ITKDLKVLN RKCTAETDOL ADIVPLNPGD
 651 LPLFGEDQO KRRNRPEAF PTAEDIFAK QHLSHYDHO VTAQSVNVL
 701 EOTSPALM SYHLPLVQHV QFIDLMESY LSLSLIDFA IOLMLBSLV
 751 EAPLLKSSD LVGSTTSLC LCIVAVLRHY HACLLINQO MAOVEGLCG
 801 VVHGNRSD GSSAERCILA YLYDLYTSCS HLKNGEGELF SDFCSKVNT
 851 IYCNVEXES NMRAPPEMI DTLENPAHT FTYTGIGKSL SNPNRNSF
 901 VCHALMHVC GHHPDRVND IAILCABLTV YCKSLSAEWL GYLKALCCSS
 951 NNGTCGFNDL LCNVDVSDLS FHDSLATEVA ILIARQCLL EDLIRCAIP
 1001 SLINACSRQ DSVFGARLTC RILHLFKTP QLNPCOSDGN KPTVGIRSSC
 1051 DRHLLAASN RIVDGAFAV LKAVFLGDA ELKSGFTYV GSTEELPEEE
 1101 GGGSGGRQO GGRNISVETA SLDVYAKYVL RSICQEWG ECKLSLCEB
 1151 SMDLPVLS SAQORLMQL ICYHRLLDN EDENPOROR IRIILQNLQ
 1201 WTVROSSLEL QLMIKOTPNN EMNSLENIA KATIEVFOOS AETGSSGSE
 1251 ASNPSSSKT KPVLSLERS GVLVAPLIA KLPTVOGHV LKAAGEBELEK
 1301 GGHGSSSKR ERDROKSM SLISOPLLS LVLTCLKGD EOREGLISTL
 1351 YSOVHOIVNN WRDQYLDCC KPKOLMHEAL KRLNLVGVG FDTVORSTQO

1401 TEMAMALLE IISGVDMQ SNNELFTTVL DMLSVLNGT LAADSSISO
 1451 GSWENKRAY MNLAKKLOKE LGERQSDLE KYNQOLPLRK QTRDVITEEP
 1501 OCSLIDTKN KIAGFDSIFK KEGLOVSTKO KISPMWLFEG LKPSAPLSWG
 1551 WFTVAVDRR VARGEQOQL LLYHTHLRPR PRAVYLEEPLP LPPEDEBPA
 1601 PLLPEEKA PEPRTDKAP AAPPSTEERK KSTKCKKS QPATTEDEYG
 1651 MGRNSGPYG VTPPDLHH PNCOSTHLN YKQSIGLYT ONQPLPACG
 1701 RVDPRPVRL PMOKLTPRT YPGLPTTMT GWGLEPSSY KTSVYRQOOP
 1751 AVPGQRLQO QLOSGMGO SSVHQMPSS SYGLQTSQY TPVSHVGLQ
 1801 QHTGPAGTAV PPSVSSQPYQ STHESTNPTL VDETRHLQOR PSGYHQOAP
 1851 TYGHGLTSTQ RFSHOTLOOT PMISTMTMS AOVQAGVRS TAILPEQOQO
 1901 QOQOQOQOQO QOQOQOQOQO QYHIRQOQ QOILRQOQOQ QOQOQOQOQO
 1951 QOQOQOQOQO QOQOQOQOQO APOPOPOSO POFQROGLQO TQOQOQTAL
 2001 VROLQQLSN TOPPSTNIF GRY

11AA: SEQUENCE 1.0
 ID Q9UW6 PRELIMINARY: PRT: 2212 AA.

AC Q9UW6: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP230.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99214851; PubMed=10198638;
 RX Ito M., Yuan C.X., Malik S., Gu W., Fondell J.D., Yamamura S.,
 RA Fu Z.Y., Zhang X., Qin J., Roeder R.G.;
 RT "Identity between TRAP and SMCC complexes indicates novel pathways for
 RT the function of nuclear TRAP and SMCC complexes and diverse mammalian activators.";
 RL Mol. Cell 3:361-370(1999).
 DR EMBL; AF117755; AAD2033.1; -;
 DR InterPro; IPR001241; DNA_topoisomII;
 DR PROSITE; PS00177; TOPOISOMERASE_II; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 2212 AA; 247332 MW; E959525836147630 CRC64;

Q9UW6 Length: 2212 April 1, 2002 16:32 Type: P Check: 8071

1 MKOSMPSLHT KILFCYFHL TNSWCLRRYG LGMAAFGLI SYEHRPLKRP
 51 RPLGPPDYV PODPKOKEDE LTALNVKQF NNQPAVSGDE HGSANVSFN
 101 PAKISSNFS IIAEKLRCNT LPTDGRKRPQ VNQKDFMLV TARSSAINT
 151 WFTDLAGTRP LTQAKKAVI ESKKEVFGY LAKYTVPMR AAMLKMTCA
 201 YVAAISETKV KKRHVDPEME WTQITIKYLM EQLKMAEYV RGPAGSGGC
 251 GSTIGPLPD VVALRQMDY TEKAMPMQ DGMLDHNEFL TWVLECFEKI
 301 RGEDELLKL LPLLLRYSG EFVOSAYLSR RLAVFCTRR ALQLDGVSSH
 351 SSHVISAQST SLPTTPAPQ PPTSGSTSP FSDLLMCPQH RPLVGLSCI
 401 LOTILLCCPS ALVWHYSLTD SRKTSGLD HLPPIASNL PEGSATFO
 451 QVRAKLEIRE QOIKERQAV EVRWSFDKQ EATAGFTIGR VHLTEVLDS

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501 HSPERSPSN SLDSLNCRIE GLGPKSKGHE ISSDDDAVVS LCEMAVWSC
551 RSGHRAMVY AKLEKROAE IEAERGGESE AADEKSIAS GSLSPASAPI
601 FQDVLQELD TQAPMLTDR SESERVEFN LVLLFCELIR HDVFSHMYT
651 CTLLSRGDLA FGAPGRPPS PRDDPADPE HKEAEGSSSS KLEDPGLSES
701 MDIDPSSSVL FEDMEKPDFS LFSPTMPCBG KGPSPEKPD VEKEVKKPPK
751 EKIGITGLV YDQPRHVOA THFPITPQES CSHECNOPLV VLGVCQORD
801 DARHAIKIT KDILKVLNR GTAETDQIAP TVPLNPGDLT FLGEDQOKR
851 RRRPEAPPT AEDIFAKFH LSHYDQHYT AOVSRNVLEQ ITSFALMSY
901 HPLVQHVQF IPDLMEYSLS ISGLIDFAIO LLNELSYEA ELLIKSSDLV
951 GSYTSLCLC IVAVLRHYA CLLNODOMA QVFEGICGV KHGMNRSBG
1001 SAERCLAYL YDLYTSCSHL KMKFGLFSD FCSKYKNITY CNVEPSESNM
1051 RMAEPHIDT LEMPAHFTT YTGIGKSLSE NPANRYFVC NALMHVCVGH
1101 HDPDRVNDIA ILCAEILGYC KSLSAEWLGV LKALCCSSNN GTGCFNDILC
1151 NVDVSDLSFH DSLATFVAIL IARQCLLED LIRCAIPSL LNAACSPQDS
1201 EPGARLICRI LHLFETPOL NPCQSDGNKP TVGIRSSCDR HLAAQONRI
1251 VDGAVFVAVL AVEVLGDAEL KSGGFTVTG TEELPEEBEG GSGGRRQGG
1301 RNISVETASL DVAKYVLRs IQQEWVGER CLKSCEDSN DLDQPVLSA
1351 QAQMLQOLIC YPHRLDNEB GENPORQRIK RILONLDMT MROSSLLOL
1401 MIKOTPNNEH NSLENIARA TIEVQBSAE TGSSSGSTAS NMPSSSKTKP
1451 VLSLERSGV WLVAPLIAKL PTVQGHVYAK AAGELEKQ HIGSSSKER
1501 DRQOKSMXL LSQOPLSLV LTLCKAGQDEQ REGLLTSLYS QVHOIVNNWR
1551 DDQYLDCKP KOLMEALKL RLNLVGMPD TVQSTQOQT EMAMLLLEII
1601 ISGTVMQSN NELETTYLDM LSVLNGTLA ADMSSISQGS MEKKRAYMN
1651 LAKLOKELE EROSDLEKY ROLPLPKOT RDVITCEPQ SLIDTKENKI
1701 AGFDSIRKE GLOVSTKQKI SPWDLFEGLK PSAPLSMGF GYVVRDRA
1751 RGEQORLLL YTHLRPRPR AYLEPLPLR PEDEPPAPT LLEPEKKAPE
1801 PPKTDKGA A PRSTEEKKK STKGKRSOP ATKTDYGMG PGKSGPGVT
1851 VPPDLHHPN PGSITHLNR QGSIGLYTON QPLPAGPRV DYVRVRLPM
1901 OKLPTPTYP GVLPTMTG VGLPESSYKT SVYRQQOPAV PQGRLRQOL
1951 QOSGMGLGS SVHOMTPSSS YGLQTSQGYT PYSHVIGLQ HTGPAQWVP
2001 PSYSOPYQS THSTNPTLV DPTRLQORP SGYVHQAPT YGHGLTSTOR
2051 FSHQTLQOTP MISTMTPMSA QGVQAGVST AILPEQOQO QQQQQQQQOQO
2101 QQQQQQQQO QYHTRQOQO QILRQOQOQO QQQQQQQQO QQQQQQQQO
2151 HQQQQQQQA POPOPQOP OFORQGLQOT QQQQOQTAIV ROLQOOLST
2201 QOPSTNIFG RV

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11AA SEQUENCE 1.0
PRELIMINARY: PRT: 72 AA.

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DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE= BLOOD, AND BRAIN;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT "Identification of a Delta isoform of preprotachykinin mRNA in Human
RT Mononuclear Phagocytes and Lymphocytes."
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF050657; AAC15703.1;
DR InterPro: IPR002040; Tachykinin.
DR InterPro: IPR003580; Protachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
DR SMART: SM00203; TK; 2.
FT NON_TER 1
FT NON_TER 72
FT NON_TER 72
SQ SEQUENCE 72 AA: 8274 MW: 200282BA41EAD16 CRC64;

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09Y494 Length: 72 April 1, 2002 16:32 Type: P Check: 3943 ..

1 DSDQIKELP EPPEHLQRI ARRPKQPF GLMKRQAGH GQISHKHKHT
51 DSVGLMGKR ALNSVAYERS AM

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11AA SEQUENCE 1.0
ID_09H6A8 PRELIMINARY: PRT: 566 AA.
AC 09H6A8
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CDNA: FLJ22428 FIS, CLONE HRC09055.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK026081; BAB15354.1;
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 3.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 3.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS50082; WD_REPEATS_2; 2.
DR PROSITE: PS50294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
SQ SEQUENCE 566 AA: 63864 MW: C2C50AB6F6CD5CB2 CRC64;

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09H6A8 Length: 566 April 1, 2002 16:32 Type: P Check: 4809 ..

1 MDEGTPLLP DSVLYQIFLS LQPADVLQAG LYCRQMOAVS RDEFLMKRQF
51 YRYQVARDV PRHPAAMSWY EEFQRLYDVT PCVEVQTLRE HTDQVHLHSF
101 SHSGYQFASC SKDQTVKIMS NDLTISLHS ADMRPYNSY TQSQFNKDD
151 SLLASGVFL GPHNSSGEI AVISLDSFAL LSRVNRKPYD VFGCWLETST
201 LISGLNHRIG DITSCSVLMT NNAFQDVESE NVNVVKKLEK IONLNASTVR

251 TVWVADCSR DSDLLLEAG DPATSPCRIF DLGSDNEEV AGPAPAHKE
 301 GLHFHLDVL EGRNQPLSE RMLETVAEL LAQGHTRPE RSATGASKY
 351 LIFTTGCLTY SPOIGIKOI LPHQMTAGB VLGEGRGSDA FFDALDHVID
 401 IGHITIGML SPDNRVLVYN SRAMPNGAVY ADPMOPPIA EEIDLVEFDL
 451 KTRREVRAL RAHRYTPND ECFEFLDVS RDFVSGAEG RHGTYMRHY
 501 NICARLHE DVNSVVEFP QEOELLTAS DDATKAMS PRYRVLOAP
 551 RPRRTFFSW LASQRR

IIAA_SEQUENCE 1.0
 ID_09HB06 PRELIMINARY; PRT: 159 AA.

AC_09HB06 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE HYPOTHEICAL 18.5 KDA PROTEIN (SIMILAR TO F-BOX AND WD-40 DOMAIN
 DE PROTEIN 5).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.O., Zhang P.P.,
 RA Qiu W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel Human CDNA clones with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CERVIX CARCINOMA;
 RA Strauberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF217998; AAG17240.1;
 DR EMBL: BC000850; AAH00850.1;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40. 2.
 DR SMART: SM00320; WD40. 2.
 DR PROSITE: PS50082; WD_REPEATS.2: 1.
 DR PROSITE: PS50294; WD_REPEATS_REGION. 1.
 DR Hypothetical protein; Repeat; WD repeat.
 KW SEQUENCE 159 AA; 18545 MW; 2DDBF544D00E68 CRC64;

Q9HB06 Length: 159 April 1, 2002 16:32 Type: P Check: 4523

1 MGLSPDNLYL YVNSRPNPG AVYADPMOPR PIAEIDLIV FDLTMRVVR
 51 RALRAHRAVT PNDECFIFL DVSRRFVAG AEDRHGYIWD RHYNICIARL
 101 RHEGVVNSV ESPQELL TASDATIKA WSPRTMRVL QAPRRPRTF
 151 FSWLASQRR

IIAA_SEQUENCE 1.0
 ID_09BY45 PRELIMINARY; PRT: 175 AA.

AC_09BY45 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE HTPAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;

RA Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.;
 RT "A novel gene expressed in human liver non-tumor tissue.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF212238; AAK14924.1;
 SO SEQUENCE 175 AA; 19766 MW; 0133956D40539F83 CRC64;

Q9BY45 Length: 175 April 1, 2002 16:32 Type: P Check: 3438

1 MWLYNPVYE AEYFTRPMF VIAFLSPSL IFLAKFLKA DTRSRQACL
 51 AASLALALNG VFTNTIKLIV GRPRDPFFYR CFPDGLASHD LMTGDKDV
 101 NEGRKSPFGS HSPFAPAGLA FASFLAGKL HCFTRQGRGK SWRECAPLSP
 151 LIFAVALS RTCDYKHHNQ GPFKW

IIAA_SEQUENCE 1.0
 ID_09BT44 PRELIMINARY; PRT: 649 AA.

AC_09BT44 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE TRINUCLEOTIDE REPEAT CONTAINING 11 (THR-ASSOCIATED) PROTEIN, 230 KDA
 DE SUBUNIT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=RETINOBLASTOMA;
 RA Strauberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC004354; AAH04354.1;
 SO SEQUENCE 649 AA; 73313 MW; CD4030E5A095B08A CRC64;

Q9BT44 Length: 649 April 1, 2002 16:32 Type: P Check: 1992

1 MHEALKILN LVGMPDTQV RSTQOTTEMA MLLELIISG TVDMQNNEL
 51 PTTVLDMLSV LINGTLADM SSISQSMEE NKRAYINLAK KLOKELGERQ
 101 SDSLEKVRQL LPLPKQTRDV ITCEPOGSLI DTKGNKIAGF DSIFKEGSLQ
 151 VSTKQKISPM DLFEGKLPSA PLSMGMPGV RYDRVARGE EQQRLILYHT
 201 HLRPRRAYV LEPRLRPED EEPRAPTLE PKKAREPRK TDKGGAAPRS
 251 TEERKKSTK GKRRORATK TEDYGMGRG SGRYGVYPR DLLHNPFGS
 301 ITHNLVROGS IGLYTQNPRL PACGRVDRY RYVRLPMQKL PTRRTYREVL
 351 PTTMTGVML EPSSYKTSVY RQQQPAVPOG QRLROOLOOS QGMIGQSSVH
 401 QMTSSSYGL QTSQGYTPYV SHVGLQDHTG PACTWPRSY SSOPYQSTNP
 451 STNPLVDPRT RHLQDRPSG VHQDAPTYGH GLTSQRFESH QTLQOTPAIS
 501 TWTPMSAGV QAGVSTAIL PEQQQQQQQQ QQQQQQQQQQ QQQQQQQQYH
 551 IROQQQQQIL RQQQQQQQQQ QQQQQQQQQQ QQQQQQQQHQ QQQQQAAPQ
 601 PQPQSPQPFQ RQGIQOTQOQ QQTALVRLQ QQQLSNTQRP PSTNIFGRY

IIAA_SEQUENCE 1.0
 ID_09BS08 PRELIMINARY; PRT: 433 AA.

AC_09BS08 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE UNKNOWN (PROTEIN FOR IMAGE:3951723) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY ADENOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004541; AA04541.1; -
 FT SEQUENCE 1
 SO SEQUENCE 433 AA; 48413 MW; 952DFC6E113C39F CRC64;

09BS08 Length: 433 April 1, 2002 16:32 Type: P Check: 5292 ..

1 ARGNNSTYQF SQFNKDDSL LASGFLGPH NSSSGEIAVI SLDSFALLSR
 51 VNRKRYDVG CWLFTSLIS GNLHRIQDIT SCSVLMNNA FQDSESVN
 101 VVKRLFKTQ LMASTVRVYM VADCSRDPD DILLEAGDPA TSPCRIFDLG
 151 SDNEEVAVGP APAHAKGELR HFLDRVLEGR AQPOLSERAL ETKVAELLAQ
 201 GHTKPEPSA TGAASKYLIF TTGCLITYSPH QIGIQILPH QMTRAGPVLG
 251 EGRGSDAFED ALDHVIDIHG HIIMGISPD NRYLYNSRA WPNAGVAVDP
 301 MOPPIAEI DLVLEDKTM REVRALRAH RAYTPNDEC FFLDVSDF
 351 VASGVEDHGG YIMDRHNYC LARLRHEDV NSVFSPOQ ELLLTASDA
 401 TIKAWRSPT MRVLQAPRP PRTEFSLAS ORR

11AA_SEQUENCE 1.0 PRELIMINARY; PRT; 173 AA.
 ID_044981 PRELIMINARY; PRT; 173 AA.
 AC_044981

DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE C54G6.3 PROTEIN.
 GN C54G6.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Tin-Wollam A., Graves T., Ozersky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF03698; AAB97561.1; -
 SO SEQUENCE 173 AA; 20156 MW; 053E67461C2D59F3 CRC64;

044981 Length: 173 April 1, 2002 16:32 Type: P Check: 8718 ..
 1 MALKVRDEC TKLVGYOFLN SHICLISLI QLLVCCMAVA QHVSNTMHS
 51 KILKDFLEG SLPLEAVDAV IPDIRLFHYL WGRIGVAVY LDGEGRLIM
 101 CVSHCLTFE SLPYFTISHP KCLFLFWPLF QVSWLKRFKG KLFNFERRKA
 151 QMDPRLPLT TAMFESAVYL EKF

11AA_SEQUENCE 1.0 PRELIMINARY; PRT; 206 AA.
 ID_061761 PRELIMINARY; PRT; 206 AA.
 AC_061761

DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE F56C3.9 PROTEIN.
 GN F56C3.9
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Stoneking T.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF067214; AAC17009.1; -
 SO SEQUENCE 206 AA; 24599 MW; 3F530D03A57CD7A9 CRC64;

061761 Length: 206 April 1, 2002 16:32 Type: P Check: 3281 ..

1 MTQOKHMF5 TETALRKFOI NTQSDTIYV LNYLAESEY FHILRTGFS
 51 EMTAEVNNLN DVPFADLVF LSYVCPDGE FDDTIQNHNI TPLVFSRDL
 101 VEPWAKREYH KYNSEAFON EYDTELLVO LCYLHSONY SEIDVFKKI
 151 ALIDNPLVVD RLVQETDSD VQSFETKIL QYRPYTERKR PQMFEDMDHT
 201 PYSAYV

11AA_SEQUENCE 1.0 PRELIMINARY; PRT; 1264 AA.
 ID_P91767 PRELIMINARY; PRT; 1264 AA.
 AC_P91767

DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE NEUROGLIAN.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylsia;
 OC Sphingidae; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxId=7130;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=LARVAL NERVE CORDS;
 RX MEDLINE=97167642; PubMed=9015260;
 RA Chen C. N., Lampe D. J., Robertson H. M., Nardi J. B.;
 RT "Neuroglial is expressed on cells destined to form the prothoracic
 RT glands of Manduca embryos as they segregate from surrounding cells and
 RT rearrange during morphogenesis.";
 RL Dev. Biol. 181:1-13(1997).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: U50719; AAC47451.1; -.
 DR HSSP: P20241; 1CFB.
 DR InterPro: IPR003962; FN1I1.Repeat.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_MHC.
 DR InterPro: IPR001005; MyD_DNA_bind.
 DR InterPro: IPR000130; Zn_MTPeptide.
 DR Pfam: PF00041; fn3; 5.
 DR Pfam: PF00047; Ig; 6.
 DR PRINTS: PRO0014; ENTPEPIL.
 DR SMART: SM00408; ICG2; 4.
 DR SMART: SM00410; IG_Like; 2.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KM Repeat.
 SQ SEQUENCE 1264 AA; 139733 MW; 02CE935D000F429C CRC64;

P91767 Length: 1264 April 1, 2002 16:32 Type: P Check: 6396 ..

1 MCTFLCFIA IAAQAALLT SPKMKVQPT QEELIFQVA AGEVDKFFII
 51 ECGEAGEGER GPKYRWING KPEFTYSDN RIIOQSRCGT LVYSKPRDED
 101 LGYOGEFAYN EMGTAASNSV FVRAELNSF KETDGOQVVK AEEGRFKFLT
 151 CEPPDGHPR KYWMLQGDQ GOLKTINNS MTLDPGGLM FSNVFRNDAS
 201 VDAVYICTAN SIFRNEYKFG NKIYLDVYQT GISPTLNRHA PERQITTTTI
 251 EKALGKRYVE LYCIYGGTFL PQIYWKDGH NIIPSASITQ DNYGKTLVVK
 301 YPAYEDSGTY TCEVSNVGT ALSYSIQLNI EAAPFTVER DVQNLAEGET
 351 AVIRCEAGGT PYRKITWIHN GKPIEQAEPN PRQVYANST VITDLVKRKT
 401 GNYGNATSS IGYVYKDYVI NVQSIPEIK EGPENLTQV GSEAVLKCRV
 451 FGAPKEIVW MRDQVITGG KYNTSEGLD VIRDVSFTDV GYQCYAKNK
 501 FGKSAFSGSL AVKRTVITD KPEDIYVAAG SSATFRNAN ADDSLKTLIV
 551 WLHDGOLIDE ENQPRFRMTN DYSLLISDTT ELDSGOYTCI AKTAIDEARA
 601 QATLVQDQRP NEPALDVEEC GAATATLRMR SMGDNRAVY RYQIHNTSF
 651 TRPSMAAAD HVPALDTSWT VQLSPWANYT FRVIAVKNIG PSPSPSHSY
 701 CTTQDPVPYK NPDNVKGGES DPTNMVIEWS KMPQIEHNGP GFIYLVSWBR
 751 NIGDEWNRK QVRDQOTEX IVTNTPTFOP YKIKYAVNF KQTSNVTPE
 801 VIGWSEDRP LQAPANFTLY QVTTGTALL SMAVAPESV RGHFGYKIQ
 851 TWTGSEDRL KEILYKADST SALVTKRPF KKNNAIILY NGRFNGPPSD

11A SEQUENCE 10 PRELIMINARY; PRT; 912 AA.

AC 017532;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE B0564.7 PROTEIN.
 GN B0564.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Paloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lightning J.;
 RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Spoat J., Wollman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL: Z73422; CAA97769.1; -.
 DR InterPro: IPR000822; Znf_C2H2.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 KM Zinc-finger.
 SQ SEQUENCE 912 AA; 103309 MW; 69A0A0EEFA9D7DD8 CRC64;

Q17532 Length: 912 April 1, 2002 16:32 Type: P Check: 558 ..

1 MMSRGAPTIC RTIPCRQFSV AAGSAGPAE IDOLFHSIAA APTQVLVNR
 51 TVLESTEEF KWLBNPIKS IDQITTAQM AITVKSSTQN KAFSKSIDIA
 101 KVLPRFYEY EGPKEVDAL REVVLQNSKG KYSTDIONLF LEKKISQSDL
 151 QVVPFDLVM IIRYKSSID QNVIESIATS LISRIEKELA NPADLLAIIA
 201 GDCYEKSKNF HNEAFKRAE RLVAVMGMAE KCALLKHMAV NKQRNRLIG
 251 AINNAISSS QVLTVSQIVS VTGSCSALTY YPKIARKIS NDLEKNSVL

301 AQMDVLISIA DSFTIRMGD QKSMNLVYR ALENVQANP ARLSKFSVGL
 351 ARIGESPSCP LAKALKPELV KEKASTPNNM LNIVESLAF QELEVAHDS
 401 VLKSPFVDI MNSWMEIHDR LRRAMTLLMT SSAKAYDMOG KYEGPTVKE
 451 TPARGINED AKTIRNARQL KYSSNHSECD RYFLKSLFLX APQDHCQLP
 501 NVEDGCAFD AYVMDPRNSN LYNTSOWGS KKRPLFEFG WLQTQNTET
 551 SCEINTVGOE QUGLRMESA GEPDVVEFET ELDYCSSTEID QOKFONMVI
 601 TPFPAADVDP KPVCIYADDI FETMTARKI HFSIYIFAK NVELAEPKL
 651 LYTTEKKYNA HLDGSVAODE GLPMWTKDDG QRAPDLSRQK NDYTLDFET
 701 NINNEDEGFS YCWTDCISTK NTTWVPRQLM PPSKRSKMLY LILPEESNI
 751 MYLSKAYGS LQLMKKHKKM GQPPQVGCY INFNCOTSKY MEGGSHVCE
 801 QCLNSMNDKP CSVCLKPYTS EPTQKLKROG PCPDFLCSN SSTMGIVLIP
 851 CGCHWQCNL EDAYERNNKH LEPLIEKIKY CPEPCRIEY RKLKRPFWHQ
 901 QDEHTLEWN SA

11AA-SEQUENCE 1.0
 ID: 09V010 PRELIMINARY; PRT: 823 AA.
 AC 09V010;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CG5481 PROTEIN.
 GN ROBO2 OR CG5481 OR CG5574 OR CG14347 OR CG14348.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flosler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AE003586; AAF51373.1; .
 DR HSSP: P56276; 1TLK.
 DR Flybase: Fgn0024195; robo2.
 DR InterPro: IPR003962; F011-repeat.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003598; I9_c2.
 DR InterPro: IPR003600; I9_1like.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; i9; 5.
 DR PRINTS: PR00014; FNTYPEIII.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00408; Igc2; 4.
 DR SMART: SM00410; IG_1like; 1.
 DR PROSITE: PS00178; AA-trna_LIGASE_L; UNKNOWN_1.
 KW Repeat.
 SQ SEQUENCE 823 AA; 89715 MW; 36FC0B91F36F2F19 CRC64;

09V010 Length: 823 April 1, 2002 16:32 Type: P Check: 4431 ..

1 MOTTVEKKNP FTENQCAEGN PPTIQWFKD GRCLKDTGTS HINMLPAGSL
 51 FFLKTVHSR ESDACTYCE AKNEFVARS RNATLOYAFL RDEFLRPNAN
 101 TRYAGEVAL MECGAPRSG EPQISWRKNG QTLNLVGNKR IRIVDGNLA
 151 IDEARQSDG RQCVKKNV GTRESATAFL KVHVRFLLR GQNGTAVVG
 201 SSVFQCRIG GDPDPVLMR RTASGGMNPR RVHVLDRSL KLDVTLDEM
 251 GEYTCADNA VGGITATGIL TVHAPKFEVI RPKNQLVEIG DEVLEPCQAN
 301 GHRPFLYMS VEGNSLLLP GYRGRMEVT LTREGSVLS IARFARSDG
 351 KVVTCNALNA VGSVSSRTV SVDTQFELP PIIEQPVNO TLVKSIVVL
 401 PCRTLGTPV QVSWYLDGIP IDVQEHERRN LSDAGALTIS DQRRDEGL
 451 YTCVASNRNG KSMGTYLR DTPNPINKF FRAPELSTV GPPGRPOME
 501 KGENSVTLGW TRSNKVGSS LVGVYIEMFG KNETDGVAV GRYVNTTFT
 551 QTCGLPGVNY FELIRAESH GLSLPSMSE PIVTGVTSSE NNSFTLMFSS
 601 LIHYPSLRH PORYNSGLD LSEKASILS GDVVELSNAS VVDSISMLT
 651 WOVCNRLTGG STADPSTAH RHLIRASFL MQINKRYE GRYVYAROLP
 701 NPVNNPAPV TSNTNPLGGS TSTSASASAS ASALISTKPN IAAGRROGE
 751 TNOSGGCAPT PLNTYRMLT ILNGCGASSC TTIGLVQYTL YEFFIYFPK
 801 SVEGKPSNSR IARTLEDEL SNF

11AA-SEQUENCE 1.0
 ID: 09VKA3 PRELIMINARY; PRT: 1677 AA.
 AC 09VKA3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CG17215 PROTEIN.

WVA3	Length: 1677	April 1, 2002 16:32	Type: P	Check: 6286
1	MCHYFRLSD	ALAKGLTLTD	FITGARLIAL	NLTNGAVOSY
51	IQHYDEGLQ	IGKKPAGSYP	WFDDETSSTP	LRSPEAFSP
101	YPIFSCSQR	WLVYSIAIP	PIGRHGRGF	ISIDIDVSL
151	PEGSRQKMO	QLQTHNRIGA	RSLFLGSRM	GAIDESTJND
201	HRTSMVPKR	LNRIKIEPVS	PKLSANQNT	PRRIKIRMT
251	SVYARAPRS	AALSFIIKY	RREHPGKLA	EYVSIWRKMS
301	GTIOETPHV	HFEEDVEVP	ISNDVIDIVE	CDYRQPSAET

351	TLTGSWSMR	GSYQCLORGG	FYSLRHPRDF	NGTIMEIMQ	EQDQINISNY
401	SEVEKCLPCA	PGCDTCTGPE	PCLANYHWP	RISLTTISIG	CACSTFVLAC
451	YLFRRRRYKV	FKVASPIFLM	ITLIGCAIMY	LERODEHTKD	NDCSEEDDEE
501	LQAAIREWVK	IPRIDILPRK	SSESVAERKS	TGNVLAKKND	ERSQOTDCK
551	DTTSKTRCK	LESDDSWAL	LKKRPATKD	NKTAUVNONI	PNTKSSKDF
601	TENKSGNKH	STVTSNEKL	RSEYENSQT	KSDAITSLSN	NQLSSESPER
651	LNLKLRIBEA	SKPTWKRP	PVLKSNQNY	SANKSENAL	DAKQQTATNT
701	EETHGCIIL	KVRQSNLTY	VEKPSRQCK	GSQTSDFPRG	AREPIYENS
751	AVDSRKAAE	IMPENYKSE	EKKIDNSDT	KTVITITGSH	ITAKMDGCH
801	FKERETGVDK	AARRVLIIAC	ILCTIFLIE	VIGGILSHSL	AIATDAHNL
851	TDLASFLST	SALHLAGRPS	SERLYGMHR	AEVIGAMSI	FETWVTGIL
901	YVMAIMRWVN	QDFELDAKIM	LITSALALIE	NVIMAMOLQ	GHSLSRPGVH
951	KMSKDSAGVL	GSKMILLGK	SYMQYAAKG	HENINVRAAI	IHYVGDIQS
1001	EGVEVALIIT	FPEPEAFMD	SCTEPFVSL	VLVYTFKILR	DVLWLMLEAT
1051	PDFMDEEVK	QTELSISGE	HVHNLRIMAL	SINKVALSAH	LAISKDADQ
1101	LILEEATLIL	HKRPKFETT	IQEEYSPQM	ENCGGCLSPS	DKSGKRKSD
1151	PEKGGKRGKR	KRGSDMAIF	PLIDTWCIA	TKWTHMGFC	ITYSLLMKT
1201	WRVSLTYRVK	SAHKIKLNDQ	QDQWVPIIL	LVMLIYLGTW	TISATPTAEV
1251	ILDSQLEKFK	QCSYNMWDHS	LAIGEYFLIA	WGIRVCYNVR	NAESLYNEAR
1301	LISALYAIYA	LVNIAMVYEH	VHLEFPAGPD	YKYMIGFPT	QLSTTTTIAL
1351	VFGPKILRVF	KGQGDKWQK	AKVRSITASF	SLNGVGLVPE	ESPDLYQENE
1401	ELKEQVQKLA	HOIEFMKTVH	MOHNNHLKP	KPGGYFTTS	TSPQAPYSKN
1451	TVSTAQDTGT	KDENSVKDCS	IELDGQGGT	TLVEAIGEFN	PHLADTFKGL
1501	IVQEDERPQS	DEEBALIAQ	FRLLEAPILD	DSLNLYYOLN	DLDDTEHVRL
1551	HQTVAAQMDL	TSSEETMTVT	QVNSPSPRPV	GVELLPPISS	DSSTASSSLY
1601	AIHTRSPNHR	SGVLLMPQNL	ESPLSLGSDA	ITITEQVLEH	NPRHLDLLE
1651	DENNTSCSL	SNLDSKTL	D GRTPIVY		

401 PLADKESK WY

11AA SEQUENCE 1.0

ID 09GPP7 PRELIMINARY: PRT: 1406 AA.

AC 09GPP7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ROUNDABOUT 2.
 GN ROBO2 OR CG5481 OR CG5574 OR CG14347 OR CG14348.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pubmed-11163265;
 RA Rajagopalan S., Nicolas E., Vivancos V., Berger J., Dickson B.J.;
 RL "Crossing the midline: Roles and regulation of Robo Receptors."; A
 RL Neuron 28:767-777(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pubmed-11163179;
 RA Simpson J.H., Bland K.S., Fetter R.D., Goodman C.S.;
 RL "Short-range and long-range guidance by Slit and its Robo receptors: A
 RL Combinatorial Code of Robo Receptors Controls Lateral Position."; A
 RL Cell 103:1019-1032(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Pubmed-11163180;
 RA Rajagopalan S., Vivancos V., Nicolas E., Dickson B.J.;
 RL "Selecting a Longitudinal Pathway: Robo Receptors Specify the Lateral
 RL Position of Axons in the Drosophila CNS."; A
 RL Cell 103:1033-1045(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Pubmed-11163264;
 RA Simpson J.H., Kidd T., Bland K.S., Goodman C.S.;
 RL "Short-range and long-range guidance by Slit and its Robo receptors:
 RL Robo and Robo2 play distinct roles in midline guidance."; A
 RL Neuron 28:753-766(2000).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF312579; AAC1425.1; -
 DR Flybase: FBgn0024195; robo2.
 DR InterPro: IPR003962; FNIII_repeat.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.
 DR PRINTS: PRO0014; FNTPETII.
 DR SMART: SM00060; FN3; 3.
 DR SMART: SM00409; IG; 5.
 DR SMART: SM00408; ICG2; 5.
 DR SMART: SM00410; IG_Like; 3.
 KW Repeat.
 FT VARIANT 805 806 SE -> F*.
 FT VARIANT 1070 1070 G -> S.
 FT VARIANT 1077 1077 T -> A.
 SQ SEQUENCE 1406 AA; 153139 MW; 3EF8302A64EC28DD CRC64;

09GPP7 Length: 1406 April 1, 2002 16:32 Type: P Check: 6657

1 MPYDRRAV PFLLLLAGL NGLFVGALK GENPRIIEH MDTYPKNP
 51 FTFNCAEGN PPTIOWERD GRELKTDTGS HRIMLPAGCL FLKYIHSR
 101 ESFAGTWCE AKNEGVARS RNATLOVAFL RDEFLEPAN TRVAGEVAL

151 MECCAPRGSP EFOISMRKG QTLNLYGNKR IRIVDGNLA IOEARQSDG
 201 RQCVVKNV GRESATAFL KVHVRPELLR GPONOTAAYG SSVVQCRG
 251 GDELDPVLMR RTASGNMPL RRHVLEDRS LKLDVTLDE MCEYCEADN
 301 AVGGIATGCI LTVHAPPKVF IRPNQLVEI GDEVLPEQCA NGHPRLTYW
 351 SVGNSSLLL PCYRCRMEV TLTPEGRSVL SIAFRAREDS GAVYCNALN
 401 AVGSVSRFV VSDTQFELP PLITEGPNV QTLVKSIVV LPCRFLGTPV
 451 PQVSWLDCI PIDVQEHRR NLSAGALTI SDLQREDEDS LYTCAVSNRN
 501 GKSSMSGYLRL LDTPTNPNIK FFRAPDELSTY PGPPGRPQW EKGESVTLT
 551 WTRSNKRVGS SLVGYIEMF GKNETDQWVA VGTRVONTTF TQTLPLGVN
 601 YFELIRAENS HGLSLPSPMS EPITVGTIRYF NSGLDLSSEAR ASLISGDVVE
 651 LSMASVVDST SMKLWQILN GKVEGEVYV ARLQLPPIVW NPAPVTSNTN
 701 PLIGSTSTSA SASASASALI STRPNIAAG KRDETNQSG GGAPTPLNTK
 751 YRMULTLNGG GASCTITGL VQYTLYEFEI VPFRKSVGEK PENSRIARTL
 801 EDVPSAPRG MEALLNLSA VELKWKAPEL KDRHGVILAN HIVYCIDIA
 851 HNESRLITNV TIDAASPTLV LANLVEGMY TVGVAAGNNA GVGYCVPAT
 901 LRLDPITKRL DFINQRPPI NODHVNDVLT QPWFILLGA ILAVMLSPFG
 951 AMWFVARKHM MKKQALNTM RGNHTSVLK MPBLSARNGN GWNLDSSITG
 1001 MWRRPSPGD SLEWKDHIA DYAPVCGAPG SPAGGTSNG GSGAGSGAS
 1051 GGDIDHGHG SERNOQRYVG EYSNIPDTYA EVSSFQKAPS EYGRHGNASP
 1101 APYATSSILS PQOQOQOQOQ RYQGRVPYGY GLDRPHNPH QOQOQOQOQA
 1151 QOTHQOQAL QOHOQLPPSN IYQOMSTTSE IYPTNTGPSR SVYSQOYYYP
 1201 KDKORIHIT ENKLNSCHTY EAAPGAKOSS PISSOPASVR RQOLPPNCIS
 1251 GRESARFXYL NTDQCKNQN LLDLDGSSMC YNLASGCG GSPSTMAMLM
 1301 SHEDEHALYH TADGDLDME RLYVKVDEQO PQOQOQOLLP LVPQHPAEGH
 1351 LOSWRNOSTR SSRKNGQECI KEPSELIYAP GSVAERSILL SNSGSGTSSQ
 1401 PAGHNV
 11AA SEQUENCE 1.0
 ID 028733 PRELIMINARY: PRT: 6875 AA.
 AC 028733;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TITIN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CE12;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-6805 FROM N.A.
 RC STRAIN=CE12;
 RX MEDLINE=92258380; PubMed=1582406;

RA Labelt S., Gautei M., Lakey A., Trinick J.;
RT "Towards a molecular understanding of titin.";
RL EMBL J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 4305-5320 FROM N.A.
RC TISSUE=PSOAS MUSCLE;
RX MEDLINE=90238553; PubMed=2129545;
RA Labelt S., Barlow D.P., Gautei M., Gibson T., Holt J., Hsieh C.L.,
RA Francke U., Leonard K., Mardale J., Whiting A., Trinick J.;
RT "A regular pattern of two types of 100-residue motif in the sequence
of titin.";
RL Nature 345:273-276(1990).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: X64696; CAA45937.1; -;
DR EMBL: X17329; CAA35207.1; -;
DR HSSP: P56276; 1TLK.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00041; fn3; 50.
DR Pfam: PF00047; Ig; 15.
DR PRINTS: PR00014; FNTHPEI1.
DR SMART: SM00060; FN3; 48.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; Ig_Like; 15.
KW Muscle protein; Myosin; Repeat.
FT NON_TER 1
FT 6875
SQ SEQUENCE 6875 AA; 759127 MW; 50CA5B84F366C55 CRC64;

Q28733 Length: 6875 April 1, 2002 16:32 Type: P Check: 9453

1 EYFRVCAEN KVGVGPIET KPIILAINPI DRPEPENLH IADKGETEY
51 LKMRPDVYG GSPNLSTHYE RRLKSTDWE RVHKSIKEH HLYVKCEVN
101 QIYERVRQTK NEGGEEDWK TEEVYKEDL QKPVLDLKLK GYLTVKAGET
151 IRLKAGVRGK PEPEYVWTKD KDATDFTRSP RAKIDTSADS SKFSLTKAKR
201 SDGKGYVYTA TMTAGSFWAY ATVAVLDKPG PVANLKIPDY SSDRCTIRND
251 PPEDDGCEI QNYLIEKCES KRWVSTYSA TVLPGTTVT RLIEGNEYIF
301 RVRAENKIGT GPTESEKPIV AKTKYDRGR PDPEVTKVS KEEMTVVMS
351 PEYDGKSTT GYLEKKEKH SVRWVPYKNS AIPERLKYQ NLIPGHEYOF
401 RVKAENEIGV GEPSLPSRPV VAKDPIPPG PPINKLVVDT TKSSITLSWG
451 KPYVDGAPI IGYVEVVRPK IADASDEGW KRCNAAQVLY RTEFTVSLD
501 ENQYEFRCV AQNOYVIGRP AELKEATKPK EILEPEIDL DASMKLVVY
551 RAGCPTRLFA IVRGRPAKV TWKRVGIDNV VRKQVLDVY TMAFLVIPS
601 TJDDSGKYSL TLVNPAGEKA VEVAVRVLDY PGPVSLKVS DVTKTSCHVS
651 WAPPENDGS QVTHIVRKR DAEKRTMSIV NPEVKTSQ VTNLVPGNEY
701 YRVTAVNEY GGPVADVPK PVLASDGLSE PDPRLLEVY EMTKNSATLA
751 WLPLRDGA KIDYIISYR EEDQPADRWY EYSVVKDSL VITGLKEGK
801 YKFRVAARNA VGVSLPREAE GYFAKQOLI PKIILMPEOI TIKAGKKLRI
851 EAHVYKPOP ICKWKKGEDD VTSSHLAVH KAESSSILIT KDVTKDSGY
901 YSLTSENSG TDTQIKIVY MDRGPPPOP FDISIDADA CSLSHIPL

951 DGSNTNTNY VEKODVSRGD WYALASVTK TSCRICKLIP GGEYFRVRA
1001 ENRFGISEPL QSPKMLAOP EGVSEPKNA RVTKVKDCI EVAMDRPSD
1051 GSPITGYLI ERKGRNSLIM VKANDTAVRS TEYPCAGLVE GLEVSFRYA
1101 LKAGSSPPS KPEVTVART PVDPGKPEV IDVTKTSVSL IMARKKHOG
1151 SKIIGYFVA CKLPEDKVR CNTPHOIPH EEYTVGLEB NAOYFRAIA
1201 KTAVINISQS ELRFEVTIHA ENVPRIOLS VAKMSLTVK AGTVNCLDAT
1251 VFGKMPPTS WKKESTVLKP AEGIKMAMOR NCLTELEFS NKKDGDYTI
1301 TAENSSGSKS ATKIKLVDR PGPPASVKIN KMSDRAMS WEPLLEDGS
1351 EITNYIVDR ETSSRNMAOV SANVPITCS VEKLIGHEV QPRICAENKY
1401 GVDDPVFTEP AIAKNPYDP GRDPPVYSN VTKDHMTVSW KPPADGSGP
1451 ITGYLLEKRE THAVNMTKVN RKVIERIK ATGLQEGTEY ERYVAINKA
1501 GPGKPSDASK AVYADPLYP PGPPAPPKVY DTRSSVSLS WCKPAYDGS
1551 PIIGYLVEVK RADTDNWRRC NLPOKLQKTR FEVTGLMENT EQOFRYAAN
1601 KVGYSPPSDV PDKHCPOIL IPPEGLDAD LRKTLILRAG VYMRLYVPYK
1651 GRPPKITWS KPNVLRERI GLDIKSTDF TFLRCENVK YDAGYILTL
1701 ENSCGKKGYT IVVKVLDTPG PPVAVTYKEI SRSAITWMD PIVDGGSTI
1751 INVVEKRD AERKSWTVTT ECSKTSFRVS NLEBGSYFF RYAEENEGI
1801 GDPGETRDV KASETPGPVY DLKLVYTKS SCNIGMKRPR SDGSGRTGY
1851 VYDFLTEENK WQVVKSLSL QYSTKDLNEG KYTFPRSAE NNGESTPSE
1901 ITVYAKDHY AFDLDKLDL DLYLAKENS NFKLKPIDHOG KAPSVYTKK
1951 GEDPLATDR VSSESAVNT TLVYVDCOKS DAKGYITTLK NYAGTKEGTL
2001 SIYVGCKPGI PTGPIKPEVY TAAITLTKG PPKDDGSEI TWYLEKRS
2051 VNNKWTCAS AVOKTTFRYT RLHEGMEYF RVSAENKYG GGLKSEPIV
2101 AKHPFVPPDA PPPNIIVDR HDSVSLWTD PRKTGGSPIY GYHIEKERN
2151 SLMKRANKT PIRMKDFKYT GLTEGLEVEF RVMAINAGV GRPSLPSEY
2201 VALDPIPPG KPEVINVTRN SVLLIWTEPK YDGGHKLTY IYKRDLPK
2251 TWKKAHHNV PDCAFTVTDL VEGGKYEFRI RAKNTAGALS APSESTGII
2301 CKDEYAPTI VLDPTIKDGL TIKAGDPIYL NAKSIIGKPL PKSSMSKAK
2351 DIRPSDITOI TSTPTSSMLT VKIYSRKDAE EYITATNPF GKKEHVRVT
2401 VLDVPGPPG IEISNVSAEK ATLWTPPLE DGGSPIKSYV LEKRETSRL
2451 WYVVAEDIS CRHVYTKLIQ GNEYLFRSA VNHYGKEPV QSEPVAMVR
2501 FGPPGPPGK EYSNVTKNTA TVSMKRPTD GGSSEITGYV ERREKGLRW
2551 VRATKTPVD LCKCVTGLQE GNTEYFRSA ENRAGIGPPS DASNYIMKD
2601 VAAAPPPSN ARVDTTKKS ASLAMKPHY DGLLEITGY VEHOKVGDST
2651 WVKDTGPAL RITEFVVDL HTKEKYNFRI SAINDAGVE PAVIPDEIV
2701 EREMAPDFEL DAELRRLVY RAGLSIRIV PIRGRAPAV TWTKDINKL

2751 TRANIENYES FTLLIIPBCN RYDTGKFVMT IENPAGKKSQ FVNVRLDLP
2801 GPVLNLRPTD ITRDSVTLHM DLPLIDGSR ITNVIYKRE ATRKSYSTVT
2851 TKCHKCTYKV TGLSECEYF FRVMAENYEG IGESETEKER VAKASERSPR
2901 D3JLNDITK STVSJLAMPKP KHDGSKITG YVIEAQRKGS DOWTHITTVK
2951 GJECVAVNLT EGEYEYFQVM AVNSAGRSAP RESRPVIYKE QJMLPELDLR
3001 GIYQKLVIAK AGDNIKVEIP VLGRRKPIYV WKKGDOVLKO TORVANNENTA
3051 T3TILLINSEC VRSDGPIYPL TAKINIGEVG DVITIOVHDI PGPPGPPIKF
3101 DEVSDFVTF SWEPPENDGG VPISNVIEM RQTDSTTWE LATTVIRTTY
3151 KATRLTTGVE YQFRVKAQNR YGVGCIISA SIYANYPEKV PGPPGPIQYV
3201 AVTKDSMTIS WHEPLSDGGS PILGYHVERK ERNGIIMQTV SKALVGNIF
3251 KSSGLTIDGIA YEFVIAENM AGSKSPSKPS EPVLALDPID PGKPIPLNI
3301 THHTVILKMA KPEYTGGEFKI TSYIYERDL PNGRMILKANF SNLENEFYV
3351 SGLTEDAAYE FRYIAKNMAG AISPSEPSD AITCRDQVEA PRLVDVRFK
3401 DVIYKAGEA FPLEADVSGR PPTFMWTKD GKELEGTGKL ERIADESTY
3451 LINKDSRRD SGAYILTATD PGGFAKHIFN VKVILDRGPP EGPLAVSEYV
3501 SEKCVLSWLP PLDDGAKIE HYIVOKRETS RLANTNVASE VOYTKLKVTK
3551 LKGNEXIYFR VMAVNNKYGVG EPLESEPIYLA VNPYGPDPDP KNEVTTIK
3601 DEMVVCWGHF DSDGSEITN YIVERRDKAG QRWVKCNKKT VDDLREKVSQ
3651 LLEGHEYFR IMAENAGIS APSRTSPYK ACDAVEFRGP PGNPRVLDTIS
3701 RSSISIAMNK PIYDGGSEIT GYMVEIALPE EDEWKIVTPP AGLKATSYTI
3751 TNLVENEYK IRIYAMNSEG LGEPALVPQT PKAEDRLPP EIELDLDRK
3801 LVVIRACCTL RLFVPIKGRP DPEVAKWTREH GESLIDKASIE STISSYLLIV
3851 GNVNREDSGK YILLVENSNG SKSAFVNVRY LDTPGPQDL KYKEVTKTSV
3901 TLTWDPPLLD GSKIKINYIV EKRESTRKAY STVATNCHKT SMKVDLOQEG
3951 SSYFRVYLAE NEYGIGLPAE TAESYKASER PLPPKITLV DVTRNSVLS
4001 WEKREHDGGS RILGYIVEMQ SKGSDKMATC ATYVTEATI TGLIQEEYS
4051 FRVSAQNEKG ISDPROLSVP VIANDLVIPR AFKLEFNTFT VLAGEDLKID
4101 VPJIGREPTP VTWHKDDVPL KQTRRVNAES TENSSILSIK EACREDVGHY
4151 VVKLSNAGE ATEFLNAILL DKPGPTGPV KMDEVTAESI TISMEPKYD
4201 GGSINNIVYV EKRDSTTTW QIVSATVART TIKASRLKTG CEQOFIYAE
4251 NRJGKSTYLN SEPVAQYPF KVPGPPTGTF VTLSSRDSME VQMEPVPNDG
4301 GSHVIGYHLE RKERNISILMV KLNKTIPIQT KFKTTGLEEG IEYEFVSAB
4351 NIVGICKPSK VSECYVARDP CDPGRPERI IVTRNSYTLQ WKKPTIDGGS
4401 KITGYVVEKK ELPDGRWMA SFTNIMDTQF EVTGLVEDHR YEFVIAARNA
4451 AGVSESESES TGAITRAREI DPPRISMDPK YKDTIVVHAG ESERIDADIY
4501 GKPIPTQWMI KGDQELSNIA RLEIKSTQFA TSLSVKDAFR VDSGNVYLA
4551 QNVAGERSVT VNVKVLDRPG PPEGPIVSG VTAEKCTIAM KPPLDDGSD

4601 IINYIVERRE TSRLVTVVD ANVOQLSCKV TKLEEGNEYI FRVMAVNNKY
4651 VGEPLESEPV IAKNPFVVPD APKAPECTTV TKDSMIYWE RASOGGSEI
4701 LGYVLEKRDK EGIRWTRCHK RLIGELRLRV TGLIENHNYE FRVSAENAG
4751 LSEPPSPSAY QKACDPIYKP GPPNNPKYMD ITRSSVFLSW SKPIYDGGE
4801 IQGYIVEKCD VSVGEWTMCT PPTGINKTNI EVEKLEKHE YNPRICAVNK
4851 AGVGDHADV GPYIYEKLE APDIDLDEL RKIINRAGC SLRLPYPIG
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4951 SGTSAFVTV RVLDTPPSPV NLKYTEIKD SVSITMEPPL LDGSKIKNY
5001 IYERKDRSTR STAAVYTNCH KSMKIDOLQ EGSYIYFRVY AENEGIGLIP
5051 ARTADPIKVA EYPOPPKIT VDDVTRNSVS LSWTKPEHDG GSKIIQYIVE
5101 MQAKHSEKWS ECARVKSLEA VITNLQGE YLFRRYAVNE KGRSDRSLA
5151 VPIVANDLVI EPDVKPAESS YSVQYGDOLK IEVPISGRPK PIITWTKDGL
5201 PLKQTRINY ADSLDLTLS IKETHKDDSG HYGITVANNV GOKTASIEII
5251 TLDPKDPKPK PYKPFDEVSAB SITLSMNPPL YTGCGQITNY IYHKRDTTIT
5301 VMDVSATVA RTLLKVTYTK TGTEYQRIE PENRYGOSFA LDSEPIYAOY
5351 PYKEPGRPGT PEVTATSKDS MVVOMHEPIN NGSPILGYH LERKERNISIL
5401 WTKVDSIIH DTQFKALNE EGIEYEFVY AENIVYGKA SKNSECYVAR
5451 DPCDDPGTPE AIIVKRNEIT LQWTKPYVDG GSNITGYIVE KNDLPEGRMM
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5551 EVELPRISMD PKFRDTIVN AGEYFRLEAD VHOKPLPTIE WLRGQEVBE
5601 SARCEIKNMD EKALLIVKDA IRIDGQYIL RASNVAGSKS FRYNKKVILDR
5651 PGPEGPVQV TGVTCCKCTL TWSPLLODGG SDIPHYVEK RETSRLAMTV
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5801 NKRRTVDLRF RVTGLTEDEH YEFVSAENA AGVGEPSPAT VYKACDPYF
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5951 LEAPELDLDS ELRKGIYVRA GGSARIHIP KGRPTPDITW SREEGEFTDK
6001 VOYKEGVNFT QLSINDORN DAKYIYKLE NSSGTKAFAV TYKVLDTQCP
6051 POUYAKVEYK KDSAVLWMEP PIIIDGAKVR NYIYDKREST RAIYANVSK
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6151 VTLIDVSQTS ASLMEKPEH DGGSVGLGY VEMQPKTEK MSVAVESKVC
6201 NAVVTGLSSG HEYQFRVYK NEKGS DPRV LGVPIYAKDL TIQPSKLPF
6251 KRYSVAGED IKIEIPVIGR PRPEIFWYKD GEPLRQTRV NYEETATSTI
6301 LHIKSSKOD FGKYTTTATN SAGTATENLS VIVLEKGRPP VGVVREDEIS
6351 ADFVULSWEP PAYTGCGQIS NIYIEKRDIT TTMHIVISAT VARTTIKVTK

DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE.

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GN F10A8.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Rongling C.M., Benito M.,
RA Carreira A.D., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006200; AAD14518.1; -
DR InterPro: IPR000326; PA_PTPase.
DR Pfam: PF01569; PAP2; 1.
DR SMART; SM00014; acidppc; 1.
SQ SEQUENCE 302 AA; 33739 MW; 9E1C6D7DAFD569D6 CRC64;

09ZU49 Length: 302 April 1, 2002 16:32 Type: P Check: 2420 ..

1 MOEIDLSVHT IKSHGGRVAS KHKHDWILV ILAIEIGLN LISPFYRYVG
51 KDMWTDLKYP FRONTVPWIS VPYAVALLPI IVFVCFYLKR TCVYDLHHSI
101 LGLLFAVLIT GYTDSIKYA TGRPRPNFYW RCFPDGKELY DALGVCVCHG
151 KAEVKEGHR SPSGHTSWS FAGLTLSLY LSGKIKANN EGHVAKLCIV
201 IFPLAACIV GISRVDDYWH HMDDVFAGL IGTLVAFYCY RQFYRPNYHE
251 EGAGPAYER AAGRGVPTV SSQNGDALRA MSLQMSSTSL ENNESTSTRA
301 PR

11AA-SEQUENCE 1.0
ID 09ZSD3 PRELIMINARY; PRT; 182 AA.
AC 09ZSD3;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE GAMETOPHYTIC ANTHERIDIOGEN-INDUCED PROTEIN.
GN ANI1.
OS Ceratopteris richardii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.
OX NCBI_TaxID=49495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HNN;
RA Men C.K., Smith R.H., Banks J.A.;
RT "ANI1: A sex pheromone-induced gene in Ceratopteris gametophytes and
RT its possible role in sex determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113324; AAD13287.1; -
SQ SEQUENCE 182 AA; 22213 MW; 9061F4AD8B4033DB CRC64;

09ZSD3 Length: 182 April 1, 2002 16:32 Type: P Check: 6830 ..

1 MAQRRESYL LCAVATCSLL LMPNASAY EDDEKETPEN YSKSTTYV
51 GKIEKDPEDY YKSTTYVEE EKEPEFYRK KPYVYGDKR PKVYVYKKEK
101 EKYHRRPKT VYVYKRPYA YKPKPVVIT KPVVYIYKRP KPVVYIYKRP
151 AYVYKHEKP YNYHYSYDKK PDFSPPEYK GPY

11AA-SEQUENCE 1.0
ID 09X160 PRELIMINARY; PRT; 290 AA.
AC 09X160;
DT 01-NOV-1999 (TREMBlrel. 12, Created)

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DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE F9L1.2 PROTEIN.
GN F9L1.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
RA Altati H., Araujo R., Hansen N., Buehler E., Chao Q., Conn L.,
RA Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
RA Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
RA Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome I BAC F9L1 sequence.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007591; AAD39637.1; -
DR InterPro: IPR000326; PA_PTPase.
DR Pfam: PF01569; PAP2; 1.
DR SMART; SM00014; acidppc; 1.
SQ SEQUENCE 290 AA; 32702 MW; BF14A9A0C23B4429 CRC64;

09X160 Length: 290 April 1, 2002 16:32 Type: P Check: 4011 ..

1 MEPIHGAHT IRSAGVTAR FHMHDWILV LLIIVEIVLN VIEPFRVVG
51 EDMLTDLRYP LODNTIPFMA VPLIAYVLPF AVICVYFYFR NDVYDLHNAI
101 LGLLFSVLIT GYTDAIKDA VGRPRDPFW RCFPDGIGIF HNVTKNVLCI
151 GAKDVYKEGH KSPSGHTSW SFAGLGFLSL YLSGKIRVD QRGHAKLCI
201 VILPLVVAL VGSVRDDYWH HMDDVFGA IIGLVATPC YLQFPPEYD
251 PDGCPHAYE QMLADSRNDV QDSAGMHLVS VROTELESVR

11AA-SEQUENCE 1.0
ID 09SV85 PRELIMINARY; PRT; 705 AA.
AC 09SV85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 81.4 KDA PROTEIN (FRAGMENT).
GN F24G24.170.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Scheller C.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049488; CAB39790.1; -
DR InterPro: IPR001064; Crystalin.
DR InterPro: IPR001876; ZnF-RanBP.
DR InterPro: IPR001965; PHD.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR003006; IG_MHC.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SMART; SM00249; PHD; 4.
DR SMART; SM00547; ZnF_RBZ; 1.

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KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 705 AA; 81384 MW; 13751CA016F99B19 CRC64;
Q9SV85 Length: 705 April 1, 2002 16:32 Type: P Check: 9930
1 GKKRKNITK IQIPVIVAMS SVGVFHKVEM DENLYFYVKL TQTDYPTSSG
51 EVLWADSTGD DQPLDQPLFL CPDARIKFKH LKIQREDGDI FDYDFKHPHY
101 ISSRHFPSKR SGDQGESL DCEDEGICLK PVVPLFWCN KESDSREQC
151 GCGRDSMLSA SYVACLOCEK KFKKECVESP LEIKHPHLF HSLRLYYHPA
201 PEFCICCKTE VEMIFYHCLT CNLSMHPVCA MKVPEFIDH PKSPHPPLTF
251 PPTQASLVCH FCALIKKLDP TYICTKCVFV HKKGLGFPH VIRLSRHTNR
301 ISFTSSLPCG KLSGVCVHQ VDNDYGAISC KKCDAYFVHS KCALQRHWD
351 GKDLSEVPEE DMIDIDGEPF KRIADGILH PPHSHLHQ TTRAYDENTY
401 CCGCALPIYE GQFYSCIESD FILHEHCANA PMKRPPLHP HPLILVATR
451 GPGNEEGTFQ CDACHRKGTG FFEYHHTDOE NIFMDIHCA SIFPEFYOG
501 HEHPLFLPSE PNKWRGCOMC TFEYVNLNLN CLECDYILCF HCATLPIYVR
551 YKHDSHFLKI CNGKEANDQS YWCEICEGKI EGTERTAFYN TPKKDTSYK
601 CNACTTLHQ RCLLGIDITYM KPGETVKDYLL SSIKYASEGQ SKESITDVOI
651 LINSPTRPPI CTRCLRCRPF PIFFKGHNTI PCSMDCVEDS AMRSYQRLLY
701 SFLMG
11AA_SEQUENCE 1.0
AC Q9SV87 PRELIMINARY; PRT; 85 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AT2G15340 PROTEIN.
GN AT2G15340.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman K.A., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Talon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
DR EMBL: AC006920; AAD22290.1;
SQ SEQUENCE 85 AA; 8733 MW; 7FDCP6BDEDD2C9F8 CRC64;
Q9SVJ7 Length: 85 April 1, 2002 16:32 Type: P Check: 8684
1 MALSSQKKR RGAGVLTAT AGGDMLALA PLPOAQVQL VIQTLAVQTL
51 EYRILVVLAP LGDLGGVGD PTALGARPHP MLXFP
11AA_SEQUENCE 1.0
AC Q9MAG7 PRELIMINARY; PRT; 667 AA.

AC Q9MAG7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE F12M16.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Shin P.,
RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Huizar L., Kremetska I., Lenz C., Li J., Liu S., Luros S.,
RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
RA Federisiel N.A., Theologis A., Ecker J.R.;
RA "Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome
RT I.";
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC008007; AAF69544.1; -
DR InterPro: IPR001965; PHD.
DR InterPro: IPR001876; Znf-RanBP.
DR SMART: SM00249; PHD; 4.
DR SMART: SM00547; Znf_RBZ; 1.
SQ SEQUENCE 667 AA; 76885 MW; E54B20F8325B2844 CRC64;
Q9MAG7 Length: 667 April 1, 2002 16:32 Type: P Check: 2190
1 MNSNSVGEFR EGEIDGNPL ITLLSQTEN PSSREAAVDS DGGTVDDLSTV
51 EPLILCPTLR LKVKNLKPYT SDSDRSPFL VVSSHPTTIO SGHOQPEYML
101 QSYCKLPL PLFWCDKNP NIDFCIRAC TTIBGTSYV VCVTCGDPFH
151 KCVGAPLEF KHPYPSLSL QLYSPSGRV LSCCQKPIY GMYNYCPTSN
201 FTLHFCARF PTPVIDHPK RHPHPLTFP KQSLPCVHC SLIKKIPTY
251 ICIRAFVYH QDCIYFPYVI KISRHHHS YSSLSGKW SCGVCROEVD
301 NDYGAVSCNK CDDYFVHSRC ALRRDIMDI ELEGVEELE IIVEPITIS
351 DGIILHFSHG HNLKLDTSKA YDENKLCQAC TLPYEGGV SGVDECDPIL
401 HEACANAPCK KYHALNPYPL TLKVTNEYH DNKGRFCDA CORESCGFYV
451 VDDFRGVAD TKDYKFKIDI RCASVSEPP YLGHEHPLYL ALNPEEESA
501 ICHIOESKD ESFCKKILNC IECDFVICK CATLPIYKARY QHDKHFLKFY
551 EAKEANDHSE WDCYGERRIA DLRRKGFYSC DDCCTTLHID CLIGEDMYMK
601 PCHTMYNMT GSRKHQOKL HHSNMTLSR PCSCEGGERC ROKIYFEYKE
651 KIIFCAVSCQ KLVIDYS
11AA_SEQUENCE 1.0
AC Q9M82 PRELIMINARY; PRT; 314 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE PHOSPHATIDATE PHOSPHOHYDROLASE.
GN F16B3.23.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Ranning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Niernan W.C., Fraser C.M.:
 RT "Arabidopsis thaliana chromosome III BAC F16b3 genomic sequence."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC021640; AAF32467.1; -
 DR InterPro: IPR000326; PA_PTPase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 314 AA; 35184 MW; 5F1E8546058C497 CRC64;

Q9M82 Length: 314 April 1, 2002 16:32 Type: P Check: 6307

1 MFEAQLGHT LRSQMTVAR THMDWILV LVLIECVLL IHPEFRFVG
 51 KIMMTDLSYR LKSNVYPTNS VPVYAMLLPL VIFIFITFRR RDVYDHLNAV
 101 LGLLYSLVLT AVLTDALKNA VGRPRDFEW RCFPDGKALY DSLGDIYCHG
 151 DKSVIREGKH SFPSSGHTSMS FSGIGFLSLY LSGKIQAFDG KGHVAKLCIV
 201 ILPLFLFALY GISRDYDWH HMODYFAGGL LGLAISTICY LQFFPPYHFR
 251 EGMGPYAFYQ VLEARVQGA ANGAVQPPR QVNNGEEDG GFMGLHLVDN
 301 PTMRREDE TGRC

11AA SEQUENCE 1.0
 ID Q9M82 PRELIMINARY; PRT; 676 AA.

AC Q9M82; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE HYPOHETICAL 78.2 KDA PROTEIN.
 GN ATAG10370.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

RA [1]
 RP SEQUENCE FROM N.A.
 RA Murphy J., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL161517; CAB78160.1; -
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR001876; Znf-RanBP.
 DR SMART: SM00249; PHD; 4.
 DR SMART: SM00547; Znf_RBZ; 1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 676 AA; 78165 MW; 25D71F73FB1585E0 CRC64;

Q9M05 Length: 676 April 1, 2002 16:32 Type: P Check: 7623

1 MDNLFFVYK LTQTDYPTSS GEVLAMDSTG DDQPLDPLF LCPDARIKHF
 51 KLIQREDGD IFDYDEKPHR YISSPHPSK RSGDQGESL LODDEGICK
 101 LPVPLFWCN NKESDSREFQ CGGCRDSMLS ASYIACIQCE KPFHKECVES

151 PLEIKHPTHL FSLRLYYHP APEFCICCKT EYEMIFENCL TGNLSMHPYC
 201 AMKRVFFID HKSHRPHLT FFFQASLYVC HFCALKKLD PVIYCTKCVF
 251 VHKGCIGEP HVRISRPTH RISTSSIPC GLKSCGVCHO QVNDYGAYS
 301 CKKCDAYFVA SKCALQRHWA DGKLEVEPE EDMIDGEP FKRIADGIIL
 351 HPHSHNLHL QTRAYDENT YCRGCAIPY EGOFYSCIES DILHEHCAN
 401 APRMKRPHL PHPLTLVAT RCPGNEGTE QCDACHKGT GFYEHHDDQ
 451 ENIFMDIHC ASIFEPFOYQ GHEHPLFPLS EPKMKGRQM CYEYVNLNL
 501 NCLECYIIC FHCATLPYKV RYKDSHPLK ICKGKEAND SWCEICEBK
 551 IEEGTERAFY NTPKRDTSFY KGNACCTTLH QRLCLGIDTY MKRGETWKDY
 601 LSSIKYASEG QSKESITDQ ILNNSPTPR ICTRCICRCP PPIFFKGHT
 651 IFCSMQVED SAMRSYQRL YSFLMG

11AA SEQUENCE 1.0
 ID Q9LRV1 PRELIMINARY; PRT; 681 AA.

AC Q9LRV1; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CHP-RICH ZINC FINGER PROTEIN-LIKE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RA [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones."
 RL DNA Res. 7:131-135(2000).
 DR EMBL: AB028611; BAB01837.1; -
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR001841; Znf_ring.
 DR SMART: SM00249; PHD; 2.
 DR SMART: SM00184; RING; 2.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
 SQ SEQUENCE 681 AA; 78805 MW; ABCB58E239519FC9 CRC64;

Q9LRV1 Length: 681 April 1, 2002 16:32 Type: P Check: 6135

1 MSSVGFQDV ENDEKSYLYV TLITQKHTPS SAVESSGDDI PLQPLFSCPY
 51 ARIIRSHKPV EKNYDGVNFF NFHPNSYPH FPRTRTSYOQ GSLLDYDHH
 101 NICKFVYVPL FWCNNKTPDS NEFCGCEE SKTSRSYVAC LECGNKPKHQ
 151 CVESPLEIHN PSHPHSLRL YSNPTHWCI CCGRLYSNMF YHCYTCDSLMS
 201 DPICAMEPIR FVVDHPRKSH HPITFFPTQA TLACNICGLV KMLDPTYICI
 251 QCVFVIHKOC MGYPIVIRIS RHQHRISFAS SLFYGNLSCG VCHQAVDNNY
 301 GAYSCGKDA YFVHSCAFH RNWVDGKELE GVSEEDDIID DGEPPERISD

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351 GYLHPHSH HLRLEISKVY DENKYGCS EPIYEGFYS CKECPILHE
401 SCANPRMR HPLHPPLTL NVATKELGN EGYHONVCG RDTGFEYEH
451 HIGERFRID LRCAISREPF EYCHKHPIC IASELEKVA COICGKSS
501 KLNCECDYI ICFRCATPY KYRYKDSHF LRIRDKKAS DEPDCEVC
551 GRIEYKERE SPWDRKREMR FYKNCDCCTT LHVECLLGR MYMKPGNSVK
601 DISKSLGI EGTOWTDYV FLNLSLRPI CTCGMRCLE PLYFGYNTI
651 FCSWECIGYG DTVEHPTSN PFSSIVLEL M

!!A..SEQUENCE 1.0
<ID 09LNZ0> PRELIMINARY: PRT: 734 AA.
AC 09LNZ0:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P9C16.28.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Klecavaca J., Kim C., Altati H., Bel Q., Chin C., Chlou J., Choi E.,
RA Com L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thayeri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
RA Theologis A., Ecker J.R.;
RT Genomic sequence for Arabidopsis thaliana BAC F9C16 from chromosome
RT I."
RN [2]
RP Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RN [4]
RP Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altati H., Bel B., Chin C., Chlou J., Choi E.,
RA Com L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thayeri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RN [6]
RP Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP EMBL: AC022314; AAF79671.1;
DR EMBL: AC022314; AAF79671.1;
DR InterPro: IPR000345; Cyrc heme-bind.
DR InterPro: IPR002219; DAG-pe-bind.
DR InterPro: IPR001965; PHD.
DR SMART: SM00249; PHD; 3.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00081; DAG-PE-BIND_DOM_2; 1.
SEQUENCE 734 AA; 84111 MW; DABBFEOFC0A33FABI CRC64;

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09LNZ0 Length: 734 April 1, 2002 16:32 Type: P Check: 5875

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1 MNSVGEFRRK EIDGKSFYV TLTOTDNPST SGELAMDSG GDDLPLQPLF
51 FCPAARINFA KLRKMHND DDDDAEDDN GDKKESDD NKGDSDDDN
101 EDNEDDDND DDDDDDDDD DDDDDDDDDG DDNDGDCD DDDGILLPF

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151 DSTPHFSTR SGDOGESL DCNHPDYCKL PVVLEWCNN KERSTVGEBC
201 GACKMTLCE SYFACLOCG KFKKEVESP PEIKHPSHP. HSLRLCSFOT
251 RLISGCCRI TFGMYOCTT CNLSMHVCA MRVPLVVDH PSHHPHLSF
301 PFTQASTVCH ICARKILNDP TYICIQCFV IHKCGMFPB TIRISHPHR
351 ISFTSLPSR TILSCVCHQ VDNNGAYSC NNCDGFEVHS KCAHPKWD
401 GKELEVPPE DDLIDGEPF ERISDGIHH PHSHLRHE MSITDESKY
451 COGALPIYE GQFYSCEBD FILHSCANA PRMKRRLPX HPITLKFAV
501 RNSFTSQFR CAVCDRHNG FFEHGEDK MFLDLRCL IREPLVQGH
551 MHPFLMDD TESLISCOM KKSYYQLF CLECEYSLC KCVTPPYKVR
601 YKDSHFLTI CDVKEASDEL DMCDCGSKI EEEKEREYMW DDRERELRY
651 KCNDCTALH VDCILGVDMY MKPTDYISV ITLISGTR KDLMTPLNNS
701 LTRPICTCL SRCPPIFFK GHTKIFCSLY CSED

!!A..SEQUENCE 1.0
<ID 09LIS2> PRELIMINARY: PRT: 90 AA.
AC 09LIS2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SELF-INCOMPATIBILITY ASSOCIATED RIBONUCLEASE (FRAGMENT).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BOA CASTA;
RA Ma R., Oliveira M.M.;
RT "Molecular Characterization of Almond Cultivars Using S-RNase Gene
RT Sequences as Markers."
RN [2]
RP Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157010; AAF82614.1;
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; ribonuclease_T2; 1.
DR PROSITE: PS00530; RNase_T2_1; 1.
FT NON_TER 1 90
FT TER 1 90
SEQUENCE 90 AA; 10654 MW; D862FE388684C2076 CRC64;

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09LIS2 Length: 90 April 1, 2002 16:32 Type: P Check: 2503

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1 OFVQWPPTN CERVIRKPCS KPRPLQYFTI HGLMPSNYSN PRIPSNCTGS
51 OFKKOMLYPY LQSVLKKSMP DVESGNDTKF WEGEMWKNHGT

!!A..SEQUENCE 1.0
<ID 09LIS2> PRELIMINARY: PRT: 374 AA.
AC 09LIS2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PHOSPHATIDIC ACID PHOSPHATASE ALPHA (EC 3.1.3.4).
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vigna.
OX NCBI_TaxID=3917;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. EPACE-1; TISSUE=LEAF;
RA Franca M.G.C., Matos A.R., d'Arcy-Lameta A., Zully-Fodil Y.,

```

RA Pham-Thi A.T.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF165891; AAF89579.1; -.
 DR InterPro: IPR000326; PA_PTase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Hydrolase.
 SQ SEQUENCE 374 AA; 42336 MW; B50DAD5707D0A0BC CRC64;

09LQ07 Length: 374 April 1, 2002 16:32 Type: P Check: 92 ..

1 MASWMDLRRL FGFOSITRPF ODLSSRRIGI SAVSGAHSS INFPLIDKN
 51 EIDFRTREYQ LGSHTVSSHG YAVARTHKH WLILLLLVLV ALGLYVHPF
 101 HRFYKDMMT DLRYPLKST VPWMSIPIYA VLLPIYELV VYIRRDYVD
 151 LHHAVLGLLF SLITNAVITE AIKNGVGRPR PDEFWRCEPD GKDYDKLD
 201 VICHGKGVV KEGYKSPSG HTSWFSGLG FLSLYLSGI KAFDRGHYA
 251 KICVFLRPL FASVIGISRV DDYMHMDV FAGLLGLTV STFCYIQFP
 301 PFHSEGWGP VAFYRMLRS ROMQVPRNP NSGHAQLTEV QAEGEQGQC
 351 HCGWGLSLR DRNATLNDIE SGRC

11AA SEQUENCE 1.0
 ID 09LQ08 PRELIMINARY; PRT; 307 AA.

AC 09LQ08;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PHOSPHATIDIC ACID PHOSPHATASE-LIKE PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Kaneo T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Nakamura Y.;
 RX PubMed=10907853;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
 RT TAC and BAC clones."
 RL DNA Res. 7:217-221(2000).
 DR EMBL: AP000414; BAB01172.1; -.
 DR InterPro: IPR000326; PA_PTase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 SQ SEQUENCE 307 AA; 34951 MW; 06E394DD1C79DB3B CRC64;

09LQ08 Length: 307 April 1, 2002 16:32 Type: P Check: 3777 ..

1 MAXIMLGSHS VSHGWKVAR EHLCDMLIVL VLGIDIVLN VIEFHRIG
 51 PDMITDLTFP FYEDTIPMA VPICILVPI CIFIYVYYYR RDYVDLHNAI
 101 LGIGFSLVLT GVTDSIKDA VGRPRNPFY RCFPNKRPV PDKRVVCHG
 151 VKIIEGYK SPSGHTSMS FAGLTFELAY LSGKIKVEDR RGHVAKLCV
 201 FLPLISILI GISRDYWH HMTDVFAGAI IGIFVASFSY LHFFPIYDE
 251 NGNAPHAYFR MLEIRSTGRA TTMRTTGSRG MLDNDVEPGN SASSPDRHR

301 ESTDSDF

11AA SEQUENCE 1.0
 ID 09LUS4 PRELIMINARY; PRT; 221 AA.

AC 09LUS4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SELF-INCOMPATIBILITY ASSOCIATED RIBONUCLEASE.
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CODIFICADA;
 RA Ma R., Oliveira M.M.;
 RT "Molecular Characterization of Almond Cultivars Using 5-RNase Gene
 RT Sequences as Markers."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF157008; AAF82612.2; -.
 DR InterPro: IPR001568; RNase_T2.
 DR Pfam: PF00445; ribonuclease_T2; 1.
 DR PROSITE: PS00530; RNASE_T2_1; 1.
 SQ SEQUENCE 221 AA; 25844 MW; 073C2F245BD8FF2C CRC64;

09LUS4 Length: 221 April 1, 2002 16:32 Type: P Check: 4935 ..

1 MGILKSLAE IVLGFAFFEC YWSSGSYDY FQFVQMPPT NCRVTRKSK
 51 PRDLQYFTIH GLMPNSNP TPSCNCSKE DDRNVSPQLR NKLKRSMPDY
 101 ESNNDIKFNE GEMNKHGICS EQLNQOYF ERSQDMKSH NITELIKANS
 151 IYPSATQNMW YSDIVSPIK ATKRPILRC KQDKTQLLH EYFCYEYNA
 201 LKQIDCNRTS GCWNSVNSIF P

11AA SEQUENCE 1.0
 ID 09FVLI PRELIMINARY; PRT; 322 AA.

AC 09FVLI;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PHOSPHATIDIC ACID PHOSPHATASE BETA (EC 3.1.3.4).
 OS Vigna unguiculata (Cowpea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OX NCBI_TaxID=3917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. EPAGE-1; TISSUE-LEAF;
 RA Franca M.G.C., Matos A.R., d'Arcy-Jameta A., Zully-Fodil Y.,
 RA Pham-Thi A.T.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF171230; AAF89745.3; -.
 DR InterPro: IPR000326; PA_PTase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Hydrolase.
 SQ SEQUENCE 322 AA; 36224 MW; 67B7B572DCAAF8E CRC64;

09FVLI Length: 322 April 1, 2002 16:32 Type: P Check: 8335 ..

1 MPEIQGMHT IRSHGTRVAR IHMDWLILL LVYIDAVLN IIEPFRFVG
 51 EGMNTDLRNP LKGNITPFMA VPVAILLPL AVFLVYFYFR KQYDFHNAI
 101 LGLFSVLIT AVYTDAIKDG VGRPRDPFW RCFPDGKGFV DPTSDVRCST
 151 GQGVIAKEGT KVPSPGHTSM SFAGLVYLSW KLSGKIRVED RGHVAKLCL

201 VEPILVAM IAGSRVDDYV HHMDVFPAG LICITIASFC YLQFYPPYD
251 LDGMDGHAF OMLAESRNGS QPSTVNNNEIH HVOSSSELQAV SYITPQMDA
301 DFRVNSWDS PMLGASQNV TH

11AA SEQUENCE 1.0
ID 09FVJ1 PRELIMINARY: PRT: 162 AA.

AC 09FVJ1: PRELIMINARY: PRT: 162 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SE-RNASE (FRAGMENT).
GN SE-RNASE.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CODIFICADA; TISSUE=PISTILS;
RA Ma R.-C., Oliveira M.M.;
RT "Detection of S-RNase related sequences in almond.";
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF177923; AAC09286.1; -
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; Ribonuclease_T2; 1.
DR PROSITE: PS00530; RNase_T2_1; 1.
FT NON_TER 1 162
FT NON_TER 162 162
SQ SEQUENCE 162 AA: 19094 MW: 440078B97171736C CRC64;

09FVJ1 Length: 162 April 1, 2002 16:32 Type: P Check: 7946

1 QFVQWPPTN CRVTRKCSKP RPLQYFTIHG LMPNSYNSPT PSNCNSKFD
51 DRVSPQLRN KLRSMPPVE SGNDTKFMEG EMNKHGICSE QTLNQFYRE
101 RSODMKSHN ITELKNAI VPSATQWRY SDIVSPIKRA TKRTPILCK
151 QDKTQLLHE VV

11AA SEQUENCE 1.0
ID 09FVJ0 PRELIMINARY: PRT: 172 AA.

AC 09FVJ0: PRELIMINARY: PRT: 172 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SG-RNASE (FRAGMENT).
GN SG-RNASE.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BOA CASTA; TISSUE=PISTILS;
RA Ma R.-C., Oliveira M.M.;
RT "Detection of S-RNase related sequences in almond.";
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF177924; AAC09287.1; -
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; Ribonuclease_T2; 1.
DR PROSITE: PS00530; RNase_T2_1; 1.
FT NON_TER 1 172
FT NON_TER 172 172
SQ SEQUENCE 172 AA: 20104 MW: 76BDAA0A077FFD9AB CRC64;

09FVJ0 Length: 172 April 1, 2002 16:32 Type: P Check: 5836

1 QFVQWPPTN CRVTRKCSKP RPLQYFTI HGLMPSNYSN PRIPNSCTGS
51 QFRKQNLVRY LQSVLAKSWP DVDSGNDTKF WEGEMKHGT CSERLNIHQ
101 YFORSYAMWK SHNITELLON ASIVPHPTQT WKYSIDIESPI KTATKTPVL
151 RCKPDPQNK SQPKTQLLHE VV

11AA SEQUENCE 1.0
ID 09FM61 PRELIMINARY: PRT: 685 AA.

AC 09FM61: PRELIMINARY: PRT: 685 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SIMILARITY TO CHP-RICH ZINC FINGER PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and YAC clones.";
RL DNA Res. 5:41-54(1998).
DR EMBL: AB009050; BAB09245.1; -
DR InterPro: IPR002219; DAG-PE-bind.
DR InterPro: IPR001965; PHD.
DR SMART: SM00109; C1; 3.
DR SMART: SM00249; PHD; 3.
SQ SEQUENCE 685 AA: 79297 MW: 427694EFD5D2BC4F0 CRC64;

09FM61 Length: 685 April 1, 2002 16:32 Type: P Check: 7091

1 MSEVGVFRKE EIDGKFLAY TLTOTETPTS SGDAALAAAK AMYFVVDLP
51 LQPLFCPSV RIKFLSKPK NHDDHHGG FMEHPLNSTP HPCCTRSHDQ
101 QGESLLDCDK DYCKLVYIP LFWCNKKEFR YGFEDCRACN GNIFTSYFT
151 CLQCGKFKK ECVESPLEIK HPSHPFSLR LFSGSSNQKC SCCKYTPPM
201 YHCTTCELS MNPVCAMRPV PLVVDHFKSH PHPLSEFPDQ ASTVCNICAM
251 IKKLDPYIC IQCVVINKG CMGPHILIRI SRHPHISFT SSLPRGNFSC
301 GVCROOVNN YGANSCEICD DYVHSKCSL LPRIMDGKEL EGVPEDDKI
351 DGEPRKRIA DGIILPHHS HHMLREIDKA YDGNKYCRGC ALPIYEGOFY
401 SCWECDFILH ESCANAPRMK RYPLRPHLT LKGTTRHNE QKGVKCSBC
451 RRDNGFFYE YRKEKEIFOL DLRCASIIER EDYQGHQHL PLPDTKKKT
501 RCOMKYESK ESKLIECD YSICFCATF PYKARYKHS HPLTIDGKE
551 ESDEPWCCEV CEGKIEYKE TGYMWGKKT ELKYVCNDC CVALHVDLF
601 GRMVIKPEE TEKEVLSFD FFSFEDYWKV MDVRLNLS LSRPLNGCK
651 CRCPPIFYK GDLIFCSWY CLKIENPTP SRVSW

11AA SEQUENCE 1.0
ID 09CAP2 PRELIMINARY: PRT: 421 AA.

AC 09CAP2: PRELIMINARY: PRT: 421 AA.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HYPOTHETICAL 47.7 KDA PROTEIN.
GN T5M16.25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE#21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White D., Alonso J., Altieri H., Araujo R., Bowmen C.L., Brooks S.Y.,
RA Buehlerr E., Chan A., Chen Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
RA Miltner J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utecherback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL: AC010704; AAG51667.1; -
DR InterPro: IPR003409; MORF.
DR Pfam: PF02493; MORF; 7.
KW Hypothetical protein.
SQ
SEQUENCE 421 AA; 47731 MW; 08361C916235663 CRC64;
O9CAP2 length: 421 April 1, 2002 16:32 Type: P Check: 8387 ..

1 MSQKILTRQ SSLRSPPT RSSIQLSSI TECDDFNETS HHRREDDLEA
51 GEHEEKORRR KPVKSGSMN RIKGLAFTL ACISFLSLSS FLLEPDELTF
101 TSNLLGLI EYALAFRAS RNMAVINGTV IAIKQIRVRS RIKHKRPVQ
151 WYIGDSKPER IKEETRLVY KEGVQFSGS DYEGERNRG KNGSGVYY
201 YVNGRREGDW INGRYDGYI ECMSKSGKYK GQYKQGLRHG PGVYWFYTD
251 SYSGEMFNGO SHGFGVGTCA DGSSFVGEEK FGYNHGLGTY HERNDDKYAG
301 EYEGDKINGF GYVHFANGHY YEGAMHEGRK OGYGTYRFT GDIKSGEMD
351 GNLVNLPRD SDPVRAVOS ARERAKNGVN QRRIDEVIR AVAAANKAAT
401 AARVAAVKAV QNOMDKICD N

11AA_SEQUENCE 1.0
ID O9AWT8 PRELIMINARY: PRT: 362 AA.
AC O9AWT8:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE ALPHA.
GN P0480E02.6.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(ga3) genomic DNA, chromosome 1, PAC
clone:P0480E02."
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002913; BAB21200.1; -
DR SEQUENCE 362 AA; 40682 MW; 8C4F1141F8BF5176 CRC64;
O9AWT8 length: 362 April 1, 2002 16:32 Type: P Check: 2435 ..

1 MDGRREVQIG PHTIOTNGVR LARNHLDHW VILLAAVVI ALHFAFPESR
51 FPGKDMNTVP SYPKQSTVP AMGVPIISIV CPVITPLSVY IARRVYDLH
101 NATGLVLSV LITAVVTVV KNAYGRPRPD FFWRCPPDCK QLYDQVTDV
151 ICHGEKSFLL DGRKSPSGH TSMSEAGLGF LSLYLSGKIK VEDROGHVAK
201 LCMILPLLI ASLVGSKID DYRNHMDVF AGGLLGFIMA MLCYIAHFFPP
251 PYNHGFSAP LSKFYHGMV GDRMHTSICL RSFKMPTPTM QKASSQCVGI
301 MSLYDYTLA GHQEMWKLK VCNIPMLKT EEAACTVAS NGVFLTLVS
351 LROERNLHRI TA

11AA_SEQUENCE 1.0
ID O88542 PRELIMINARY: PRT: 2074 AA.
AC O88542:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE OPA-CONTAINING PROTEIN 1.
GN TNRC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Philibert R.A., King B.H., Cook E.H., Lee Y.-H., Shubblefield B.,
RA Damschroder-Williams P., Dea C., Palotie A., Tengstrom C.,
RA Martin B.M., Gims E.I.;
RT "The association of a dodecamer insertion variant with mental
retardation."
RL Mol. Psych. 0:0-0(1998).
DR EMBL: AF071310; AAC83164.1; -
DR MGD: MGI:1926212; Tnrc11.
DR InterPro: IPR001241; DNA_topoisom_1.
DR PROSITE: PS00177; TOPOISOMERASE_II; UNKNOWN_1.
DR SEQUENCE 2074 AA; 231808 MW; 293224D9BF46208 CRC64;
O88542 length: 2074 April 1, 2002 16:32 Type: P Check: 415 ..

1 MNOKDNFVLV TARSSAINT WFTDLAGTKP LTHLAKVVI FSKKEVGY
51 LAKYTVPMR AAWLIKMTCA YVAMSETKV KKNTRADPT EWTQITRYL
101 WEOIQMAEY YRPGPAGSG CGSTIGPLPH DYEMAIRQMD YNEKLALPMF
151 QDGMNDRHEF LTVVLECFEK IRGEDELLK LLLPLLRIS GFYQSAVLS
201 RLIAVFCSTR LALDQGVSS HSHVIAAOS TSLPTTPAP QPPTSTPST
251 PPSDLMCPQ HRPVFGSLC ILQITLLCP SALVMHYSLT DSRITGSPL
301 DILPIAPSNL PMPGNSAFT QOYRAKLREI EOIIRKRGCA VEVRKSPFKC
351 QEATAGFTIG RVLHTLEVLD SHSPERSDFS NSLSDLCNRI FGLGSKDGH
401 EISSDDAVV SLCEMAVSC KRSGRHRAV VAKLLEKRA EIEARCGES
451 EADEKGSVA SGLSAPSPAP IFQDVLLQFL DTQAPMLTP RSESRRVFF
501 NLVLFCELI RHDVFSNMV TCTLISRGDL AFGAPGRPP SPFDDPTDDP

551 ERKEAEGSSS SKLEDPGLISE SMDIDPSSIV LEFDEMEKPDF SLFSETPMCE
 601 GKGSPPSEKP DVEKEVKEPPA KEKIEGLIGI LYDQPRNHQV ATHPIPIPEE
 651 SCSEHCNORL VLFPGVKQR DDARHAIKTI TKDILKVLNR KQIAETDOLA
 701 PIVPLNPGDL TFLGEDGQK RRRNRPEAPF TAEDIFAKPQ HLSHYDQHV
 751 TQAVRNATLE QITSPALGMS YHLPIVQHVQ FIFDLMEYVL SISGLIDAI
 801 QLLNELSYVE AELLIKSSDL VGSYTSLSL CIYAVLRHYH ACLILNDOM
 851 AQVFGELGV VKHGMRSDG SSAERCLAY LYDLVYSCSH LKSKFGLFS
 901 DCSKVNKNTI YCNVPSSEN MRWAPFEMID TLENPAHNF TYTGKRLS
 951 ENPANRYSFV CNAIMHCVG HHDPDRVNDI AILCAELTGY CKSLSAEWLG
 1001 VLKALCCSSN NGTCGFNDLL CNDVSDLSF HDLAFVAVI LIARQCLLLE
 1051 DLRCAAPIS LINAACSEOD SEFGARLTCR ILHLFKTQV LNPOSDGNK
 1101 PTVGIRSSCD RHLLAASQNR IYDGAFAVL KAFVILGDAE LKSGFTVPG
 1151 GTEELPEEBG GGGSSGRROG GRNIVETAS LDVYAKYVLR SICQEWVGE
 1201 RCLKSLCEBS NDLODPVLSS AQOARLMQLI CYPHRLDNE DGENQORRI
 1251 KRILANLDM TMRÖSSLELO LMIKQTPNTE MNSLLENIAK ATIEVQOSA
 1301 EFGSSSGSTA SNMPSSTKT PYLSLERSG VMLVAPLIAK LPTVQGHVL
 1351 KAAGELENG QHLGSSSRKE RDRQKQKMS LLSQDPFSL VLTICKGDE
 1401 QREGLAŠLH SQVHOIYVNM RENQYLDCK PKOLMEALK LRLNVGMF
 1451 DTVORSTOOT TEMAQLLEI IISGTYMOS NNELFTTVLD MLSVLINGTL
 1501 AADMSISOG SMEENKRAYM NLVKKLOKL GERÖSDSLK VHOLLPLPKO
 1551 NRQVITCEPO GSLIDTKGN IAGFDSIFKK EGLÖVSTKÖK ISPMELFEGJ
 1601 KPSTAPLSMA WEGTVRVDRR VARGEEOQL LYHTHLRDR PRAYVLEPLP
 1651 LPPEDEEPPA PALLEPEKKA PEPPKTDKPG AAPPSTEERK KKSITGKKRS
 1701 QPATKNEGYG MGPGRSGPYG VTVPDDLH ANPGSISHLS YROSSMGLYT
 1751 QNOPLPAGP RVDPYRPVRL PMOKLPTPT YPGVLPTMS TWMGLEPSSY
 1801 KTSVTRQOOP TVPOGÖRLQ QLOOSÖGMLG ÖSSVHÖMTPS SSYGLÖTSOL
 1851 SSPSLÖGYTS YVSHVGLÖH TGPADPTRL ÖÖRPSGVHÖ QAPTYGHGLT
 1901 STÖRFSHÖTL ÖÖTPMGÖTMT PLSAQVÖAG VRSÖTSLPEÖ ÖÖÖÖÖÖÖÖÖÖ
 1951 ÖÖÖÖÖÖÖÖÖÖ ÖÖÖÖÖÖÖÖÖÖ ÖÖYHIRÖÖÖ ÖÖÖMLRÖÖÖ ÖÖÖÖÖÖÖÖÖÖ
 2001 ÖÖÖÖÖÖÖÖÖÖ ÖÖÖPHÖÖÖÖÖ AAPPÖPÖPÖS ÖPÖFÖRÖGLÖ ÖTÖÖÖÖÖTAA
 2051 LVROIQÖQLS NTÖPÖPSTNI FGRY

11AA-SEQUENCE 1.0

AC 09D788; PRELIMINARY; PRT: 158 AA.

DR 01-JUN-2001 (Tremblrel. 17, Created)
 DR 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
 GN 2310022A04RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AK009455; BAB26299.1;
 DR MGD: MGI:1919160; 2310022A04RIK.
 SQ SEQUENCE 158 AA: 17517 MW; B05FA8090DA3C14 CRC64;

09D788 Length: 158 April 1, 2002 16:32 Type: P Check: 7438 ..

1 MGTALGAEL GVRVLLPFAF LVTELLPFPQ RRIQPEELML YRNPVEAEY
 51 PPTGRMFVIA FLTPLSLIEF AKELRKADAT DSKQACLAAS LALALNGVFT
 101 NIILIVGRP RPDEFYRCFP DGLAHSDLTG TGDEDEVNKG RKSPSGHSS
 151 CMSFMGTT


```
! FINDPATTERNS on geneseqp: allowing 0 mismatches
```


$$1 \quad 1 \quad (H, K, R) P \sim P(F, Y, W) (F, Y, W)$$

April 1, 2002

15 1 Jan 2014 Sequence of red tide with eubacteria

1 to match
accident. ~~1~~ (H,K,R)P(H,K,R)P-P-P(E,Y,W)(E,Y,W) - pattern searched
arg. to a function
35: THERS
PPKPOOWE
WLM
(R)P(K)P-P-P(W)(F) - pattern matched

AAP40479, ck: 2062 len: 45 ! Aap40479 Substance P analogue. 11/1991

1  (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(W)(F)
RPKPQWF

AAP40481 ck: 1633 len: 45 ! Aap40481 Substance P analogue. 11/1991

1 (H,K,R)P(H,K,R)P~P~P(F,Y,W)(F,Y,W)
(R)P(K)P~P~P(W)(F)
35: THERS RPKPFQWF WLL

AAP614805 ck: 722 len: 45 ! Aap61480 Sequence of undeca peptide substar

1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)	
	(R)P(K)P-P-P(F)(F)	
35: THERS	RPKPQQFF	GLM

AAP70431 ck: 5532 len: 163 ! Aap70431 Human beta-preprotachykinin. 1/1995

1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
92: QRIAR RPKPQGF GLMGR

AAP80312 ck: 722 len: 45 | Aap80312 Sequence of neuropeptide substance

1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)	
	(R)P(K)P-P-P(F)(F)	
35: THERS	RPKPQOFF	GLM

AAp80313, ck: 2062 len: 45 ! Aap80313 Sequence of neuropeptide antagonists

1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)	
	(R)P(K)P-P-P(W)(F)	
35: THERS	RPKPQWF	WLL

AAP80314 ck: 2062 Len: 45 ! Aap80314 Sequence of neuropeptide antagonists

1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(W)(F)
35: THERS RPKPQWF WILL

AAP80315 ck: 1410 Len: 45 ; AAP80315 Sequence of neuropeptide antagonists

1 (H,K)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQQFF WLM

AAP80316> ck: 1633 len: 45 ! Aap80316 Sequence of neuropeptide antagonists

1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(W)(F)
35: THERS RPKPEQWF WILL

AMIP80317 ck: 2107 len: 45 | Aap80317 Sequence of neuropeptide antago

35: THEIRS
 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
 (R)P(K)P-P-P(W)(F)
 RKPQOWF WLM

AAP80320 ck: 765 len: 45 | Aap80320 Sequence of neuropeptide antago

35: THERS

(H,K,R)	P(H,K,R)	P-P-P(F,Y,W)(F,Y,W)	
(R)	P(K)	P-P-P(F)	HLM
		RPKPQOFF	

AA058563 ck: 2062 len: 45 | Aa05856 D-arginine 1, D-proline 2, D-tr

35: THEIRS
 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
 (R)P(K)P-P-P(W)(F)
 RPPQWF
 WLL

AAR13162, ck: 722 len: 45 | Aar13162 Static acid-bonded polypeptide

35: THEIRS GLM
 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
 (R)P(K)P-P-P(F)(F)
 PPKPOFF

PAR1144 Yck: 2062 len: 45 ! Aar11144 Substance P analogue. 5/1991

35: THERS
 (H,K,R)^P(H,K,R)^{P-P-P}(F,Y,W)(F,Y,W)
 (R)^P(K)^{P-P-P}(W)(F)
 :RPKQWF
 WLL

AAR18543 ck: 722 len: 45 ! Aar1854 Undecapeptide substance P. 7/19

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35:  THERS
      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPOOFF
      GLM

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:AAR21966³ ck: 704 len: 45 ! Aar21966 Cyclic substance P [D Cys 5, hc

35: THERS $(H, K, R)^{P(H, K, R)} P-P-P(E, Y, W)(E, Y, W)$
 $(R)^{P(K, P-P-P(E, Y, W))}$
 RPKPCOFE GXM

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AAr21965, ck: 4 len: 45 | Aar21965 Cyclic substance P [Cys 5,9]. 6
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35: THERS

	(H,K,R)P(H,K,R)P-P-P(E,Y,W)(E,Y,W)	
	(R)P(K)P-P-P(E)(F)	
	RPKPCOFF	CIM

AAR21967 ck: 9726 len: 45 1 Aar21967 Cyclic substance P [Cys 5,11].

35: THERS

AAR21960 ck: 1726 len: 45 ! Aar21960 Cyclic substance P [Hcys 5,9].

35: THERS

	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)	
	(R)P(K)P-P-P(F)(F)	
	RPKXOFF	XLM

ck: 1490 len: 45 ! Aar21961 Cyclic substance P [Hcys 5,11].

1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS RPKPQOFF GLX
AAR21932 ck: 3913 len: 43 1 Aar21932 Substance P (1-9) fragment. 6/1992
35: THERS (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
RPKPQOFF G
AAR21934 ck: 1501 len: 45 1 Aar21934 Substance P [Tyr7] and fragment (7
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR21935 ck: 1109 len: 45 1 Aar21935 Substance P [Pro 9] or [D-Pro 9].
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF PLM
AAR21936 ck: 1217 len: 45 1 Aar21936 Substance P or (7-11) [Ethionine 1
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLX
AAR21937 ck: 677 len: 45 1 Aar21937 Substance P or (7-11) [Norleucine
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLT
AAR21938 ck: 722 len: 45 1 Aar21938 Substance P [Me-Leu 10]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR21940 ck: 898 len: 45 1 Aar21940 Substance P [Pro 10]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GPM
AAR21942 ck: 722 len: 45 1 Aar21942 Substance P [Metet 11]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR21944 ck: 857 len: 45 1 Aar21944 Substance P [Pro 11]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLP
AAR21946 ck: 722 len: 45 1 Aar21946 Substance P [Me-Phe 8]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLX
AAR21951 ck: 254 len: 45 1 Aar21951 Substance P [Glu 3]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR21954 ck: 722 len: 45 1 Aar21954 Substance P [Me-Gly 9]. 6/1992
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR21958 ck: 464 len: 45 1 Aar21958 Substance P [Ala 9] or [D-Ala 9
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF ALM
AAR21962 ck: 722 len: 45 1 Aar21962 Substance P [Me Gly 6, Met (O2)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR21963 ck: 722 len: 45 1 Aar21963 Substance P [P-Chloro-Phe 7,8].
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR28442 ck: 722 len: 45 1 Aar28442 Substance P. 3/1993
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR28443 ck: 980 len: 45 1 Aar28443 Neurokinin 1 ligand #1. 3/1993
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF GLM
AAR28445 ck: 1520 len: 45 1 Aar28445 Neurokinin 1 ligand #3. 3/1993
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF MLM
AAR28680 ck: 344 len: 58 1 Aar28680 Galanin(1-12)-Pro-Spanide amid
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
48: YLLGP (R)P(K)P-P-P(F)(F)
RPKPQOFF WLL
AAR28392 ck: 1785 len: 45 1 Aar28392 Bradykinin receptor antagonist
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35: THERS (R)P(K)P-P-P(F)(F)
RPKPQOFF WLX

1	<u>AAAR5229</u>	ck: 2172 len: 526	1	Aar45229 APP-REP 751 amyloid precursor prot
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	<u>396: DKYLE</u>			
1	<u>AAAR32798</u>	ck: 4680 len: 46	1	Aar32798 Tyr-1 substance P used for binding
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>36: HERSY</u>			
1	<u>AAAR2646</u>	ck: 722 len: 45	1	Aar42646 Neurokinin 1 receptor affinity-con
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR42647</u>	ck: 1453 len: 45	1	Aar42647 Neurokinin 1 receptor affinity-con
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR2649</u>	ck: 1520 len: 45	1	Aar42649 Neurokinin 1 receptor affinity-con
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR5243</u>	ck: 722 len: 45	1	Aar85243 Substance P peptide. 8/1997
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR5244</u>	ck: 3804 len: 46	1	Aar85244 Substance P analogue peptide Cys-6
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMC
1	<u>35: THERS</u>			
1	<u>AAAR9003</u>	ck: 677 len: 45	1	Aaw09003 Substance P analogue, acts as subs
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLL
1	<u>35: THERS</u>			
1	<u>AAAR9004</u>	ck: 2602 len: 45	1	Aaw09004 Spanide analogue, acts as substan
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		WLX
1	<u>35: THERS</u>			
1	<u>AAAR7310</u>	ck: 722 len: 45	1	Aar77310 Substance P. 3/1996
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR7982</u>	ck: 1342 len: 45	1	Aar74982 [D-Arg1, D-Phe5, D-Trp7,9, Leu11]
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR2620</u>	ck: 4569 len: 254	1	Aaw32620 Bacillus smithii nitrile hydrat
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(H)P(R)P-P-P(F)(F)(W)		
		HPRPQSFH		EARAK
1	<u>56: RPPHH</u>			
1	<u>AAAR3181</u>	ck: 477 len: 45	1	Aaw33181 Mono-DTPA-Lys1 Substance P. 1/1
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(K)P(K)P-P-P(F)(F)		
		KPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR3180</u>	ck: 722 len: 45	1	Aaw33180 Mono-DTPA-Arg1 Substance P. 1/1
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR26509</u>	ck: 2172 len: 526	1	Aaw26509 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	<u>396: DKYLE</u>			
1	<u>AAAR26510</u>	ck: 8039 len: 521	1	Aaw26510 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	<u>396: DKYLE</u>			
1	<u>AAAR26393</u>	ck: 2172 len: 526	1	Aaw26393 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	<u>396: DKYLE</u>			
1	<u>AAAR26394</u>	ck: 8039 len: 521	1	Aaw26394 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	<u>396: DKYLE</u>			
1	<u>AAAR16339</u>	ck: 9887 len: 435	1	Aaw16339 DAB389-SP-Gly fusion toxin. 9/1
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMG
1	<u>424: HKTHA</u>			
1	<u>AAAR4616</u>	ck: 722 len: 45	1	Aaw04616 Substance P peptide for mass sp
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			
1	<u>AAAR7975</u>	ck: 242 len: 45	1	Aaw79775 Substance P. 1/1999
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	<u>35: THERS</u>			

1	AAW50978	ck: 765	len: 45	1	Aaw50978 Substance P analogue [D-Arg1,D-Pro	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	35: THERS				WLM			
1	AAW50966	ck: 2062	len: 45	1	Aaw50966 Substance P analogue, spantide I.	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	GLM
	35: THERS				WLL			
1	AAW50968	ck: 1410	len: 45	1	Aaw50968 Substance P analogue, [D-Pro2,D-P	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
	35: THERS				WLM			
1	AAW50969	ck: 2107	len: 45	1	Aaw50969 Substance P analogue, [D-Pro2,D-T	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	WLM
	35: THERS				WLM			
1	AAW50972	ck: 1633	len: 45	1	Aaw50972 Substance P analogue, [D-Arg1,D-P	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	WLL
	35: THERS				WLL			
1	AAW50958	ck: 2062	len: 45	1	Aaw50958 Substance P analogue, [D-Arg1,D-P	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	WLL
	35: THERS				WLL			
1	AAW50942	ck: 1633	len: 45	1	Aaw50942 Substance P antagonist (SP1). 7/19	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	GLM
	35: THERS				WLL			
1	AAW44744	ck: 2172	len: 526	1	Aaw44744 APP-REP 751 protein from PCLL602.	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	396: DKYLE				GLMG			
1	AAW44745	ck: 8039	len: 521	1	Aaw44745 APP-REP 751 protein from PCLL621.	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	396: DKYLE				GLMG			
1	AAW42978	ck: 2172	len: 526	1	Aaw42978 Amyloid precursor protein mutant A	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	396: DKYLE				GLMG			
1	AAW42979	ck: 8039	len: 521	1	Aaw42979 Amyloid precursor protein mutant A	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	396: DKYLE				GLMG			
1	AAW42973	ck: 722	len: 45	1	Aaw42973 Substrate P reporter epitope. 5	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
	35: THERS				GLM			
1	AAW30985	ck: 722	len: 45	1	Aay30985 Non-crosslinked protein particl	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
	35: THERS				GLM			
1	AAW34864	ck: 8364	len: 252	1	Aay34864 Chlamydia pneumoniae transmembr	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
	207: GYVCE				TLRLR			
1	AAW13564	ck: 940	len: 1,415	1	Aay13564 Drosophila Robo 2 polypeptide. 7	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(K)P-P-P(Y)(W)	SVEN
	357: COANG				SVEN			
1	AAW08402	ck: 7245	len: 1,414	1	Aay08402 Drosophila sp. ROBO2 extracellu	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(K)P-P-P(Y)(W)	SVEN
	357: COANG				SVEN			
1	AAW03156	ck: 722	len: 45	1	Aay03156 Substance P. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
	35: THERS				GLM			
1	AAW03157	ck: 3988	len: 46	1	Aay03157 Substance P-Glycine. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	35: THERS				GLMG			
1	AAW03158	ck: 7513	len: 47	1	Aay03158 Substance P-Glycine-Lysine. 6/1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	35: THERS				GLMG			
1	AAW03159	ck: 1449	len: 48	1	Aay03159 Substance P-Glycine-Lysine-Arg1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
	35: THERS				GLMG			
1	AAW03162	ck: 3913	len: 43	1	Aay03162 Substance P fragment P/1-9#. 6/	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	G
	35: THERS				G			

1	AAW99689	ck: 677	len: 45	1	Aaw99689 Substance P analogue #6. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLL
1	AAW99690	ck: 2602	len: 45	1	Aaw99690 Substance P analogue #7. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF	WLX
1	AAW99691	ck: 2602	len: 45	1	Aaw99691 Substance P analogue #8. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF	WLX
1	AAW74445	ck: 9834	len: 1,218	1	Aaw74445 Human nucleotide pyrophosphohydroly	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(Y)(F) KPRPDXYF	WYHND
1	AAW92709	ck: 1217	len: 45	1	Aaw92709 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLX
1	AAW92711	ck: 860	len: 42	1	Aaw92711 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92715	ck: 722	len: 45	1	Aaw92715 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92716	ck: 898	len: 45	1	Aaw92716 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92717	ck: 1217	len: 45	1	Aaw92717 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLX
1	AAW92718	ck: 857	len: 45	1	Aaw92718 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLP
1	AAW92719	ck: 722	len: 45	1	Aaw92719 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92677	ck: 1109	len: 45	1	Aaw92677 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	PLM
1	AAW92678	ck: 1109	len: 45	1	Aaw92678 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	PLM
1	AAW92679	ck: 254	len: 45	1	Aaw92679 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92680	ck: 722	len: 45	1	Aaw92680 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92681	ck: 722	len: 45	1	Aaw92681 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92682	ck: 4	len: 45	1	Aaw92682 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM
1	AAW92683	ck: 1726	len: 45	1	Aaw92683 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF	GLM

1	35: THERS	RPKPXQFF	GLM	
1	<u>AAW92684</u>	ck: 1523 len: 45 1 Aaw92684 Human tachykinin agonist beta-amy1	1	<u>AAW92731</u>
	(H,K,R)P(H,K,R)P-D-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw92731 Human tachykinin agonist beta-a
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPXQFF	GXM		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92685</u>	ck: 9726 len: 45 1 Aaw92685 Human tachykinin agonist beta-amy1	1	<u>AAW92656</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 2107 len: 45 1 Aaw92656 Human tachykinin agonist beta-a
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQQFF	GLC		(R)P(K)P-D-P(W)(F)
1	35: THERS			RPKPQOWP
1	<u>AAW92686</u>	ck: 1490 len: 45 1 Aaw92686 Human tachykinin agonist beta-amy1	1	<u>AAW92657</u>
	(H,K,R)P(H,K,R)P-D-P(F,Y,W)(F,Y,W)			ck: 2062 len: 45 1 Aaw92657 Human tachykinin agonist beta-a
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPXQFF	GLX		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOWP
1	<u>AAW92665</u>	ck: 3913 len: 43 1 Aaw92665 Human tachykinin agonist beta-amy1	1	<u>AAW94412</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 4310 len: 46 1 Aaw94412 Cancer protease-sensitive amino
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	G		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92666</u>	ck: 1501 len: 45 1 Aaw92666 Human tachykinin agonist beta-amy1	1	<u>AAW79663</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw79663 Substance P derivative having c
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	GLM		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92667</u>	ck: 1217 len: 45 1 Aaw92667 Human tachykinin agonist beta-amy1	1	<u>AAW79663</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw79663 Substance P derivative having c
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	GLX		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92668</u>	ck: 1217 len: 45 1 Aaw92668 Human tachykinin agonist beta-amy1	1	<u>AAW79663</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw79663 Substance P derivative having c
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	GLX		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92674</u>	ck: 464 len: 45 1 Aaw92674 Human tachykinin agonist beta-amy1	1	<u>AAW79663</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw79663 Substance P derivative having c
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	ALM		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92675</u>	ck: 464 len: 45 1 Aaw92675 Human tachykinin agonist beta-amy1	1	<u>AAW79663</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw79663 Substance P derivative having c
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	ALM		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF
1	<u>AAW92676</u>	ck: 722 len: 45 1 Aaw92676 Human tachykinin agonist beta-amy1	1	<u>AAW79663</u>
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)			ck: 722 len: 45 1 Aaw79663 Substance P derivative having c
	(R)P(K)P-D-P(F)(F)			(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
	RPKPQOFF	GLM		(R)P(K)P-D-P(F)(F)
1	35: THERS			RPKPQOFF

44: GGGGG	(R)P(K)P-P-P(F)(F) RPPQQFF				
1	<u>AA06258</u> ck: 3738 len: 54 1 Aab06258 Substance P analogue #2. 10/2000	1			
44: GGGGG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPPQQFF				
1	GLM				
35: THERS	AA06260 ck: 1196 len: 45 1 Aab06260 Substance P. 10/2000	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPPQWFF				
1	GLM				
157: KNAV	AA05042 ck: 1234 len: 348 1 Aag05042 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
142: KNAV	AA05043 ck: 69 len: 333 1 Aag05043 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
135: KNAV	AA05044 ck: 3694 len: 326 1 Aag05044 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
157: KNAV	AA06751 ck: 8736 len: 342 1 Aag06751 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPPNFFY				
1	RCPPN				
153: KNAV	AA06752 ck: 9625 len: 338 1 Aag06752 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPPNFFY				
1	RCPPN				
105: KNAV	AA06753 ck: 4240 len: 290 1 Aag06753 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPPNFFY				
1	RCPPN				
182: KNAV	AA00034 ck: 5300 len: 361 1 Aag00034 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPNFFY				
1	RCPPD				
157: KNAV	AA00035 ck: 8399 len: 336 1 Aag00035 Arabidopsis thaliana protein fragm	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPNFFY				
1	RCPPD				
105: KNAV	AA03023 ck: 717 len: 336 1 Aag03023 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
142: KNAV	AA03024 ck: 6784 len: 321 1 Aag03024 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
135: KNAV	AA03025 ck: 5563 len: 314 1 Aag03025 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
176: KNAV	AA03500 ck: 957 len: 367 1 Aag03500 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
157: KNAV	AA03501 ck: 1234 len: 348 1 Aag03501 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
142: KNAV	AA03502 ck: 69 len: 333 1 Aag03502 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
157: KNAV	AA03842 ck: 1234 len: 348 1 Aag03842 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
142: KNAV	AA03843 ck: 69 len: 333 1 Aag03843 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
157: KNAV	AA03844 ck: 3694 len: 326 1 Aag03844 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				
135: KNAV	AA04936 ck: 1234 len: 348 1 Aag04936 Arabidopsis thaliana protein fr	1			
	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
1	RCPPD				

1	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	
157: KNAVg			
1	AAG14937 ck: 69 len: 333 1 Aag14937 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
142: KNAVg			
1	AAG14938 ck: 3694 len: 326 1 Aag14938 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
135: KNAVg			
1	AAG17706 ck: 1234 len: 348 1 Aag17706 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
157: KNAVg			
1	AAG17707 ck: 69 len: 333 1 Aag17707 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
142: KNAVg			
1	AAG17708 ck: 3694 len: 326 1 Aag17708 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
135: KNAVg			
1	AAG21999 ck: 386 len: 398 1 Aag21999 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
207: KNAVg			
1	AAG22000 ck: 1234 len: 348 1 Aag22000 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
157: KNAVg			
1	AAG22001 ck: 69 len: 333 1 Aag22001 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
142: KNAVg			
1	AAG30400 ck: 2030 len: 324 1 Aag30400 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
137: KDAVg			
1	AAG30401 ck: 3697 len: 302 1 Aag30401 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
135: KDAVg			
1	AAG30402 ck: 2710 len: 272 1 Aag30402 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RRRPDFFW	RCFPD	1
105: KDAVg			
1	AAG30526 ck: 3692 len: 119 1 Aag30526 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(H)P-D-P(Y)(F) RPHPMLYF	F	1
111: TALGA			
1	AAG30528 ck: 9507 len: 93 1 Aag30528 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(H)P-D-P(Y)(F) RPHPMLYF	F	1
85: TALGA			
1	AAG38754 ck: 8835 len: 342 1 Aag38754 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(Y) RPHPMLYF	F	1
157: KDAVg			
1	AAG38755 ck: 9712 len: 338 1 Aag38755 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(Y) RPHPMLYF	RCFPD	1
153: KDAVg			
1	AAG38756 ck: 4354 len: 290 1 Aag38756 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(Y) RPHPMLYF	RCFPD	1
105: KDAVg			
1	AAG42826 ck: 4761 len: 361 1 Aag42826 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(Y)(W) RPHPMLYF	RCFPD	1
182: KVATG			
1	AAG42827 ck: 7060 len: 336 1 Aag42827 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(Y)(W) RPHPMLYF	RCFPD	1
157: KVATG			
1	AAG42828 ck: 2550 len: 284 1 Aag42828 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(Y)(W) RPHPMLYF	RCFPD	1
105: KVATG			
1	AAG50469 ck: 9507 len: 93 1 Aag50469 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(H)P-D-P(Y)(F) RPHPMLYF	F	1
85: TALGA			
1	AAY96513 ck: 8290 len: 860 1 Aay96513 Human zslg43 polypeptide. 9/200		

1	682: LELGV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(H)P-P-P(W)(F)	VSLDG	152: KLIVG	RPRPDFFY	RCP	
1	AAV58787 ck: 2030 len: 324	1 Aay58787 Arabidopsis phosphatidic acid phos (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	AAV32382 ck: 722 len: 45	1 Aay32382 Cell differentiation, prolifera (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM	
1	157: KDAVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	35: THERS	RPKPOQFF	
1	AAV58788 ck: 1560 len: 382	1 Aay58788 Arabidopsis phosphatidic acid phos (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(W)	RCEPD	1	AAV53610 ck: 4816 len: 248	1 Aay53610 The nitrile hydratase alpha sub (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W)	EARAK
1	203: KVATG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(W)	RCEPD	1	AAW23571 ck: 7240 len: 191	1 Aaw23571 Arabidopsis EST encoded protein (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y)	RCEPD
1	AAV58789 ck: 1234 len: 348	1 Aay58789 Arabidopsis phosphatidic acid phos (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	AAW0285 ck: 2082 len: 600	1 Aaw0285 Human polypeptide SEQ ID NO 343 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	SWLAS
1	156: KDCVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	AAW2450 ck: 7719 len: 119	1 Aaw2450 Human kidney related polypeptid (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(F)	VX
1	AAV58791 ck: 9121 len: 377	1 Aay58791 Soybean phosphatidic acid phosphat (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	AAU12377 ck: 668 len: 1,218	1 Aau12377 Human PRO1188 polypeptide seque (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F)	WYHND
1	181: KNAVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	369: CKATG	KRPDKXF	WYHND
1	AAV58792 ck: 5772 len: 356	1 Aay58792 Soybean phosphatidic acid phosphat (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	AAV62768 ck: 722 len: 45	1 Aag62768 Amino acid sequence of substanc (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
1	157: KDAVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCEPD	1	35: THERS	RPKPOQFF	GLM
1	AAV54319 ck: 165 len: 2,108	1 Aay54319 Amino acid sequence of a murine PC (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	LEPLP	1	AAV62769 ck: 3988 len: 46	1 Aag62769 Amino acid sequence of substanc (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	1,672: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	LEPLP	1	35: THERS	RPKPOQFF	GLMG
1	AAV54320 ck: 8484 len: 2,057	1 Aay54320 Amino acid sequence of a human PC (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	LEPLP	1	AAV62770 ck: 7513 len: 47	1 Aag62770 Amino acid sequence of substanc (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	1,612: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	LEPLP	1	35: THERS	RPKPOQFF	GLMG
1	AAV66557 ck: 668 len: 1,218	1 Aay66557 Membrane-bound protein PRO1188, 4/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(F)	WYHND	1	AAV62771 ck: 1449 len: 48	1 Aag62771 Amino acid sequence of substanc (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	369: CKATG	KRPDKXF	WYHND	1	35: THERS	RPKPOQFF	GLMG
1	AAV76061 ck: 24 len: 162	1 Aay76061 Rat skin cell transmembrane protei (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y)		1			

1	AA62772	ck: 3988	len: 46	1	Aag62772 Amino acid sequence of carboxy-est	(R)P(K)P-D-P(E,Y,W)(F)	GLM
	35: THERS					REKPOOFF	
1	AA62773	ck: 7513	len: 47	1	Aag62773 Amino acid sequence of carboxy-est	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62774	ck: 1449	len: 48	1	Aag62774 Amino acid sequence of carboxy-est	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62775	ck: 3988	len: 46	1	Aag62775 Amino acid sequence of carboxy-est	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62776	ck: 7513	len: 47	1	Aag62776 Amino acid sequence of carboxy-est	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62777	ck: 1449	len: 48	1	Aag62777 Amino acid sequence of carboxy-est	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 3913	len: 43	1	Aag62780 Amino acid sequence of a substance	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	G
	35: THERS					REKPOOFF	
1	AA62780	ck: 5532	len: 163	1	Aag99353 Human atypical tachykinin protein	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	92: QRIR					REKPOOFF	
1	AA62780	ck: 722	len: 45	1	Aag99354 Substance P peptide. 9/2001	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 722	len: 45	1	Aab84527 Amino acid sequence of human subst	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 3910	len: 46	1	Aab84528 Amino acid sequence of a modified	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 9228	len: 214	1	Aag98279 Human secreted protein, SEQ ID	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	RCPPD
	106: KLIIG					RRPPDFV	
1	AA62780	ck: 947	len: 45	1	Aab99350 Substance P tachykinin-related	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLR
	35: THERS					REKPOOFF	
1	AA62780	ck: 722	len: 45	1	Aab98866 Chimeric analgesic peptide #22.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLM
	35: THERS					REKPOOFF	
1	AA62780	ck: 3988	len: 46	1	Aab98867 Chimeric analgesic peptide #23.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 7513	len: 47	1	Aab98868 Chimeric analgesic peptide #24.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 1449	len: 48	1	Aab98869 Chimeric analgesic peptide #25.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 3988	len: 46	1	Aab98870 Chimeric analgesic peptide #26.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 7513	len: 47	1	Aab98871 Chimeric analgesic peptide #27.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 1449	len: 48	1	Aab98872 Chimeric analgesic peptide #28.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	
1	AA62780	ck: 3988	len: 46	1	Aab98873 Chimeric analgesic peptide #29.	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)	GLMG
	35: THERS					REKPOOFF	

1	<u>AAB98874</u> ck: 7513 len: 47 Aab98874 Chimeric analgesic peptide #30. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLMGK	1	<u>AAB91414</u> ck: 765 len: 45 Aab91411 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF HLM
1	<u>AAB98875</u> ck: 1449 len: 48 Aab98875 Chimeric analgesic peptide #31. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLMGK	1	<u>AAB91412</u> ck: 1410 len: 45 Aab91412 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLM
1	<u>AAB98878</u> ck: 3913 len: 43 Aab98878 Chimeric analgesic peptide #34. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF G	1	<u>AAB91413</u> ck: 2107 len: 45 Aab91413 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF WLM
1	<u>AAB98879</u> ck: 1410 len: 45 Aab98879 Chimeric analgesic peptide #35. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLM	1	<u>AAB91414</u> ck: 1633 len: 45 Aab91414 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF WLM
1	<u>AAB98880</u> ck: 4676 len: 46 Aab98880 Chimeric analgesic peptide #36. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLMG	1	<u>AAB91415</u> ck: 1109 len: 45 Aab91415 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF WLL
1	<u>AAB98881</u> ck: 2107 len: 45 Aab98881 Chimeric analgesic peptide #37. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF WLM	1	<u>AAB91422</u> ck: 7516 len: 44 Aab91422 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF PLM
1	<u>AAB98882</u> ck: 5373 len: 46 Aab98882 Chimeric analgesic peptide #38. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOFF WLMG	1	<u>AAB91423</u> ck: 7257 len: 44 Aab91423 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GL
1	<u>AAB92070</u> ck: 722 len: 45 Aab92070 Substance P. 6/2001 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLM	1	<u>AAB91427</u> ck: 7257 len: 44 Aab91427 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GL
1	<u>AAB91402</u> ck: 981 len: 45 Aab91402 Tachykinins peptide SEQ ID NO:578. (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLM	1	<u>AAB91429</u> ck: 1109 len: 45 Aab91429 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF PLM
1	<u>AAB91409</u> ck: 1520 len: 45 Aab91409 Tachykinins peptide SEQ ID NO:585. (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLM	1	<u>AAB91432</u> ck: 7516 len: 44 Aab91432 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF LM

1 AAB91434 > ck: 2062 len: 45 | Aab91434 Tachykinins peptide SEQ ID NO:610.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(W)(F)
35: THERS RPKPQOWF WLL

1 AAB91436 > ck: 722 len: 45 | Aab91436 Tachykinins peptide SEQ ID NO:612.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB91438 > ck: 385 len: 45 | Aab91438 Tachykinins peptide SEQ ID NO:614.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(R)P-D-P(F)(F)
35: THERS KRPDPQWF GLM

1 AAB91440 > ck: 1449 len: 48 | Aab91440 Tachykinins peptide SEQ ID NO:616.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GLMGK

1 AAB91444 > ck: 3913 len: 43 | Aab91444 Tachykinins peptide SEQ ID NO:620.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF G

1 AAB91449 > ck: 722 len: 45 | Aab91449 Tachykinins peptide SEQ ID NO:625.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB91450 > ck: 722 len: 45 | Aab91450 Tachykinins peptide SEQ ID NO:626.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB91451 > ck: 8055 len: 44 | Aab91451 Tachykinins peptide SEQ ID NO:627.
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GL

1 AAB92023 > ck: 344 len: 58 | Aab92023 Galanin peptide SEQ ID NO:1199. 6/
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(W)(F)
48: YLLGP RPKPQOWF WLL

1 AAB92031 > ck: 344 len: 58 | Aab92031 Galanin peptide SEQ ID NO:1207. 6/
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(W)(F)
48: YLLGP RPKPQOWF WLL

1 AAB70690 > ck: 4219 len: 209 | Aab70690 Human hDPP protein sequence SEQ ID

1 (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
106: KLIWG RRPDPDFY RCEPD

1 AAB49755 > ck: 736 len: 45 | Aab49755 Complex sugar bound peptide (SB
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(R)P-D-P(F)(F)
35: THERS KRPDPQWF GLM

1 AAB65180 > ck: 668 len: 1,218 | Aab65180 Human PRO1188 (UNQ602) protein
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(R)P-D-P(F)(F)
369: CKATG KRPDPKXF WYHND

1 AAB50544 > ck: 722 len: 45 | Aab50544 Prolyl endopeptidase inhibitor
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB50306 > ck: 722 len: 45 | Aab50306 Substance P. 3/2001
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(K)P-D-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB56000 > ck: 24 len: 162 | Aab56000 Skin cell protein, SEQ ID NO: 3
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(F)
152: KLIWG RRPDPDFY RCF

Databases searched: *A-Genealogy*
2500, Release 25.0, Released on 25Oct2001, Formatted on 13Dec2001

Total finds: 245
Total length: 91,837,149
Total sequences: 522,463
CPU time: 09:07.03

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:29 ; Search time 38.86 Seconds
(Without alignments)
20.968 Million cell updates/sec

Title: US-09-988-792-1

Perfect score: 61

Sequence: 1 RPKPQGFGLM 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

(Total number of hits satisfying chosen parameters: 517

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	7 AAP61480	Sequence of undeca
2	61	100.0	11	9 AAP80312	Sequence of neupoc
3	61	100.0	11	12 AAR13162	Static acid-bonded
4	61	100.0	11	12 AAR11854	Undecapeptide subs
5	61	100.0	11	13 AAR21938	Substance P [Me-Ile
6	61	100.0	11	13 AAR21942	Substance P [MeMet
7	61	100.0	11	13 AAR21946	Substance P [Me-Phe
8	61	100.0	11	13 AAR21954	Substance P [Me-Glu
9	61	100.0	11	13 AAR21962	Substance P [Me-Glu
10	61	100.0	11	13 AAR21963	Substance P [p-Chl
11	61	100.0	11	13 AAR28442	Substance P. Synt

12	61	100.0	11	14 AAR42646	Neurokinin 1 recep
13	61	100.0	11	16 AAR85243	Substance P peptid
14	61	100.0	11	16 AAR77310	Substance P. Synt
15	61	100.0	11	18 AAW33180	Mono-DTPA-Arg1 Sub
16	61	100.0	11	18 AAW04616	Substance P peptid
17	61	100.0	11	19 AAW42973	Substance P report
18	61	100.0	11	20 AAY30985	Non-crosslinked pr
19	61	100.0	11	20 AAY03156	Substance P. Synt
20	61	100.0	11	20 AAW92715	Human tachykinin a
21	61	100.0	11	20 AAW92719	Human tachykinin a
22	61	100.0	11	20 AAW92720	Human tachykinin a
23	61	100.0	11	20 AAW92708	Human tachykinin a
24	61	100.0	11	20 AAW92680	Human tachykinin a
25	61	100.0	11	20 AAW92681	Human tachykinin a
26	61	100.0	11	20 AAW92676	Human tachykinin a
27	61	100.0	11	20 AAW92731	Human tachykinin a
28	61	100.0	11	20 AAW79662	Substance P deriva
29	61	100.0	11	20 AAW79663	Substance P deriva
30	61	100.0	11	21 AAB18483	Peptide substrate
31	61	100.0	11	21 AAB23027	Human/rat tachykin
32	61	100.0	11	21 AAY32382	Cell differentiatl
33	61	100.0	11	22 AAG62768	Amino acid sequenc
34	61	100.0	11	22 AAG62768	Substance P peptid
35	61	100.0	11	22 AAB84527	Amino acid sequenc
36	61	100.0	11	22 AAB98866	Chimeric analgesic
37	61	100.0	11	22 AAB82070	Substance P. Unid
38	61	100.0	11	22 AAB91436	Tachykinins peptid
39	61	100.0	11	22 AAB91449	Tachykinins peptid
40	61	100.0	11	22 AAB91450	Prol-1 endopeptida
41	61	100.0	11	22 AAB50544	Substance P. Unid
42	61	100.0	11	22 AAB50306	Tyr-1 substance P
43	61	100.0	12	16 AAR83298	Substance P analog
44	61	100.0	12	16 AAR85244	Substance P analog
45	61	100.0	12	20 AAY03157	Cancer protease-se
46	61	100.0	12	20 AAW94412	Amino acid sequenc
47	61	100.0	12	22 AAG62769	Amino acid sequenc
48	61	100.0	12	22 AAG62772	Amino acid sequenc
49	61	100.0	12	22 AAG62775	Amino acid sequenc
50	61	100.0	12	22 AAB84528	Amino acid sequenc
51	61	100.0	12	22 AAB98867	Chimeric analgesic
52	61	100.0	12	22 AAB98870	Chimeric analgesic
53	61	100.0	12	22 AAB98873	Chimeric analgesic
54	61	100.0	13	20 AAY03158	Substance P-Glycin
55	61	100.0	13	22 AAG62770	Amino acid sequenc
56	61	100.0	13	22 AAG62773	Amino acid sequenc
57	61	100.0	13	22 AAG62776	Amino acid sequenc
58	61	100.0	13	22 AAB98868	Chimeric analgesic
59	61	100.0	13	22 AAB98871	Chimeric analgesic
60	61	100.0	13	22 AAB98874	Chimeric analgesic
61	61	100.0	14	20 AAY03159	Substance P-Glycin
62	61	100.0	14	22 AAG62771	Amino acid sequenc
63	61	100.0	14	22 AAG62774	Amino acid sequenc
64	61	100.0	14	22 AAG62777	Amino acid sequenc
65	61	100.0	14	22 AAB98869	Chimeric analgesic
66	61	100.0	14	22 AAB98872	Chimeric analgesic
67	61	100.0	14	22 AAB98875	Chimeric analgesic
68	61	100.0	14	22 AAB91440	Tachykinins peptid
69	61	100.0	20	21 AAB06258	Substance P analog
70	61	100.0	8	AAP70431	Human beta-preprot
71	61	100.0	129	22 AAG93533	Human atypical tac
72	61	100.0	401	18 AAW16339	DAB389-SP-Gly fusi
73	61	100.0	487	18 AAW6510	Amyloid precursor
74	61	100.0	487	18 AAW26394	Amyloid precursor
75	61	100.0	487	19 AAW44745	Amyloid precursor
76	61	100.0	487	19 AAW42979	Amyloid precursor
77	61	100.0	492	14 AAW45229	APP-REP 751 amylo1
78	61	100.0	492	18 AAW6509	Amyloid precursor
79	61	100.0	492	18 AAW6509	Amyloid precursor
80	61	100.0	492	19 AAW44744	APP-REP 751 protei
81	61	100.0	492	19 AAW42978	Amyloid precursor
82	61	100.0	492	19 AAW42978	Substance P [Tyr7]
83	58	95.1	11	13 AAR21937	Substance P or (7-
84	58	95.1	11	13 AAR21951	Substance P [Glu 3

85	58	95.1	11	13	AA828445	Neurokinine 1 lig	158	49	80.3	9	6	AA850634	Substance P-like p
86	58	95.1	11	14	AA842649	Neurokinin 1 recep	159	49	80.3	9	20	AAW92714	Human tachykinin a
87	58	95.1	11	16	AAW90003	Substance p analog	160	49	80.3	9	22	AA891446	Tachykinins peptid
88	58	95.1	11	18	AAW33181	Mono-DHPA-lysi Sub	161	49	80.3	11	22	AA891437	Tachykinins peptid
89	58	95.1	11	19	AAW97975	Substance P. Mamm	162	49	80.3	13	13	AA829593	Vertebrate stromel
90	58	95.1	11	20	AAW99689	Substance p analog	163	48	78.7	13	4	AA830142	Sequence of peptid
91	58	95.1	11	20	AAW92679	Human tachykinin a	164	48	78.7	11	9	AA880317	Sequence of neurop
92	58	95.1	11	20	AAW92666	Human tachykinin a	165	48	78.7	11	13	AA821966	Cyclic substance p
93	58	95.1	11	20	AAW91402	Tachykinins peptid	166	48	78.7	11	13	AA821967	Cyclic substance p
94	58	95.1	11	22	AA891409	Tachykinins peptid	167	48	78.7	11	13	AA821960	Cyclic substance p
95	56	91.8	10	6	AA850633	Substance p-like p	168	48	78.7	11	19	AAW50969	Substance p analog
96	56	91.8	10	13	AA821933	Substance P (2-11)	169	48	78.7	11	20	AAW92683	Human tachykinin a
97	56	91.8	10	20	AAW92663	Human tachykinin a	170	48	78.7	11	20	AAW92685	Human tachykinin a
98	56	91.8	10	22	AA891423	Tachykinins peptid	171	48	78.7	11	20	AAW92656	Human tachykinin a
99	56	91.8	10	22	AA891427	Tachykinins peptid	172	48	78.7	11	22	AAW98881	Chimeric analgesic
100	56	91.8	10	22	AA891445	Tachykinins peptid	173	48	78.7	11	22	AA891413	Tachykinins peptid
101	56	91.8	11	13	AA821945	Substance P (Pro 1	174	48	78.7	12	22	AAW98882	Chimeric analgesic
102	56	91.8	11	13	AA821936	Substance P or (7-	175	47	77.0	11	21	AA806260	Substance P. Unid
103	56	91.8	11	13	AA821941	Substance P (pGLu	176	46	75.4	8	20	AAW92711	Human tachykinin a
104	56	91.8	11	13	AA821944	Substance P (Pro 1	177	46	75.4	10	22	AA891410	Tachykinins peptid
105	56	91.8	11	20	AAW922709	Human tachykinin a	178	46	75.4	10	22	AA891422	Tachykinins peptid
106	56	91.8	11	20	AAW922717	Human tachykinin a	179	46	75.4	10	22	AA891432	Tachykinins peptid
107	56	91.8	11	20	AAW922718	Human tachykinin a	180	46	75.4	17	21	AA806257	Substance p analog
108	56	91.8	11	20	AAW92667	Human tachykinin a	181	45	74.6	10	20	AA806939	Substance P from B
109	56	91.8	11	20	AAW92668	Human tachykinin a	182	45	74.6	10	22	AA864746	Substance p amino
110	56	91.8	11	20	AAW92670	Human tachykinin a	183	45	73.8	11	5	AA840479	Substance p analog
111	56	91.8	11	20	AAW92672	Human tachykinin a	184	45	73.8	11	9	AA880313	Sequence of neurop
112	56	91.8	11	21	AA808614	Peptide identified	185	45	73.8	11	9	AA880314	Sequence of neurop
113	56	91.8	11	22	AA890350	Substance P tachyk	186	45	73.8	11	11	AA805856	D-arginine 1, D-pr
114	56	90.2	11	13	AA821939	Substance P (Ile 8	187	45	73.8	11	12	AA811144	Substance P analog
115	56	90.2	11	13	AA821943	Substance P (Met 7	188	45	73.8	11	13	AA821968	Cyclic substance p
116	56	90.2	11	13	AA821949	Substance P (Pro 3	189	45	73.8	11	13	AA821969	Cyclic substance p
117	55	90.2	11	13	AA821958	Substance P (Ala 9	190	45	73.8	11	13	AA821970	Cyclic substance p
118	55	90.2	11	20	AAW92669	Human tachykinin a	191	45	73.8	11	19	AAW50966	Substance p analog
119	55	90.2	11	20	AAW92671	Human tachykinin a	192	45	73.8	11	19	AAW50958	Substance P analog
120	55	90.2	11	20	AAW92673	Human tachykinin a	193	45	73.8	11	20	AAW92687	Human tachykinin a
121	55	90.2	11	20	AAW92674	Human tachykinin a	194	45	73.8	11	20	AAW92688	Human tachykinin a
122	55	90.2	11	20	AAW92675	Human tachykinin a	195	45	73.8	11	20	AAW92689	Human tachykinin a
123	55	90.2	11	22	AA849755	Complex sugar bou	196	45	73.8	11	20	AAW92690	Human tachykinin a
124	54	88.5	11	13	AA821940	Substance P (Pro 1	197	45	73.8	11	20	AAW92657	Human tachykinin a
125	54	88.5	11	14	AA842647	Neurokinin 1 recep	198	45	73.8	11	22	AA891434	Tachykinins peptid
126	54	88.5	11	20	AAW922716	Human tachykinin a	199	45	73.8	11	22	AA850312	Galantn(1-12)-Pro-
127	54	88.5	11	20	AAW92271	Human tachykinin a	200	45	73.8	24	13	AA828680	Galantn(1-12)-Pro-
128	54	88.5	10	22	AA891451	Tachykinins peptid	201	45	73.8	24	22	AA892023	Galantn peptide SE
129	53	86.9	11	9	-AA880315	Sequence of neurop	202	45	73.8	20	22	AA892031	Galantn peptide SE
130	53	86.9	11	9	AA880320	Sequence of neurop	203	44.5	73.0	10	20	AAW99684	Substance p analog
131	53	86.9	11	13	AA821935	Substance P (Pro 9	204	44.5	73.0	10	22	AA866675	Tachykinin peptid
132	53	86.9	11	13	AA821964	Substance P (D-Ala	205	44	72.1	8	3	AA820303	Gastrointestinal m
133	53	86.9	11	19	AAW50978	Substance p analog	206	44	72.1	8	20	AAW92664	Human tachykinin a
134	53	86.9	11	19	AAW50968	Substance p analog	207	44	72.1	8	21	AA816753	P antagonist peptid
135	53	86.9	11	20	AAW92677	Human tachykinin a	208	44	72.1	8	22	AA891416	Tachykinins peptid
136	53	86.9	11	20	AAW92678	Human tachykinin a	209	44	72.1	8	22	AA891424	Tachykinins peptid
137	53	86.9	11	22	AAW98879	Chimeric analgesic	210	44	72.1	11	13	AA821965	Cyclic substance p
138	53	86.9	11	22	AA891411	Tachykinins peptid	211	44	72.1	11	20	AAW92682	Human tachykinin a
139	53	86.9	11	22	AA891412	Tachykinins peptid	212	44	72.1	20	13	AA828679	Galantn(1-12)-Pro-
140	53	86.9	11	22	AA891415	Tachykinins peptid	213	44	72.1	20	22	AA892027	Galantn peptide SE
141	53	86.9	11	22	AA891429	Tachykinins peptid	214	43.5	71.3	10	16	AA865181	S. cerevisiae sske
142	53	86.9	11	22	AA850311	Prevlin peptide #3.	215	43	70.5	11	13	AA828392	Bradykinin recepto
143	53	86.9	12	22	AA898880	Chimeric analgesic	216	43	70.5	11	14	AA823183	Ranakinin. Rana r
144	52	85.2	9	13	AA821932	Substance P (1-9)	217	43	70.5	11	16	AAW09004	Substance analogue.
145	52	85.2	9	20	AA8103162	Substance P (fragme	218	43	70.5	11	20	AAW99680	Substance p analog
146	52	85.2	9	20	AAW92665	Human tachykinin a	219	43	70.5	11	20	AAW99691	Substance p analog
147	52	85.2	9	22	AA862780	Amino acid sequenc	220	42	68.9	11	13	AA821971	Cyclic substance p
148	52	85.2	9	22	AA898878	Chimeric analgesic	221	42	68.9	11	20	AAW92691	Human tachykinin a
149	52	85.2	9	22	AA891444	Tachykinins peptid	222	40	65.6	7	20	AA8103161	Substance p fragme
150	52	85.2	11	13	AA828443	Neurokinine 1 liga	223	40	65.6	7	20	AAW92658	Human tachykinin a
151	51	83.6	11	19	AAW60208	Peptide NRP1, a su	224	40	65.6	7	22	AA862779	Amino acid sequenc
152	51	83.6	11	21	AA8167965	Carboxyfluorescein	225	40	65.6	7	22	AAW98877	Chimeric analgesic
153	50	82.0	11	13	AA821961	Cyclic substance p	226	40	65.6	7	22	AAW91443	Tachykinins peptid
154	50	82.0	11	20	AAW92684	Human tachykinin a	227	38	62.3	11	13	AA821972	Cyclic substance p
155	50	82.0	11	20	AAW92686	Human tachykinin a	228	38	62.3	11	20	AAW92692	Human tachykinin a
156	50	82.0	11	22	AA891438	Tachykinins peptid	229	38	62.3	115	21	AA816968	Arabidopsis thalia
157	50	82.0	22	13	AA828681	Galantn(1-12)-Pro-	230	38	62.3	116	21	AA816967	Galantn(1-12)-Pro-

231	38	62.3	176	21	AA616966	Arabidopsis thalia	304	34	55.7	6	22	AA691442	Tachykinins peptid
232	38	62.3	249	21	AA621479	Arabidopsis thalia	305	34	55.7	7	13	AA621956	Substance P (5-11)
233	38	62.3	249	21	AA652793	Arabidopsis thalia	306	34	55.7	11	13	AA621974	Cyclic substance P
234	38	62.3	255	21	AA621478	Arabidopsis thalia	307	34	55.7	11	13	AA628446	Neurokinine 1 lig
235	38	62.3	255	21	AA652792	Arabidopsis thalia	308	34	55.7	11	14	AA642650	Neurokinin 1 recep
236	38	62.3	257	21	AA621477	Arabidopsis thalia	309	34	55.7	11	20	AA692694	Human tachykinin a
237	38	62.3	257	21	AA652791	Arabidopsis thalia	310	34	55.7	162	22	AA672892	Human tachykinin a
238	38	62.3	475	22	AA684839	p73 gamma protein	311	34	55.7	162	22	AA673046	Human olfactory re
239	38	62.3	3722	12	AA610145	Cephalosporin anti	312	34	55.7	467	21	AA630869	Arabidopsis thalia
240	37	60.7	7	20	AA650324	Neutrophil-activat	313	34	55.7	572	22	AA603506	Human protein kin
241	37	60.7	7	21	AA652662	Human tachykinin a	314	34	55.7	582	14	AA639556	Deduced amino acid
242	37	60.7	7	21	AA675574	P antagonist peptid	315	34	55.7	583	22	AA630869	Amino acid sequenc
243	37	60.7	7	22	AA691420	Tachykinins peptid	316	34	55.7	587	12	AA639553	Deduced amino acid
244	37	60.7	7	22	AA691431	Tachykinins peptid	317	34	55.7	587	22	AA630861	Amino acid sequenc
245	37	60.7	8	13	AA628444	Neurokinine 1 lig	318	34	55.7	588	12	AA639555	Sequence encoded b
246	37	60.7	8	20	AA692710	Human tachykinin a	319	34	55.7	588	22	AA630868	Amino acid sequenc
247	37	60.7	8	22	AA691407	Tachykinins peptid	320	34	55.7	598	21	AA630868	Arabidopsis thalia
248	37	60.7	11	5	AA640481	Substance P analog	321	34	55.7	628	21	AA630867	Arabidopsis thalia
249	37	60.7	11	9	AA680316	Sequence of neurop	322	34	55.7	666	21	AA697010	S. cerevisiae esse
250	37	60.7	11	19	AA650979	Substance P analog	323	33	54.1	11	22	AA650314	Previn peptide #6
251	37	60.7	11	19	AA650972	Substance P analog	324	33	54.1	62	20	AA619487	Amino acid sequenc
252	37	60.7	11	19	AA650942	Substance P antago	325	33	54.1	77	21	AA616060	Arabidopsis thalia
253	37	60.7	11	19	AA608303	Amino acid sequenc	326	33	54.1	85	21	AA616059	Arabidopsis thalia
254	37	60.7	11	22	AA691414	Tachykinins peptid	327	33	54.1	138	15	AA662881	Murine anti-human
255	37	60.7	138	21	AA670578	Salmonella pathoge	328	33	54.1	171	18	AA623689	Potato polyphenol
256	36	59.0	9	22	AA699348	Atypical tachykin	329	33	54.1	324	17	AA692786	Canola palmitoyl-A
257	36	59.0	10	22	AA699347	Atypical tachykin	330	33	54.1	328	17	AA692789	Soybean palmitoyl-
258	36	59.0	10	22	AA691383	Tachykinins peptid	331	33	54.1	404	16	AA678621	Chicken GalInac-a1p
259	36	59.0	11	13	AA621973	Cyclic substance P	332	33	54.1	505	14	AA641941	p17 gene LptK-2 pr
260	36	59.0	11	20	AA692693	Human tachykinin a	333	33	54.1	505	16	AA685929	Protein tyrosine-k
261	36	59.0	11	22	AA699337	Human atypical tac	334	33	54.1	505	22	AA696304	Escherichia coli p
262	36	59.0	11	22	AA699358	ATT-short peptide.	335	33	54.1	566	22	AA640285	Human polyptide
263	36	59.0	12	6	AA650357	Hyalambtin dodecap	336	33	54.1	711	19	AA644842	Staphylococcus aur
264	36	59.0	12	18	AA604615	Kasasinin peptide f	337	33	52.5	6	20	AA650694	Sequence of pharma
265	36	59.0	12	20	AA692730	Human tachykinin a	338	32	52.5	6	26	AA692659	Human tachykinin a
266	36	59.0	45	22	AA699335	Human atypical tac	339	32	52.5	6	21	AA677575	P antagonist pepti
267	36	59.0	45	22	AA699357	ATT peptide. Unid	340	32	52.5	6	22	AA699351	Atypical tachykin
268	36	59.0	56	22	AA618187	Peptide #4621 enco	341	32	52.5	6	22	AA691419	Tachykinins peptid
269	36	59.0	56	22	AA630684	Peptide #4491 enco	342	32	52.5	6	22	AA691421	Tachykinins peptid
270	36	59.0	56	22	AA605809	Peptide #4491 enco	343	32	52.5	7	22	AA699350	Tachykinins peptid
271	36	59.0	68	22	AA699333	Human atypical tac	344	32	52.5	8	22	AA699349	Atypical tachykin
272	36	59.0	76	22	AA699336	Human atypical tac	345	32	52.5	11	18	AA604613	Physalaemin peptid
273	36	59.0	107	22	AA699338	Human atypical tac	346	32	52.5	11	19	AA648280	Tyrosylpeptide phy
274	35	57.4	11	13	AA621975	Cyclic substance P	347	32	52.5	11	22	AA691386	Tachykinins peptid
275	35	57.4	11	14	AA632182	Generic neuropepti	348	32	52.5	11	22	AA652031	Previn peptide #8
276	35	57.4	11	16	AA674982	[D-Arg1, D-Phe5, D	349	32	52.5	12	22	AA692032	Galanin peptide SE
277	35	57.4	11	19	AA648950	Tachykinin peptid	350	32	52.5	13	15	AA649131	Sequence of C-term
278	35	57.4	11	20	AA692695	Human tachykinin a	351	32	52.5	13	20	AA649081	Infectious pancrea
279	35	57.4	11	21	AA608313	Human tachykinin a	352	32	52.5	13	20	AA692700	Human tachykinin a
280	35	57.4	11	22	AA662781	Amino acid sequenc	353	32	52.5	29	21	AA615454	TCR beta V-N-J reg
281	35	57.4	11	22	AA696883	Chimeric analgesic	354	32	52.5	53	22	AA687377	Human gene 36 enco
282	35	57.4	11	22	AA650313	Previn peptide #5.	355	32	52.5	53	22	AA687407	Human gene 36 enco
283	35	57.4	96	19	AA698597	H. pylori GHPO 124	356	32	52.5	53	22	AA687408	Human gene 36 enco
284	35	57.4	128	19	AA648949	Preprotachykinin-C	357	32	52.5	54	21	AA628048	Human secreted pro
285	35	57.4	130	18	AA633902	Streptococcus pneu	358	32	52.5	54	22	AA675548	Human secreted pro
286	35	57.4	130	22	AA663008	Amino acid sequenc	359	32	52.5	112	22	AA623547	Human EST encoded
287	35	57.4	143	21	AA658600	Arabidopsis thalia	360	32	52.5	126	22	AA632312	Peptide #6349 enco
288	35	57.4	185	21	AA658599	Arabidopsis thalia	361	32	52.5	127	21	AA641066	Human OREF ORF830
289	35	57.4	195	21	AA658598	Arabidopsis thalia	362	32	52.5	128	20	AA637734	Protein involved i
290	35	57.4	250	21	AA656820	Arabidopsis thalia	363	32	52.5	136	21	AA625444	Pinus radiata cell
291	35	57.4	250	21	AA659507	Arabidopsis thalia	364	32	52.5	155	20	AA694272	Rat-derived eosino
292	35	57.4	296	21	AA656819	Arabidopsis thalia	365	32	52.5	181	18	AA623667	Tobacco polyphenol
293	35	57.4	296	21	AA659506	Arabidopsis thalia	366	32	52.5	181	20	AA697990	Tobacco polyphenol
294	35	57.4	304	21	AA656818	Arabidopsis thalia	367	32	52.5	209	22	AA699984	Chick limb deforma
295	35	57.4	311	21	AA659505	Arabidopsis thalia	368	32	52.5	232	21	AA638330	Human secreted pro
296	35	57.4	311	21	AA614238	Human novel protei	369	32	52.5	276	18	AA621195	Lipolytic enzyme/E
297	35	57.4	496	18	AA633901	Streptococcus pneu	370	32	52.5	293	21	AA674880	Neisseria meningit
298	35	57.4	496	22	AA663007	Amino acid sequenc	371	32	52.5	294	21	AA674878	Neisseria gonorrhoe
299	35	57.4	1092	21	AA652029	M. thermotutotroph	372	32	52.5	294	21	AA674879	Neisseria meningit
300	35	57.4	1092	21	AA651658	Methanobacter sp.	373	32	52.5	305	21	AA616920	Arabidopsis thalia
301	35	57.4	1279	22	AA639101	Human polyptide	374	32	52.5	305	21	AA623413	Arabidopsis thalia
302	35	57.4	1305	22	AA640887	Human tachykinin a	375	32	52.5	305	21	AA645709	Arabidopsis thalia
303	34	55.7	6	20	AA692712	Human tachykinin a	376	32	52.5	323	21	AA616919	Arabidopsis thalia

377	32	52.5	323	21	AAG23412	Arabidopsis thalia	450	31	50.8	208	22	AAW04463	Peptide #3145 enco
378	32	52.5	323	21	AAG45708	Arabidopsis thalia	451	31	50.8	249	22	AAW40179	Human polypeptide
379	32	52.5	323	21	AAG45713	Arabidopsis thalia	452	31	50.8	249	22	AAB94506	Human polypeptide
380	32	52.5	381	20	AAV33944	Soluble interleukin	453	31	50.8	249	22	AAW44412	Amino acid sequenc
381	32	52.5	381	20	AAG26698	Arabidopsis thalia	454	31	50.8	264	15	AAR60610	Tobamovirus moveme
382	32	52.5	402	22	AAU00427	Caenorhbditis ele	455	31	50.8	264	16	AAR67755	Tomv P30 elictor.
383	32	52.5	418	20	AAV35520	Chlamydia pneumoni	456	31	50.8	266	21	AAB18251	Plasmodium falcipar
384	32	52.5	433	21	AAG29013	Arabidopsis thalia	457	31	50.8	281	22	AAU12198	Human PRO1341 poly
385	32	52.5	452	21	AAG29012	Arabidopsis thalia	458	31	50.8	298	21	AAB07469	A human leucine-ri
386	32	52.5	462	22	AAB74596	Murine macrophage	459	31	50.8	307	21	AAV56059	HTLV-1 Tax/HLA-A2
387	32	52.5	462	22	AAB49983	Murine macrophage	460	31	50.8	307	21	AAV56083	HTLV tax/HLA-A2 re
388	32	52.5	464	20	AAV35231	Protein involved 1	461	31	50.8	307	21	AAV56086	HTLV tax/HLA-A2 re
389	32	52.5	479	21	AAG45712	Arabidopsis thalia	462	31	50.8	307	21	AAV57859	TCR beta chain and
390	32	52.5	484	21	AAG45711	Arabidopsis thalia	463	31	50.8	307	21	AAV57862	TCR beta chain and
391	32	52.5	508	22	AAB82317	Human immunoglobul	464	31	50.8	307	21	AAV57868	TCR beta chain and
392	32	52.5	531	21	AAG29011	Arabidopsis thalia	465	31	50.8	316	17	AAW05517	HCMV Toledo strain
393	32	52.5	614	20	AAV17905	Pseudomonas alpha-	466	31	50.8	349	22	AAU03566	Pseudomonas fluore
394	32	52.5	614	20	AAV17906	Pseudomonas alpha-	467	31	50.8	372	22	AAB94062	Human protein sequ
395	32	52.5	614	20	AAV17907	Pseudomonas alpha-	468	31	50.8	389	22	AAB94732	Human protein sequ
396	32	52.5	614	20	AAV17908	Pseudomonas alpha-	469	31	50.8	393	20	AAV35055	Chlamydia pneumoni
397	32	52.5	614	20	AAV17909	Pseudomonas alpha-	470	31	50.8	399	22	AAB93773	Human protein sequ
398	32	52.5	614	20	AAV17904	Pseudomonas alpha-	471	31	50.8	406	12	AAAR11349	Cytochrome enzyme
399	32	52.5	632	12	AAAR15470	Maltopentase synt	472	31	50.8	447	22	AAAB95485	Human protein sequ
400	32	52.5	712	22	AAAR18088	Peptide #4522 enco	473	31	50.8	466	21	AAAR7880	M. tuberculosis an
401	32	52.5	750	21	AAG45696	Arabidopsis thalia	474	31	50.8	477	22	AAAG3231	C glutamicum prote
402	32	52.5	766	20	AAV13457	Amino acid sequenc	475	31	50.8	477	22	AAB79682	Corynebacterium gl
403	32	52.5	768	21	AAG45695	Arabidopsis thalia	476	31	50.8	479	17	AAW04723	Aromatic acyl tran
404	32	52.5	804	21	AAB25515	Pinus radiata cell	477	31	50.8	491	21	AAAB08899	Human secreted ox
405	32	52.5	828	21	AAB25559	Pinus radiata cell	478	31	50.8	512	22	AAU02834	Taxus canadensis p
406	32	52.5	843	21	AAB25518	Pinus radiata cell	479	31	50.8	530	21	AAB29626	Cat flea HMT synap
407	32	52.5	1197	21	AAV57445	Mouse Esez2 protein	480	31	50.8	547	22	AAB92957	Human protein sequ
408	32	52.5	1291	20	AAV16101	Acetobacter xylinu	481	31	50.8	566	18	AAW11217	Leishmania tropica
409	32	52.5	1658	21	AAV57450	Mouse Esez2 protei	482	31	50.8	566	20	AAW70212	Leishmania antigen
410	32	52.5	2243	22	AAB84884	Murine protein, SE	483	31	50.8	566	20	AAV45167	Arabismania tropica
411	32	52.5	2266	22	AAB84885	Human protein, SEQ	484	31	50.8	593	21	AAAG13870	Arabisopsis thalia
412	32	52.5	2502	22	AAB82665	Porcine reproducti	485	31	50.8	593	21	AAAG16880	Arabisopsis thalia
413	31	50.8	7	3	AAAR20310	Ty78-SP5-11. Synt	486	31	50.8	612	21	AAAG13869	Arabisopsis thalia
414	31	50.8	8	19	AAAR80322	Sequence of neurop	487	31	50.8	612	21	AAAG13869	Arabisopsis thalia
415	31	50.8	8	19	AAAR50970	Substance P analog	488	31	50.8	631	10	AAAP91139	Human type IV coll
416	31	50.8	10	19	AAAR48951	Tachykinin peptide	489	31	50.8	631	10	AAAP91139	Human type IV coll
417	31	50.8	16	17	AAAR01448	Leucocyte O2- prod	490	31	50.8	631	11	AAAR07350	Human type IV matr
418	31	50.8	16	19	AAAR75724	Proline/Arginine r	491	31	50.8	631	11	AAAR07969	Complete type IV c
419	31	50.8	19	17	AAAR01452	Leucocyte O2- prod	492	31	50.8	631	19	AAAR41226	Human mature metrl
420	31	50.8	23	17	AAAR01451	Leucocyte O2- prod	493	31	50.8	644	22	AAAR20490	Human matrix metrl
421	31	50.8	26	17	AAAR01447	Leucocyte O2- prod	494	31	50.8	660	11	AAAR06420	Amino acid sequenc
422	31	50.8	26	19	AAAR75723	Proline/Arginine r	495	31	50.8	660	22	AAB84607	Chicken matrix met
423	31	50.8	27	21	AAAR4363	Amino acid sequenc	496	31	50.8	663	19	AAAR41111	Chicken matrix met
424	31	50.8	39	14	AAAR30491	Antibacterial pept	497	31	50.8	663	19	AAAR41227	Chlamydia pneumoni
425	31	50.8	39	17	AAAR01446	Leucocyte O2- prod	498	31	50.8	778	20	AAV35090	Arabisopsis thalia
426	31	50.8	39	17	AAAR94446	Synducin peptide (499	31	50.8	874	21	AAAR41705	Arabisopsis thalia
427	31	50.8	39	17	AAAR94446	Magadalin-derived a	500	31	50.8	874	22	AAAR72287	Murine ADAMTS-9 am
428	31	50.8	39	19	AAAR57722	Proline/Arginine r	501	31	50.8	882	21	AAAR41704	Arabisopsis thalia
429	31	50.8	39	21	AAAR6888	PR-39 peptide used	502	31	50.8	950	21	AAAR41703	Arabisopsis thalia
430	31	50.8	39	22	AAAR84690	Amino acid sequenc	503	31	50.8	958	21	AAAR21255	Human metalloprote
431	31	50.8	44	22	AAAR97280	PR-39 peptide. Un	504	31	50.8	1073	21	AAAR21264	Human metalloprote
432	31	50.8	44	22	AAAR51194	E. coli AMP gene P	505	31	50.8	1765	20	AAAR41668	Rat sensory neuron
433	31	50.8	58	22	AAAR21380	Human HMPF-1 mutan	506	31	50.8	1765	20	AAAR06596	Rat sodium channel
434	31	50.8	75	22	AAAR30829	Peptide #486 enco	507	31	50.8	1765	20	AAAR06597	Rat sodium channel
435	31	50.8	80	11	AAAR07349	Fragment of human	508	31	50.8	1765	20	AAAR16372	Mouse sodium chan
436	31	50.8	85	11	AAAR07338	Fragment of human	509	31	50.8	1765	20	AAAR20122	Type 5 sodium chan
437	31	50.8	94	21	AAAR16399	Arabisopsis thalia	510	31	50.8	1765	22	AAAR20123	Rat sodium channel
438	31	50.8	103	21	AAAR16398	Arabisopsis thalia	511	31	50.8	1765	22	AAAR20124	Mouse sodium chan
439	31	50.8	136	21	AAAR33870	Arabisopsis thalia	512	31	50.8	1882	22	AAAR72286	Human ADAMTS-9 am
440	31	50.8	136	21	AAAR00558	Human secreted pro	513	31	50.8	1934	22	AAAR72301	Human ADAMTS-9 alt
441	31	50.8	136	22	AAAR16275	Peptide #2709 enco	514	31	50.8	3639	14	AAAR40227	ACV5. Actinomium
442	31	50.8	136	22	AAAR28761	Peptide #2798 enco	515	31	50.8	3712	12	AAAR13896	ACV synthetase. A
443	31	50.8	136	21	AAAR04008	Peptide #2690 enco	516	31	50.8	4472	17	AAAR97245	Virulence gene clu
444	31	50.8	139	21	AAAR33868	Arabisopsis thalia	517	31	50.8	543	12	AAAR13405	Parvo virus B19 VP
445	31	50.8	143	22	AAAR70696	S cerevisiae apopt	30.5		50.0				
446	31	50.8	143	22	AAAR70787	Human protein sequ							
447	31	50.8	197	22	AAAR93848	Peptide #3180 enco							
448	31	50.8	208	22	AAAR16746	Peptide #3271 enco							
449	31	50.8	208	22	AAAR29234								

ALIGNMENTS

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX

Sequence 11 AA;

Query Match

Best Local Similarity 91.8%; Score 56; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFGFL 10
| | | | | | | | | |
Db 1 rpkpqgffgl 10

RESULT 107

AAW92718
ID AAW92718 standard; peptide; 11 AA.

AC AAW92718;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #64.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

XX WPI; 1999-189630/16.

PS Screening for neurotoxin inhibitors - by testing compounds for their
effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 37-38; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX

Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFGFL 10
| | | | | | | | | |
Db 1 rpkpqgffgl 10

RESULT 108

AAW92667
ID AAW92667 standard; peptide; 11 AA.

AC AAW92667;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #13.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

XX WPI; 1999-189630/16.

PS Screening for neurotoxin inhibitors - by testing compounds for their
effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 15-16; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX

Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFGFL 10
| | | | | | | | | |
Db 1 rpkpqgffgl 10

RESULT 109

AAW92668
ID AAW92668 standard; peptide; 11 AA.

AC AAW92668;

XX

DT 30-APR-1999 (first entry)
 XX Human tachykinin agonist beta-amyloid peptide fragment #14.
 DE
 XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /label= NLE
 XX
 XX US5876948-A.
 PN 02-MAR-1999.
 PD
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 PS (CHIL-) CHILDRENS MEDICAL CENT.
 XX Yankner BA;
 PI
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 XX Disclosure; Column 15-16; 28pp; English.
 PS
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 XX
 SQ Sequence 11 AA;
 SO
 Query Match 91.8%; Score 56; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPKPOFFGL 10
 DB 1 rpkpqffgl 10
 DE
 XX
 XX RESULT 110
 AAM92670
 ID AAM92670 standard; peptide; 11 AA.
 XX
 XX AAM92670;
 AC
 XX
 XX 30-APR-1999 (first entry)
 DT
 XX
 XX Human tachykinin agonist beta-amyloid peptide fragment #16.
 DE
 XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /label= NLE
 XX
 XX US5876948-A.
 PN 02-MAR-1999.
 PD
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 PS (CHIL-) CHILDRENS MEDICAL CENT.
 XX Yankner BA;
 PI
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 XX Disclosure; Column 17-18; 28pp; English.
 PS
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 XX
 SQ Sequence 11 AA;
 SO
 Query Match 91.8%; Score 56; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RPKPOFFGL 11
 DB 2 rpkpqffgl 11
 DE
 XX
 XX RESULT 111
 AAM92672
 ID AAM92672 standard; peptide; 11 AA.
 XX
 XX AAM92672;
 AC
 XX
 XX 30-APR-1999 (first entry)
 DT
 XX
 XX Human tachykinin agonist beta-amyloid peptide fragment #18.
 DE
 XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /label= NLE
 XX
 XX US5876948-A.
 PN 02-MAR-1999.
 PD
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 PS (CHIL-) CHILDRENS MEDICAL CENT.
 XX Yankner BA;
 PI

FT Modified-site 1
 FT /note= "Residue is ethionine"
 XX
 XX US5876948-A.
 PN 02-MAR-1999.
 PD
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 PS (CHIL-) CHILDRENS MEDICAL CENT.
 XX Yankner BA;
 PI
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 XX Disclosure; Column 17-18; 28pp; English.
 PS
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 XX
 SQ Sequence 11 AA;
 SO
 Query Match 91.8%; Score 56; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RPKPOFFGL 11
 DB 2 rpkpqffgl 11
 DE
 XX
 XX RESULT 111
 AAM92672
 ID AAM92672 standard; peptide; 11 AA.
 XX
 XX AAM92672;
 AC
 XX
 XX 30-APR-1999 (first entry)
 DT
 XX
 XX Human tachykinin agonist beta-amyloid peptide fragment #18.
 DE
 XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note= "Residue is ethionine"
 XX
 XX US5876948-A.
 PN 02-MAR-1999.
 PD
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 PS (CHIL-) CHILDRENS MEDICAL CENT.
 XX Yankner BA;
 PI

XX WPI: 1999-189630/16.
DR Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX Disclosure: Column 17-18; 28pp; English.
PS
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPQOFGIM 11
DB 2 PKPQGFfGIM 11

RESULT 112
AAB08614
ID AAB08614 standard; Peptide; 11 AA.
XX
AC AAB08614;
XX
XX 20-DEC-2000 (first entry)
DT
XX
XX Peptide identified from a databank of polypeptides and polynucleotides.
DE
XX Precursor peptide; polypeptide hormone; peptide identification.
XX
XX Unidentified.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "hydrogen attached"
FT Modified-site 11
FT Modified-site /note= "amidated residue"
FT
XX WO200050636-A1.
PN
XX
XX 31-AUG-2000.
PD
XX
XX 24-FEB-2000; 2000WO-FR00460.
PE
XX
XX 25-FEB-1999; 99US-0257525.
PR
XX
XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX
PI Camara Ferrer YJA, Thureau C, Martinez J, BERGE G, Goze C;
XX
XX WPI: 2000-572101/53.
DR
XX
XX Identifying peptide with selected function, useful particularly for
PT C-amidated hormones, by screening database for combination of nucleic
PT acid and amino acid sequences -
XX
XX
PS Disclosure: Page 22; 40pp; French.
XX
XX The specification describes a method for identifying a peptide having
CC a particular function. The method comprises preparing a database of

CC polynucleotides and polypeptides of unknown functions, screening the
CC database for a combination of nucleotides or amino acids indicative of
CC the peptide with a particular function, and identifying polynucleotides
CC and proteins which contain the peptide. The method is used to identify
CC precursor peptides with an amidated C-terminus, especially polypeptide
CC hormones, for studying physiologically active substances. The present
CC sequence represents a peptide which was identified using the method of
CC the invention.
XX
SQ Sequence 11 AA;

Query Match 91.8%; Score 56; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPQOFGIM 11
DB 2 PKPQGFfGIM 11

RESULT 113
AAB99350
ID AAB99350 standard; peptide; 11 AA.
XX
AC AAB99350;
XX
XX 24-AUG-2001 (first entry)
DT
XX
XX Substance P tachykinin-related peptide SEQ ID NO:3.
DE
XX
XX Tachykinin-related peptide; substance P; neurokinin A; neurokinin B;
KW physiologically active; tachykinin; drug; veterinary medicine;
KW agrochemical.
XX
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 11 /note= "amidated"
FT
XX WO200134637-A1.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 07-NOV-2000; 2000WO-JP07789.
PE
XX
XX 08-NOV-1999; 99JP-0317535.
PR
XX
XX (SUNR) SUNTORY LTD.
PA
XX Ikeda T, Nomoto K, Minakata H;
PI
XX
XX WPI: 2001-329069/34.
DR
XX
XX Synthesis of new physiologically-active peptide analogs of tachykinin,
PT useful as drugs, veterinary medicines and agrochemicals, comprises
PT modifying C-terminal amino-acid residues -
XX
XX
PS Claim 13; Page 23; 36pp; Japanese.
XX
XX The present invention describes a method for producing physiologically
CC active substances. The method comprises converting the amino-acid
CC residue at a specific position in a peptide into another amino-acid
CC residue to provide activity against (in)vertebrates. Also described are:
CC (1) converted unnatural tachykinin-related peptide with tachykinin-like
CC physiological activity against (in)vertebrates which is an amino-acid
CC sequence with the 5 amino-acids at C-terminal as in
CC -Phe-AAI-Gly-AA2-Met-NH2 (1) where AAI = Val, Ile, Phe, Tyr, His, Met,
CC Thr, Leu, Gly or Gln and AA2 = Ser, Ala, Val, Met, Thr, Pro or Leu; and
CC (2) drugs, veterinary medicines or agrochemicals containing the new
CC tachykinin-related peptide as the active ingredient. The peptide
CC analogues are for use as drugs, veterinary medicines and agrochemicals

CC With activity on vertebrates or invertebrates. By modifying C-terminal
CC amino-acid residues of tachykinin, the activity of tachykinin and its
CC related derivative can therefore be changed from that against
CC vertebrates to that on invertebrates or vice versa. The present sequence
CC represents a specifically claimed tachykinin-related peptide from the
CC present invention.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQPFGL 10
| | | | | | | | | |
Db 1 rpkpqgffgl 10

RESULT 114

AAR21939

ID AAR21939 standard; Protein: 11 AA.

XX AAR21939;

XX 25-JUN-1992 (first entry)

XX Substance P [1le 8].

DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI: 1992-079804/10.

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with an
CC isoleucine residue substituted at position 8. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.

XX See also AAR21932-75.

XX Sequence 11 AA;

Query Match 90.2%; Score 55; DB 13; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQPFGLM 11

Db | | | | | | | | | |
1 rpkpqgffglm 11

RESULT 115

AAR21943

ID AAR21943 standard; Protein: 11 AA.

XX AAR21943;

XX 25-JUN-1992 (first entry)

XX Substance P [Met 7].

DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI: 1992-079804/10.

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a
CC methionine residue substituted at position 7. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.

XX See also AAR21932-75.

XX Sequence 11 AA;

Query Match 90.2%; Score 55; DB 13; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0031;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQPFGLM 11
| | | | | | | | | |
Db 1 rpkpqgmfglm 11

RESULT 116

AAR21949

ID AAR21949 standard; Protein: 11 AA.

XX AAR21949;

XX 25-JUN-1992 (first entry)

XX Substance P [Pro 3].

DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW

XX syndrome; hereditary cerebral haemorrhage.
OS Synthetic.
XX W09202248-A.
XX 20-FEB-1992.
XX 29-JUL-1991; 91WO-US05323.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
XX WPI: 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Down's syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Proline
XX residue substituted at position 3. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA:
SQ
Query Match 90.2%; Score 55; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOQFFGLM 11
DB 1 rpppqgffglm 11
RESULT 117
AAR21958
ID AAR21958 standard; Peptide: 11 AA.
XX
XX AAR21958;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Ala 9] or [D-Ala 9].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "either L or D form"
XX
XX W09202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX

XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI: 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Down's syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with an Ala (D/L)
XX residue substituted at position 9. The peptide was synthesised
XX by standard solid phase synthesis. Neuronal accumulation of
XX beta-amyloid may be treated by administration of tachykinin
XX agonists. The peptide can reduce the neurotoxic effects of a beta-
XX amyloid related polypeptide on cultured neurons. The peptide and
XX its analogues are useful for controlling diseases characterised by
XX beta amyloid accumulation in the brain such as Alzheimer's disease
XX and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA:
SQ
Query Match 90.2%; Score 55; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOQFFGLM 11
DB 1 rpkpqgffglm 11
RESULT 118
AAW92669
ID AAW92669 standard; peptide: 11 AA.
XX
XX AAW92669;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #15.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI: 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 17-18; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
XX

CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||11111111
Db 1 rpkpqgffglm 11

RESULT 119

AAW92671
ID AAW92671 standard; peptide; 11 AA.

XX
AC AAW92671;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #17.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

OS
XX US5876948-A.

XX
PD 02-MAR-1999.

XX
PF 27-JUL-1991; 91US-0737371.

XX
PR 29-JUL-1991; 91US-0737371.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MEDICAL CENT.

XX
PI Yankner BA;

XX
DR WPI; 1959-189630/16.

XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX
PS Disclosure; Column 17-18; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||11111111
Db 1 rpkpqgffglm 11

RESULT 120

AAW92673
ID AAW92673 standard; peptide; 11 AA.

XX
AC AAW92673;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #19.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

OS
XX US5876948-A.

XX
PD 02-MAR-1999.

XX
PF 27-JUL-1991; 91US-0737371.

XX
PR 29-JUL-1991; 91US-0737371.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MEDICAL CENT.

XX
PI Yankner BA;

XX
DR WPI; 1959-189630/16.

XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX
PS Disclosure; Column 17-18; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||11111111
Db 1 rpkpqgffglm 11

RESULT 121

AAW92674
ID AAW92674 standard; peptide; 11 AA.

XX
AC AAW92674;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #20.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
PI WPI: 1999-189630/16.
DR
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure: Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
1111111111
DB 1 rpkpqgfalm 11

RESULT 122
AAW92675
ID AAW92675 standard; peptide; 11 AA.
XX
AC AAW92675;
XX
DF 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #21.
DE
XX Tachykinin-agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 9
FT /note="D-form residue"
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX

PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
PI WPI: 1999-189630/16.
DR
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure: Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
1111111111
DB 1 rpkpqgfalm 11

RESULT 123
AAB49755
ID AAB49755 standard; peptide; 11 AA.
XX
AC AAB49755;
XX
DF 17-APR-2001 (first entry)
XX
XX Complex sugar bound peptide (SBP) amino acid sequence.
DE
XX Sugar peptide complex; SBP; sugar bound peptide; enzymatically stable.
KW
XX Synthetic.
OS
XX JP2000319297-A.
PN
PD 21-NOV-2000.
XX
PF 30-MAR-1999; 99JP-0088030.
XX
PR 30-MAR-1999; 99JP-0088030.
XX
PA (NOGK) 2H NOGUCHI KENKYUSHO.
XX
DR WPI: 2001-184996/19.
XX
XX A process for preparation of enzymically stable sugar peptide complex
PT
PT Example 2; Page 3; App; Japanese.
PS
XX This invention relates to a process for the preparation of an
CC enzymatically stable sugar peptide complex, and includes an in vivo
CC stable inhibitor of peptide-N-glycanase (EC. 3.5.1.52). The process can
CC be used for the investigation of in vivo reciprocal recognition of

CC cell-cell and substrate-receptor interaction, and their metabolism. The
CC present sequence represents a complex sugar bound peptide (SBP) amino
CC acid sequence prepared by the process of the invention.
XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0031;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
:|||||
Db 1 krpqgffglm 11

RESULT 124

AAR21940
ID AAR21940 standard; Protein: 11 AA.

XX
AC AAR21940;

XX 25-JUN-1992 (first entry)

XX Substance P [Pro 10].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI: 1992-079804/10.

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

PS Claim 10; Page 21; 35pp; English.

CC The peptide is the tachykinin agonist substance P with a Proline
CC residue substituted at position 10. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.

XX
SQ Sequence 11 AA;

Query Match 88.5%; Score 54; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 rpkpqgffglm 11

RESULT 125
AAR42647
ID AAR42647 standard; peptide: 11 AA.

XX
AC AAR42647;

XX 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide.

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
KW hormone; intra-operativ; tumour; low energy gamma photon;
KW radionuclide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 9 /label= Megly

FT Modified-site 11 /note= "Met is Met(O2); the C-terminal is amidated"

XX WO9318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALINCRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI: 1993-320461/40.

PT Intra-operatively detecting and locating tumour tissues - using
PT specific peptide(s) labelled with low energy gamma photon
PT emitting radionuclide

XX Disclosure; Page 5; 31pp; English.

CC The method of intraoperatively detecting and locating tumoral
CC tissues makes use of peptides having selective neurokinin 1
CC receptor affinity (AAR42644: generic formula: AAR42646-R42650:
CC specific examples), peptides having selective somatostatin
CC receptor affinity (AAR42645: generic formula: AAR42651-R42660:
CC specific examples), and peptides selected from cytokines,
CC growth factors and hormones.

XX
SQ Sequence 11 AA;

Query Match 88.5%; Score 54; DB 14; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 rpkpqgffglm 11

RESULT 126

AAM92716
ID AAM92716 standard; peptide: 11 AA.

XX
AC AAM92716;

XX 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #62.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX Homo sapiens.
XX US5876948-A.
XX PD 02-MAR-1999.
XX PF 27-JUL-1991; 91US-0737371.
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI: 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 37-38; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 88.5%; Score 54; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGLM 11
DT ||||| 1
DB 1 rpkpqgfpgm 11

RESULT 127
AAW92721
ID AAW92721 standard; peptide; 11 AA.
XX
XX AAW92721;
XX AC
XX DT 30-APR-1999 (first entry)
XX DE Human tachykinin agonist beta-amyloid peptide fragment #67.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
XX Homo sapiens.
XX OS
XX PA Key Location/Qualifiers
XX PH Modified-site 11
XX FT /label= Memet
XX FT /note= "N-methyl-methionine"
XX PN US5876948-A.
XX PD 02-MAR-1999.
XX

PF 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX PA
XX PI Yankner BA;
XX DR WPI: 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 39-40; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 88.5%; Score 54; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGLM 11
DT ||||| 1
DB 1 rpkpqgfpgm 11

RESULT 128
AAB91451
ID AAB91451 standard; Peptide; 10 AA.
XX
XX AAB91451;
XX AC
XX DT 22-JUN-2001 (first entry)
XX DE Tachykinins peptide SEQ ID NO:627.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX OS Synthetic.
XX PN WO200069900-A2.
XX PD 23-NOV-2000.
XX PF 17-MAY-2000; 2000WO-US13576.
XX PR 17-MAY-1999; 99US-0134406.
XX PR 10-SEP-1999; 99US-0153406.
XX PR 15-OCT-1999; 99US-0159783.
XX PA (CONJ-) CONJUCHEM INC.
XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX DR WPI: 2001-112059/12.
XX PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PT -
XX
PS Disclosure: Page 403; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases.
CC Intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
S0 Sequence 10 AA:

Query Match 86.9%; Score 53; DB 22; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
1111111111
Db 1 rpkpqfgy1 10

RESULT 129
AAB80315
ID AAB80315 standard; protein: 11 AA.
XX
AC AAB80315;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide antagonist C which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist C.
XX
OS Swiss 3T3 cells.
XX
FH Key Location/Qualifiers
FT MISC-difference 2 /label=OTHER
FT /note="DPro"
FT MISC-difference 7 /label=OTHER
FT /note="DPhe"
FT MISC-difference 1 /label=OTHER
FT /note="DTrp"
FT MISC-difference 11 /label=OTHER
FT /note="Met-NH2"
XX
PN W08807551-A.
XX
PD 06-OCT-1988.
XX
PF 31-MAR-1988; 88WO-GB00255.
XX
PR 25-NOV-1987; 87GB-0027638.
XX

PA (IMCR) IMPERIAL CANCER RES.
XX
PI Rosengurt E, Zachary I, Woll P;
XX
DR WPI: 1988-292842/41.
XX
PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
PS Disclosure: Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
XX cells which binds selectively with polypeptides of the bombesin type and
XX binds with antagonist A and antagonist D. Antagonist A is a
XX commercially available structural variant of substance P, known as
XX [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
XX [D-Pro2] spantide. Antagonist B is also commercially available structural
XX variant of substance P, known as [D-Phe5] spantide. Substance P is an
XX 11-mer neuropeptide, of interest in studies in pain transmission. Ten
XX substance P antagonists (see AAB80313-80322) were tested for their
XX ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
XX of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
XX potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
XX potent than either A or D. Spantide (B) had no antagonist activity even
XX at 100 uM. Polypeptide antagonists A and D and novel variants are useful
XX for diagnosis and therapy, esp. of cancers where uncontrolled cell
XX growth is associated with disorders of proteins of the bombesin family.
S0 Sequence 11 AA:

Query Match 86.9%; Score 53; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
1111111111
Db 1 rpkpqffwlm 11

RESULT 130
AAB80320
ID AAB80320 standard; protein: 11 AA.
XX
AC AAB80320;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide antagonist H which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist H.
XX
OS Swiss 3T3 cells.
XX
FH Key Location/Qualifiers
FT MISC-difference 1 /label=OTHER
FT /note="DArg"
FT MISC-difference 2 /label=OTHER
FT /note="DPro"
FT MISC-difference 7 /label=OTHER
FT /note="DPhe"
FT MISC-difference 9 /label=OTHER
FT /note="DHis"
FT MISC-difference 11 /label=OTHER
FT

FT /note="Met-NH2"
XX
PN WO8807551-A.
XX
PD 06-OCT-1988.
XX
XX 31-MAR-1988; 88WO-GB00255.
XX
PR 25-NOV-1987; 87GB-0027638.
XX
PA (IMCR) IMPERIAL CANCER RES.
XX
PI Rosengurt E, Zachary I, Moll P;
XX WPI; 1988-292842/41.
DR
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, I and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||
Db 1 rpkpqgffhlm 11

RESULT 131
AAR21935
ID AAR21935 standard; Protein; 11 AA.
XX
AC AAR21935;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Pro 9] or [D-Pro 9].
XX
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /note="either L or D form"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.

XX
PF 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Pro (D/L)
CC residue substituted at position 9. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21932-75.
SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||
Db 1 rpkpqgffhlm 11

RESULT 132
AAR21964
ID AAR21964 standard; Peptide; 11 AA.
XX
AC AAR21964;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [D-Ala 4].
XX
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4 /note="D form"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX
PS Claim 13; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D-Ala
CC residue substituted at position 4. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21932-75.
XX
XX
SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 rpkpqffglm 11

RESULT 133
AAW50978
ID AAW50978 standard; peptide; 11 AA.
XX
XX AAW50978;
XX
DT 31-JUL-1998 (first entry)
XX
XX Substance P analogue [D-Arg1,D-Pro2,D-Phe7,D-His9].
XX
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX Substance P; cancer; inhibition; growth hormone releasing factor;
XX spantide.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
FH MISC-difference 1 /note= "D-form residue"
FT MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
FT
XX EP835662-A2.
XX PN
XX PD 15-APR-1998.
XX
XX PE 11-DEC-1996; 96EP-0309012.
XX
XX PR 08-OCT-1996; 96US-0727679.
XX PR 16-AUG-1996; 96IN-0001822.
XX
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX
XX PI Jaggi M, Mukherjee R;
XX DR WPI: 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,

PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX
PS Disclosure; Page 13; 49pp; English.
XX
CC The invention relates to a new composition which comprises: (1) the
CC somatostatin analogue SOM2 ACCKNPFDWKTRPSQC (3-14 disulphide bridge),
CC and (11) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
XX
SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 rpkpqffglm 11

RESULT 134
AAW50968
ID AAW50968 standard; peptide; 11 AA.
XX
XX AAW50968;
XX
DT 31-JUL-1998 (first entry)
XX
XX Substance P analogue, [D-Pro2,D-Phe7,D-Tip9].
XX
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX Substance P; cancer; inhibition; growth hormone releasing factor;
XX spantide.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
FH MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT MISC-difference 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
FT
XX EP835662-A2.
XX PN
XX PD 15-APR-1998.
XX
XX PE 11-DEC-1996; 96EP-0309012.
XX
XX PR 08-OCT-1996; 96US-0727679.
XX PR 16-AUG-1996; 96IN-0001822.
XX
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX
XX PI Jaggi M, Mukherjee R;
XX DR WPI: 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,

XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
PS
XX Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (1) the
CC somatostatin analogue SOM2 AGCKNFRDKMTPTSDC (3-14 disulphide bridge),
CC and (11) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
||||||| 11
Db 1 rpkpqgfflwm 11

RESULT 135
AAW92677

ID AAW92677 standard; peptide; 11 AA.

XX AAW92677;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #23.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX Homo sapiens.

OS

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PS 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA.

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 19-20; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
||||||| 11
Db 1 rpkpqgfflwm 11

RESULT 136
AAW92678

ID AAW92678 standard; peptide; 11 AA.

XX AAW92678;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #24.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX Homo sapiens.

OS

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PS 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA.

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 19-20; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | | | | | | | |
Db 1 rpkpqgfflpm 11

RESULT 137

AAB98879
ID AAB98879 standard; Peptide; 11 AA.

AC AAB98879;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #35.

KM Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.

OS Synthetic.

FX Key Location/Qualifiers

FT Misc-difference 2 /note- "D-form residue"

FT Misc-difference 7 /note- "D-form residue"

FT Misc-difference 9 /note- "D-form residue"

FT Modified-site 11 /label= OTHER

FT /note= "C-terminal amide"

PN W020013C371-A2.

PD 03-MAY-2001.

PF 27-OCT-2000; 2000MO-US29789.

PR 28-OCT-1999; 99US-0428692.

PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

DR WPI; 2001-397593/42.

PT New chimeric peptides used for treating pain comprise opioid receptor

PS binding group and nociceptive receptor binding group

CC Claim 10; Page 15; 34pp; English.

CC The present invention describes a number of chimeric peptides comprising

CC an opioid receptor binding moiety and a nociceptive receptor binding

CC moiety. These can be used as analgesics for the treatment of pain. Unlike

CC opioid receptor based peptides alone, tolerance does not result from

CC their long-term use. The present sequence is one of the peptides of the

CC invention.

SQ Sequence 11 AA;

OY 1 RPKPOQFFGLM 11
| | | | | | | | | | | |
Db 1 rpkpqgfflpm 11

RESULT 138
AAB91411
ID AAB91411 standard; Peptide; 11 AA.

AC AAB91411;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:587.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimidyl; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN W0200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000MO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 392; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases.

CC Intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | | | | | | | |
Db 1 rpkpqgfflpm 11

RESULT 139

AAB91412
ID AAB91412 standard; Peptide; 11 AA.

```

AC AAB91412;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:588.
XX
KM protection; endogenous therapeutic peptide; peptidase; conjugation;
RW blood component; modification; succinimideyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO20069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure: Page 392; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimideyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
XX
OY Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 RPKPOOFFGLM 11
1 ||||||| 11
1 rpkpqgffwlm 11
XX
RESULT 140.
AAB91415
ID AAB91415 standard; peptide; 11 AA.
XX
AC AAB91415;
XX
DT 22-JUN-2001 (first entry)
XX
```

KW	Tachykinins peptide SEQ ID NO:591.
DE	Protection; endogenous therapeutic peptide; peptidase; conjugation;
XV	blood component; modification: succinimidyl; maleimido group; amino;
XX	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS	Homo sapiens.
SX	Synthetic.
PN	WO20069900-A2.
PD	23-NOV-2000.
PF	17-MAY-2000; 2000WO-US13576.
PR	17-MAY-1999; 99US-0134A06.
PR	10-SEP-1999; 99US-0153A06.
PA	15-OCT-1999; 99US-0159783.
(CONJ -)	CONTUCHEM INC.
Bridon DP,	Ezrin AM, Milner PG, Holmes DL, Thibaudau K:
WPI:	2001-112059/12.
Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity	-
Disclosure:	Page 393; 733pp; English.
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptide stablestabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.	
Sequence	11 AA;
Query Match	86.9%; Score 53; DB 22; Length 11;
Best Local Similarity	90.9%; Pred. No. 0.0069;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 RPKPOQFFGLM 11
I I I I I I I I I	
DB	1 rpkpqgfpflm 11
RESULT 141	
AAB91429	
ID	AAB91429 standard: Peptide; 11 AA.
AC	AAB91429;
DT	22-JUN-2001 (first entry)
Tachykinins peptide SEQ ID NO:605.	
Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification: succinimidyl; maleimido group; amino;	

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure: Page 397; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases.
CC Intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence: 11 AA;
XX

Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 RPKPOFFGLM 11
DB 1 rpkpqgfflpm 11
XX

RESULT 142
AAB50311
ID AAB50311 standard; peptide: 11 AA.
XX
AC AAB50311;
XX
DT 08-MAR-2001 (first entry)
XX
DE Previn peptide #3.
XX
KW Asian tcd; antibacterial; Botulinum toxin inhibitor; BtxB;
KW previn; tetanus neurotoxin; buforinin.
XX
OS Bufo bufo gargarizans.
OS Synthetic.
XX

PN WO200069891-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US13215.
XX
PR 17-MAY-1999; 99US-0134446.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;
XX
DR WPI; 2001-025001/03.
XX
PT Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins -
XX
PS Claim 7; Page 29; 47pp; English.
XX
CC The present sequence is a previn compound which inhibits the enzymatic
CC activity of BtxB and tetanus neurotoxins. Previn
CC may be used to construct compounds such as buforinins.
XX
SQ Sequence: 11 AA;
XX

Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 RPKPOFFGLM 11
DB 1 rpkpqgfflpm 11
XX

RESULT 143
AAB98880
ID AAB98880 standard; peptide: 12 AA.
XX
AC AAB98880;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #36.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH FT Misc-difference 2
FT FT Misc-difference 7
FT FT Misc-difference 7
FT FT Misc-difference 9
FT FT Misc-difference 9
FT FT Modified-site 12
FT FT /label= OTHER
FT FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AM, Kream R, Misicka-Kesik A;
XX

DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15-16; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
an opioid receptor binding moiety and a nociceptive receptor binding
moiety. These can be used as analgesics for the treatment of pain. Unlike
opioid receptor based peptides alone, tolerance does not result from
their long-term use. The present sequence is one of the peptides of the
invention.
CC
CC
SQ Sequence 12 AA;

Query Match 86.9%; Score 53; DB 22; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 11
1111111111
DB 1 rpkpqgffwlm 11

RESULT 144
AAR21932
ID AAR21932 standard; peptide; 9 AA.
XX
AC AAR21932;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P (1-9) fragment.
XX
KM Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
tachykinin agonists e.g. substance P, physalamin and neurokinin
B, for treating Alzheimer's disease, Down's syndrome, etc.
PT
PS Claim 9; Page 21; 35pp; English.
XX
CC The peptide is a tachykinin agonist consisting of residues 1-9 of
substance P. The peptide was synthesised by standard solid phase
synthesis. Analogues of the peptide, with C-terminal deletions down
to substance P (1-4) were also synthesised. Neuronal accumulation of
beta-amyloid may be treated by administration of these tachykinin
agonists. The peptides reduce the neurotoxic effects of a beta-
amyloid related polypeptide on cultured neurons. The peptide and
its analogues are useful for controlling diseases characterised by
beta amyloid accumulation in the brain such as Alzheimer's disease
and Down's syndrome.
CC
CC See also AAR21933-75.
XX

SQ Sequence 9 AA;

Query Match 85.2%; Score 52; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQGFPG 9
1111111111
DB 1 rpkpqgffg 9

RESULT 145
AAY03162
ID AAY03162 standard; peptide; 9 AA.
XX
AC AAY03162;
XX
DT 10-JUN-1999 (first entry)
XX
DE Substance P fragment P/1-9#.
XX
KM Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
PF 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
XX
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Kream RM;
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence is a fragment of substance P used in the method of the
invention. The method is for enhancing opioid analgesia within a human
subject for a duration of 15 minutes comprises concurrent administration
of substance P, or one of its precursors. The method is used to elicit
opioid analgesia and anaesthesia, either prior to or after the occurrence
of a nociceptive event. The components have a synergistic effect. The
method allows use of low doses of opioid that produce little or no
physiological effect reducing conventional risks of toxicity and
addiction, and allows the use of low doses of substance P and its related
analogs that limit their in vivo physiological consequences. The
analogs that limit their in vivo physiological consequences. The
analogs that limit their in vivo physiological consequences. The
elimination of opioid analgesia if desired and on demand. The treatment
provides a durable analgesic effect, but only minimally disturbs and
interrupts the normal metabolic processes of the body.
CC
CC
SQ Sequence 9 AA;

Query Match 85.2%; Score 52; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQGFPG 9
1111111111
DB 1 rpkpqgffg 9

RESULT 146
AAW92665
ID AAW92665 standard; peptide; 9 AA.
XX
AC AAW92665;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #11.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 15-16; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congenital angiodystrophy with cerebral
XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
XX
SQ Sequence 9 AA:
XX
Query Match 85.2%; Score 52; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RPKPQGFEG 9
Db 1 rpkpqgffg 9
IIIIIIIIII
RESULT 147
AAG62780
ID AAG62780 standard; peptide; 9 AA.
XX
AC AAG62780;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a substance P fragment.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Unidentified.
XX

PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-US01529.
XX
XX 19-JAN-2000; 2000US-0489667.
XX
XX (ALLR) ALLERGAN SALES INC.
XX
XX Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
XX component) attached to a targeting moiety
XX
PS Disclosure; Page 72; 77pp; English.
XX
XX The specification describes an agent, comprising a clostridial neurotoxin
XX attached to a targeting moiety, where the targeting moiety is selected
XX from transmission compounds, and compounds substantially similar to the
XX transmission compounds. The agent may be used for treating pain, where
XX the clostridial neurotoxin component is derived from botulinum toxin
XX selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
XX The targeting moiety comprises a light chain and an amine end segment of
XX a heavy chain and comprises Substance P as the targeting moiety. The pain
XX alleviating effects persist for 2-6 months. The present sequence
XX represents a substance P fragment, and is used in the course of the
XX invention.
XX
SQ Sequence 9 AA:
XX
Query Match 85.2%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RPKPQGFEG 9
Db 1 rpkpqgffg 9
IIIIIIIIII
RESULT 148
AAB98878
ID AAB98878 standard; Peptide; 9 AA.
XX
AC AAB98878;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #34.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
XX Synthetic.
XX
XX
XX
XX
XX Key Location/Qualifiers
FT Modified-site 9 /label=OTHER
FT /note="C-terminal amide"
XX
XX W0200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX

PI Carr DB, Lipkowski AM, Kream R, Misicka-Kesik A;
XX
DR WPI: 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 85.2%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKRQQFFG 9
Db 1 rpkpqgffg 9

RESULT 149
AAB91444
ID AAB91444 standard; Peptide; 9 AA.
XX
AC AAB91444;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:620.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US13576.
XX
PR 17-MAY-1999; 9905-0134406.
PR 10-SEP-1999; 9905-0153406.
PR 15-OCT-1999; 9905-0159783.
XX
PA (CONT-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudreau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 401; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 85.2%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKRQQFFG 9
Db 1 rpkpqgffg 9

RESULT 150
AAR28443
ID AAR28443 standard; peptide; 11 AA.
XX
AC AAR28443;
XX
DT 22-MAR-1993 (first entry)
XX
DE Neurokinine 1 ligand #1.
XX
KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /label= MeGly
FT Modified-site 11
FT /label= OTHER
FT /note= "Met(O)-2-NH2"
XX
PN WO9218536-A.
XX
PD 29-OCT-1992.
XX
PF 22-APR-1992; 92MO-US03307.
XX
PR 22-APR-1991; 91EP-0200955.
XX
PA (MILCW) MALLINCKRODT MEDICAL INC.
XX
PI Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
XX
DR WPI: 1992-382047/46.
XX
PT Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX
PS Disclosure; Page 4; 22pp; English.
XX
CC This peptide or its Tyro deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain

CC tissues. See AAR28442-R28446.
XX
SQ Sequence 11 AA;

Query Match 85.2%; Score 52; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
1111111111
DB 1 rpkpqdftmlm 11

RESULT 151
AAM60208
ID AAM60203 standard; peptide; 11 AA.

XX AAM60203;

XX 18-AUG-1998 (first entry)

DE Peptide NEFL, a substrate a matrix metalloproteinase.

XX Peptide substrate; screen; matrix metalloproteinase; MMP;

KW MMP cleavage site; arthritis; periodontal disease; tumour cell invasion;

KW metastasis; identification; MMP-3.

XX Synthetic.

XX Key

FT Modified-site 1 Location/Qualifiers

FT /note= "labelled with fluorogenic group

FT 7-methoxycoumarin-4-ylacetyl"

FT Modified-site 11 /note= "lysine-2,4-dinitrophenyl quenching group"

FT US5770691-A.

PD 23-JUN-1998.

XX 05-JUN-1995; 95US-0464337.

XX 05-JUN-1995; 95US-0464337.

XX 05-JUN-1995; 95US-0464337.

XX (UNITV) UNIV KANSAS MEDICAL CENT.

XX (MINU) UNIV MINNESOTA.

XX Fields GB, Nagase H;

XX WPI; 1998-376880/32.

XX Self-quenching fluorescent peptides - useful as fluorogenic matrix

XX metalloprotease substrates

XX Disclosure: Column 9; 11pp; English.

XX AAM60206-08 represent synthetic peptide substrates that are used to

XX screen for the presence of a matrix metalloproteinase (MMP). The

XX peptides contain a MMP cleavage site, and are specific for one MMP.

XX AAM60206-07 are self-quenching fluorogenic substrates that fluoresce

XX when cleaved by MMPs. MMPs have been implicated in various diseases, e.g.

XX arthritis, periodontal disease and tumour cell invasion and metastasis.

XX It is not clear which MMPs are implicated in these diseases, and

XX identification would prove beneficial. Peptide AAM60207 is selectively

XX cleaved by MMP-3 (stromelysin 1) and can thus be used to discriminate

XX MMP-3 from other MMPs.

XX Sequence 11 AA;

Query Match 83.6%; Score 51; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RPKPOQFFGL 10
1111111111
DB 1 rpkpqdftgl 9

RESULT 152
AAY67965
ID AAY67965 standard; peptide; 11 AA.

XX AAY67965;

XX 05-APR-2000 (first entry)

DE Carboxyfluorescein cell permeant peptide #2.

XX Kaposi syndrome; fibroblast growth factor; signal peptide; PMN;

KW peptide nucleic acid; cell permeability; intracellular delivery;

KW gene therapy; cancer.

XX Unidentified.

XX Key

FT Modified-site 8 Location/Qualifiers

FT /note= "ornithine"

FT WO9964449-A2.

PD 16-DEC-1999.

XX 10-JUN-1999; 99WO-GB01848.

XX 10-JUN-1998; 98GB-0012376.

XX 10-JUL-1998; 98GB-0014888.

XX (UYBE-) UNIV QUEBENS BELFAST.

XX Nelson J, Harriott P, Wallace A;

XX WPI; 2000-097517/08.

XX New cell permeable signal peptides, useful for intracellular delivery

XX of a molecule

XX Example 1; Page 29; 33pp; English.

XX The present invention describes a cell permeable peptide comprising at

XX least the hydrophobic core of a signal peptide (or analogue) containing

XX at least 1 additional positively charged amino acid (or analogue). The

XX peptides are useful for the intracellular delivery of molecules.

XX especially peptide nucleic acids to in vivo targets. The peptides are

XX useful in commercial drug-delivery systems, in e.g. gene therapy,

XX cancer therapy and anti-infectious agent therapy. The peptides

XX facilitate biochemical and molecular biological research. The modified

XX peptides facilitate intracellular delivery of any cell-impermeable

XX substances and improve delivery into low permeability cells. Delivery

XX into sub-compartments can be achieved by modifying the signal peptides.

XX The present sequence represents a peptide used in the exemplification

XX of the present invention.

XX Sequence 11 AA;

Query Match 83.6%; Score 51; DB 21; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.015;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
1111111111
DB 1 rpkpqdftglm 11

```

RESULT 153
AAR21961
ID AAR21961 standard; Peptide: 11 AA.
XX
AC AAR21961;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [Heys 5,11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /label= OTHER
FT /note= "OTHER = homocysteine"
FT Misc-difference 11 /label= OTHER
FT /note= "OTHER = homocysteine"
XX
PN W09202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-0505323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI: 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist, substance P with
CC homocysteine substituted at positions 5 and 11, with a disulphide
CC bond formed between them making the peptide cyclic. The
CC peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA:
XX
Query Match 82.0%; Score 50; DB 13; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPOQPFGL 10
DB 111111111
1 rpkipxgffgl 10
RESULT 154
AAR21961
ID AAR21961 standard; peptide: 11 AA.
XX
AC AAR21961;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [Heys 5,11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /label= OTHER
FT /note= "OTHER = homocysteine"
FT Misc-difference 11 /label= OTHER
FT /note= "OTHER = homocysteine"
XX
PN W09202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-0505323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI: 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist, substance P with
CC homocysteine substituted at positions 5 and 11, with a disulphide
CC bond formed between them making the peptide cyclic. The
CC peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA:
XX
Query Match 82.0%; Score 50; DB 13; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPOQPFGL 10
DB 111111111
1 rpkipxgffgl 10

```

DT	30-APR-1999	(first entry)
DE	Human tachykinin agonist beta-amyloid peptide fragment #30.	
XX		
KW	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;	
KW	Alzheimer's disease; Down's syndrome; amyloidosis; human;	
XX	hereditary cerebral haemorrhage; non-inherited congenophilic anglopathy.	
OS	Homo sapiens.	
XX		
PH	Key	
FT	Modified-site	
FT	Modified-site	
FT	Modified-site	
XX		
PN	US5876948-A.	
XX		
PD	02-MAR-1999.	
XX		
PF	27-JUL-1991;	
XX		
PR	29-JUL-1991;	
PR	27-JUL-1990;	
XX		
PA	(CHIL-) CHILDRENS MEDICAL CENT.	
PI	Yankner BA;	
XX		
DR	WPI: 1999-189630/16.	
XX		
PT	Screening for neurotoxin inhibitors - by testing compounds for their	
PT	effect on beta-amyloid peptide neurotoxic effect on neuronal cells	
XX		
PS	Disclosure: Column 23-24; 28pp; English.	
XX		
CC	This invention describes a method for screening compounds for inhibiting	
CC	a neurotoxin. The method involves incubating tachykinin agonists with	
CC	neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be	
CC	used for identifying compounds for treating diseases characterised by an	
CC	undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,	
CC	Down's syndrome, and the syndromes of hereditary cerebral haemorrhage	
CC	with amyloidosis and non-inherited congenophilic anglopathy with cerebral	
CC	haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human	
CC	beta-amyloid peptide fragments.	
XX		
SO	Sequence 11 AA;	
XX		
Query Match	82.0%; Score 50; DB 20; Length 11;	
Best Local Similarity	81.8%; Pred. No. 0.022;	
Matches 9; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 RPKPQOQFGLM 11	
Db	1 rpkipxqffgxm 11	
XX		
RESULT 155		
AAW92686		
ID	AAW92686 standard; peptide; 11 AA.	
XX		
AC	AAW92686;	
XX		
DT	30-APR-1999 (first entry)	
XX		
DE	Human tachykinin agonist beta-amyloid peptide fragment #32.	
XX		
KW	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;	
KW	Alzheimer's disease; Down's syndrome; amyloidosis; human;	
KW	hereditary cerebral haemorrhage; non-inherited congenophilic anglopathy.	
OS	Homo sapiens	

XX Key Location/Qualifiers
FH Modified-site 5
FT Modified-site /note= "Residue is homocysteine"
FT Modified-site 11
FT Modified-site /note= "Residue is homocysteine"
PN US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA:
PI
XX WPI; 1999-189630/16.
DR
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PS
XX Disclosure; Column 23-24; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA:
SQ

Query Match 82.0%; Score 50; DB 20; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.022; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPOQFFGL 10
DB 1 RPKPQFFGL 10

RESULT 156
AAB91438
ID AAB91433 standard; Peptide: 11 AA.
XX
AC AAB91433;
XX
XX 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:614.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxy-; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PR 17-MAY-1999; 99US-0134406.
XX

PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX WPI; 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
XX Disclosure; Page 399; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (1)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxy/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (1) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 11 AA:
SQ

Query Match 82.0%; Score 50; DB 22; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.022; 1; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPOQFFGLM 11
DB 1 KPRPHGFTGLM 11

RESULT 157
AAR28681
ID AAR28681 standard; peptide: 22 AA.
XX
XX AAR28681;
XX
XX 22-MAR-1993 (first entry)
XX
XX Galanin(1-12)-Pro-Pro-Pro-Sp(5-11)amide (M37).
DE
XX
XX Receptor; Substance P; insulin; growth hormone;
KW acetylcholine; dopamine; somatostatin; noradrenaline;
KW endocrinology; food intake; neurology; psychiatry;
KW Alzheimer-type senile dementia; schizophrenia;
KW intestinal diseases.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..12
FT Peptide /label= galanin(1-12)
FT 16..22
FT Peptide /label= SP(5-11)
XX
XX EP514361-A.
PN
XX 19-NOV-1992.
PD
XX

PF 14-MAY-1992; 92EP-0850108.
 XX
 PR 15-MAY-1991; 91SE-0001472.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Ahren B, Barfai T, Consolo S, Hoekfelt T, Land T;
 PI Langel U, Lindskog S, Wiesenfeld-Hallin Z;
 XX
 DR WPI; 1992-384184/47.
 XX
 PR New galanin antagonist peptide(s) - used for treating
 PT Alzheimer's-type senile dementia, schizophrenia, analgesia and
 PT intestinal diseases
 XX
 PS Disclosure: Page 7; 21pp; English.
 PS
 XX The C-terminal of this peptide is amidated. MW-2392; IC50= 40nM.
 CC The peptides given in AAR26679-90 are used to treat disorders in
 CC mammals caused by the function of galanin at its receptor. The
 CC peptides may be useful in the regulation of insulin release, growth
 CC hormone release, acetylcholine release, dopamine release, substance
 CC P release, somatostatin release and noradrenaline release. They are
 CC useful in endocrinology, food intake, neurology and psychiatry, and
 CC to treat Alzheimer-type senile dementia, schizophrenia, intestinal
 CC diseases, and in analgesia. Dosage is 0.01-1000, pref. 0.1-1000
 CC microg/kg body wt.
 XX
 SQ Sequence 22 AA;
 XX

Query Match 82.0%; Score 50; DB 13; Length 22;
 Best Local Similarity 90.0%; Pred. No. 0.044; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKQOQFFGLM 11
 I | | | | | | | |
 DB 13 pppqgffgilm 22

RESULT 158
 AAP50634
 ID AAP50634 standard; Peptide; 9 AA.
 XX
 AC AAP50634;
 XX
 DT 09-MAR-1992 (first entry)
 XX
 DE Substance P-like peptide.
 XX
 KW Hair tonic; growth; regeneration.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label- pyroglutamic acid
 FT
 XX
 PN JP6020807-A.
 XX
 PD 14-OCT-1985.
 XX
 PF 28-MAR-1984; 84JP-0058390.
 XX
 PR 28-MAR-1984; 84JP-0058390.
 XX
 PA (MEIJ) MEIJI SEIKA KAISHA.
 XX
 DR WPI; 1985-293619/47.
 XX
 PT Hair tonic compsn. - comprises peptide contg. pyroglutamic acid
 PT or other aminoacid(s) residue
 XX

PS Disclosure: Page 2; 3pp; Japanese.
 XX
 CC The C-terminal is amidated. Substance P (H-RPKPEERFGLM-NH2) or
 CC this peptide derived from it can be used in aq. soln. or suspension
 CC to promote hair growth and regeneration.
 CC See also AAP50632 and AAP50633.
 XX
 SQ Sequence 9 AA;
 XX

Query Match 80.3%; Score 49; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOQFFGLM 11
 I | | | | | | | |
 DB 1 kppqgffgilm 9

RESULT 159
 AAW92714
 ID AAW92714 standard; peptide; 9 AA.
 XX
 AC AAW92714;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #60.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 37-38; 28pp; English.
 PS
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 XX
 SQ Sequence 9 AA;
 XX

Query Match 80.3%; Score 49; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOQFFGLM 11

Db 1 kpgqffglm 9

RESULT 160

AAB91446 ID AAB91446 standard; Peptide; 9 AA.

XX AAB91446;

XX 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:622.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;

KM blood component; modification; succinimidyl; maleimido group; amino;

XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PT -

PS Disclosure; Page 402; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

XX comprising a therapeutically active amino acid region (III) and a

XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

XX a less therapeutically active amino acid region (IV), which covalently

XX bonds with amino/hydroxyl/thiol groups on blood components to form a

XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth

XX factors and neurotransmitters, to protect them from peptidase activity

XX in vivo for the treatment of various disorders. Endogenous therapeutic

XX peptides are not suitable as drug candidates as they require frequent

XX administration due to rapid degradation by peptidases in the body.

XX Modifying and attaching therapeutic peptides to albumin prevents or

XX reduces the action of peptidases to increase length of activity (half

XX life) and specificity as bonding to large molecules decreases.

XX Intracellular uptake and interference with physiological processes.

XX AAB90829 to AAB92441 represent peptides which can be used in the

XX exemplification of the present invention.

XX Sequence 9 AA:

Query Match 80.3%; Score 49; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 kpgqffglm 11

Db 1 kpgqffglm 9

RESULT 161

AAB91437 ID AAB91437 standard; Peptide; 11 AA.

XX AAB91437;

XX 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:613.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;

KM blood component; modification; succinimidyl; maleimido group; amino;

XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PT -

PS Disclosure; Page 399; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

XX comprising a therapeutically active amino acid region (III) and a

XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

XX a less therapeutically active amino acid region (IV), which covalently

XX bonds with amino/hydroxyl/thiol groups on blood components to form a

XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth

XX factors and neurotransmitters, to protect them from peptidase activity

XX in vivo for the treatment of various disorders. Endogenous therapeutic

XX peptides are not suitable as drug candidates as they require frequent

XX administration due to rapid degradation by peptidases in the body.

XX Modifying and attaching therapeutic peptides to albumin prevents or

XX reduces the action of peptidases to increase length of activity (half

XX life) and specificity as bonding to large molecules decreases.

XX Intracellular uptake and interference with physiological processes.

XX AAB90829 to AAB92441 represent peptides which can be used in the

XX exemplification of the present invention.

Query Match 80.3%; Score 49; DB 22; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.033;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 kpgqffglm 11

Db 1 kpgqffglm 11

Query Match 80.3%; Score 49; DB 22; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.033;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 kpgqffglm 11

Db 1 kpgqffglm 11

AC AAR29593;
XX
DT 22-APR-1993 (first entry)
XX
DE Vertebrate Stromelysin artificial substrate.
XX
XX Enzyme inhibitors; diagnosis; screening; testing; enzyme stimulators;
KM hydrolytic enzymes; HIV protease; glycosidases; nucleases.
XX
PN EP518557-A.
XX
PD 16-DEC-1992.
XX
PF 03-JUN-1992; 92EP-0305109.
XX
PR 10-JUN-1991; 91US-0712828.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Heath WF, Lai MT, Manetta JV, Sportsman JR, Yan SCB;
PI Lai MHT;
XX
DR WPI: 1992-417420/51.
XX
XX Measurement of hydrolytic enzyme activity in large numbers of
PT samples - using resin bound substrate attached to reporter
PT molecule for easy assessment of change rate e.g. of HIV-1
PT protease
XX
XX
PS Claim 10; Page 18; 19pp; English.
XX
CC This sequence represents an artificial substrate for vertebrate
CC stromelysin. The N terminal residue may opt. be biotinylated, and
CC the C terminal opt. conjugated to FITC.
XX
SQ Sequence 13 AA;

Query Match 80.3%; Score 49; DB 13; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.039;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 11
1 :|||||1111
1 rrrpqgfglm 11

DB 1 rrrpqgfglm 11

RESULT 163
AAP30142
ID AAP30142 standard; Protein; 11 AA.
XX
AC AAP30142;
XX
XX 14-JUN-1992 (first entry)
DT
XX
DE Sequence of peptides with substance P inhibiting activity.
XX
XX Substance P antagonist; pain therapy; hypertension.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /label= D-P
FT Modified-site 7 /label= D-W
FT Misc-difference 8 /label= F,I
FT Modified-site 9 /label= D-W
FT Modified-site 11 /label= M,I
FT /note= "bonded to NH2"
XX
PN W08301251-A.

XX
PD 14-APR-1983.
XX
XX 09-OCT-1981; 81WO-DE00171.
XX
XX 09-OCT-1981; 81WO-DE00171.
PR 09-OCT-1981; 81EP-0902802.
XX
XX (FERR) FERRING ARZNEIMITTE.
PA (HORI/) HORIG J.
XX
XX
PI Horig J;
XX
DR WPI: 1983-39155K/16 (39155K).
XX
XX Undeca:peptide derivs. with substance P inhibiting activity -
PT useful for treating pain and hypertension
PT
XX
XX
PS Claim 2; Page 18; 25pp; German.
XX
XX The peptides of the invention are powerful antagonists of Substance
CC P and so are useful in human and veterinary medicine, for treating
CC pain and hypertension (esp.) chronic conditions. A 10 microm concn.
CC of the peptide produced about 50% inhibition at a Substance P concn. of
CC 7.5-20 nanom.
XX
SQ Sequence 11 AA;

Query Match 78.7%; Score 48; DB 4; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 11
1 :|||||1111
1 rpkpqgfwlm 11

DB 1 rpkpqgfwlm 11

RESULT 164
AAP80317
ID AAP80317 standard; protein; 11 AA.
XX
AC AAP80317;
XX
XX 14-SEP-1990 (first entry)
DT
XX
DE Sequence of neuropeptide antagonist E which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist E.
XX
OS Swiss 3T3 cells.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /label=OTHER
FT /note= "DPro"
FT Misc-difference 7 /label=OTHER
FT /note= "DTrp"
FT Misc-difference 9 /label=OTHER
FT Misc-difference 11 /label=OTHER
FT /note= "Met-NH2"
XX
PN W08807551-A.
XX
PD 06-OCT-1988.

PF 31-MAR-1988; 88WO-GB00255.
XX
XX 25-NOV-1987; 87GB-0027638.
XX
XX (IMCR) IMPERIAL CANCER RES.
XX
XX Rosengurt E, Zachary I, Woll P;
XX
XX WPI; 1988-292842/41.
XX
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells; and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P. It is also known as
CC [D-Pro²] spantide. Antagonist B is also commercially available structural
CC variant of substance P known as [D-Phe⁵] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
||| ||| |
Db 1 rpkpqgfwlm 11

RESULT 165
AAR21966
ID AAR21966 standard; Peptide: 11 AA.
XX
XX AAR21966;
XX
XX 25-JUN-1992 (first entry)
XX
XX Cyclic substance P (D Cys 5, hCys 10).
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX
XX key Location/Qualifiers
FH Disulfide-bond 5..10
FT Misc-difference 10
FT /Label= homocysteine
FT Modified-site 5 /note="D form"
FT
XX
XX W09202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.

PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.
XX
XX
XX Claim 11; Page 22; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a D Cys
CC residue substituted at position 5 and a homoCys at position 9,
CC with a disulphide bond formed between them making the peptide
CC cyclic. The peptide was synthesised by standard solid phase
CC synthesis. Neuronal accumulation of beta-amyloid may be treated
CC by administration of tachykinin agonists. The peptide can reduce
CC the neurotoxic effects of a beta-amyloid related polypeptide on
CC cultured neurons. The peptide and its analogues are useful for
CC controlling diseases characterised by beta amyloid accumulation
CC in the brain such as Alzheimer's disease and Down's syndrome.
XX
XX See also AAR21932-75.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
||| ||| |
Db 1 rpkpcqffgxm 11

RESULT 166
AAR21967
ID AAR21967 standard; Peptide: 11 AA.
XX
XX AAR21967;
XX
XX 25-JUN-1992 (first entry)
XX
XX Cyclic substance P (Cys 5, 11).
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX
XX key Location/Qualifiers
FH Disulfide-bond 5..11
XX
XX W09202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.

XX Claim 11; Page 22; 35pp; English.
 PS
 XX
 CC The peptide is the tachykinin agonist substance P with Cys
 CC residues substituted at positions 5 and 11, with a disulphide bond
 CC formed between them, making the peptide cyclic. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal accumu-
 CC lation of beta-amyloid may be treated by administration of tachykinin
 CC agonists. The peptide can reduce the neurotoxic effects of a beta-
 CC amyloid related polypeptide on cultured neurons. The peptide and
 CC its analogues are useful for controlling diseases characterised by
 CC beta amyloid accumulation in the brain such as Alzheimer's disease
 CC and Down's syndrome.
 CC See also AAR21932-75.
 XX
 SQ Sequence 11 AA;

 QY Query Match 78.7%; Score 48; DB 13; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.049; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1;
 DB 1 RPKPQGFGL 10
 1 RPKPQGFGL 10
 1 RPKPQGFGL 10
 RESULT 167
 AAR21960
 ID AAR21960 standard; Peptide; 11 AA.
 XX
 AC AAR21960;
 XX
 DT 25-JUN-1992 (first entry)
 XX
 DE Cyclic substance P [Hcys 5,9].
 XX
 KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /label= OTHER
 FT /note= "OTHER = homocysteine"
 FT Misc-difference 9 /label= OTHER
 FT /note= "OTHER = homocysteine"
 XX
 PN WO9202248-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 29-JUL-1991; 91WO-US05323.
 XX
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MED CENT.
 XX
 PI Yankner BA.
 XX
 DR WPI; 1992-079804/10.
 XX
 PT Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Down's syndrome, etc.
 XX
 PS Claim 11; Page 22; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist, substance P with
 CC homocysteine substituted at positions 5 and 9, with a disulphide
 CC bond formed between them making the peptide cyclic. The

CC peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX
 SQ Sequence 11 AA;

 QY Query Match 78.7%; Score 48; DB 13; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.049; 2; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 2;
 DB 1 RPKPKGFGLM 11
 1 RPKPKGFGLM 11
 1 RPKPKGFGLM 11
 RESULT 168
 AAW50969
 ID AAW50969 standard; peptide; 11 AA.
 XX
 AC AAW50969;
 XX
 DT 31-JUL-1998 (first entry)
 XX
 DE Substance P analogue, [D-Pro2,D-Trp7,9].
 XX
 KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
 KW Substance P; cancer; inhibition; growth hormone releasing factor;
 KW spantide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 XX
 PN EP835662-A2.
 XX
 PD 15-APR-1998.
 XX
 PF 11-DEC-1996; 96EP-0309012.
 XX
 PR 08-OCT-1996; 96US-0727679.
 PR 16-AUG-1996; 96IN-0001822.
 XX
 PA (NAIM-) NAT INST IMMUNOLOGY.
 XX
 PI Jaggi M, Mukherjee R;
 XX
 DR WPI; 1998-208959/19.
 XX
 PT Composition containing analogues of vasoactive intestinal peptide,
 PT somatostatin - bombesin and substance P, for treatment of tumours
 PT and for inhibiting over-expression of these peptide(s)
 XX
 PS Disclosure; Page 13; 49pp; English.
 XX
 CC The invention relates to a new composition which comprises: (i) the
 CC somatostatin analogue SOM2 AGCKNFRDWRPSDC (3-14 disulphide bridge),
 CC and (ii) at least 4 of the peptides: antagonist of vasoactive
 CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
 CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin

CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 19; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPOFFGLM 11
||| | | | | |
Db 1 rpkpqwfwlm 11

RESULT 169
AAW92683
ID AAW92683 standard; peptide; 11 AA.

AC AAW92683;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #29.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 5 /note= "Residue is homocysteine"

FT Modified-site 9 /note= "Residue is homocysteine"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

PI WPI: 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX

PS Disclosure; Column 23-24; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 RPKPOFFGLM 11
||| | | | | |
Db 1 rpkpxqffxlm 11

RESULT 170
AAW92685
ID AAW92685 standard; peptide; 11 AA.

AC AAW92685;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #31.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.

XX US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

PI WPI: 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX

SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 20; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
||| | | | | |
Db 1 rpkpcqffgl 10

RESULT 171

AAW92656
 ID AAW92656 standard; peptide; 11 AA.
 XX
 AC AAW92656;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #2.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 XX
 PN US5876948-A.
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PI Yankner BA;
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 11-12; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

Query Match 78.7%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.049;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 DB 1 rpkpqgfwlm 11

RESULT 172
 AAB98881
 ID AAB98881 standard; Peptide; 11 AA.
 XX
 AC AAB98881;
 XX
 DT 14-AUG-2001 (first entry)
 XX

DE Chimeric analgesic peptide #37.
 XX
 KW Opioid receptor binding; nociceptive receptor binding; analgesic;
 KW pain; chimeric peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /label= OTHER
 FT /note= "C-terminal amide"
 XX
 PN WO200130371-A2.
 PD 03-MAY-2001.
 XX
 PF 27-OCT-2000; 2000WO-US29789.
 XX
 PR 28-OCT-1999; 99US-0428692.
 XX
 PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 PI Carr DB, Lipkowski AW, Kream R, Misicka-Keslk A;
 DR WPI; 2001-397593/42.
 XX
 PT New chimeric peptides used for treating pain comprise opioid receptor
 PT binding group and nociceptive receptor binding group
 XX
 PS Claim 10; Page 16; 34pp; English.
 XX
 CC The present invention describes a number of chimeric peptides comprising
 CC an opioid receptor binding moiety and a nociceptive receptor binding
 CC moiety. These can be used as analgesics for the treatment of pain. Unlike
 CC opioid receptor based peptides alone, tolerance does not result from
 CC their long-term use. The present sequence is one of the peptides of the
 CC invention.
 XX
 SQ Sequence 11 AA;

Query Match 78.7%; Score 48; DB 22; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.049;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 DB 1 rpkpqgfwlm 11

RESULT 173
 AAB91413
 ID AAB91413 standard; Peptide; 11 AA.
 XX
 AC AAB91413;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Tachykinins peptide SEQ ID NO:589.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyI; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 XX
 DT Synthetic.
 XX

XX	PN	WO200069900-A2.
XX	PD	23-NOV-2000.
XX	PF	17-MAY-2000; 2000WO-US13576.
XX	PR	17-MAY-1999; 99US-0134406.
XX	PR	10-SEP-1999; 99US-0153406.
XX	PR	15-OCT-1999; 99US-0159783.
XX	PA	(CONUS-) CONJUCHEM INC.
XX	PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX	DR	WPI; 2001-112059/12.
PT	PT	Modifying and attaching therapeutic peptides to albumin prevents
PT	PT	peptidase degradation, useful for increasing length of in vivo activity
PT	PT	-
XX	XX	Disclosure: Page 392; 733pp; English.
CC	CC	The present invention describes a modified therapeutic peptide (I)
CC	CC	comprising a therapeutically active amino acid region (III) and a
CC	CC	reactive group (II) (e.g. succinimidyI and maleimido groups) attached to
CC	CC	a less therapeutically active amino acid region (IV), which covalently
CC	CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	CC	peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC	CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	CC	factors and neurotransmitters, to protect them from peptidase activity
CC	CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	CC	peptides are not suitable as drug candidates as they require frequent
CC	CC	administration due to rapid degradation by peptidases in the body.
CC	CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	CC	reduces the action of peptidases to increase length of activity (half
CC	CC	life) and specificity as bonding to large molecules decreases
CC	CC	intracellular uptake and interference with physiological processes.
CC	CC	AA990829 to AA92441 represent peptides which can be used in the
CC	CC	exemplification of the present invention.
SO	SO	Sequence 11 AA:
OY	OY	1 RPKPOQFFGLM 11
Db	Db	111111111111
		1 rpKpqgwfvlm 11
RESULT 174		
AA98882		
AB98882		standard; Peptide: 12 AA.
AA98882:		
14-AUG-2001		(first entry)
Chimeric analgesic peptide #38.		
Opioid receptor binding; nociceptive receptor binding; analgesic;		
pain; chimeric peptide.		
Synthetic.		
Key		Location/Qualifiers
Misc-difference 2		/note= "D-form residue"
Misc-difference 7		
Misc-difference 9		/note= "D-form residue"
Misc-difference 9		

FT		/note= "D-form residue"
FT	Modified-site 12	/label= OTHER
FT		/note= "C-terminal amide"
XX		
XX	WO200130371-A2.	
XX		
XX	03-MAY-2001.	
XX		
PE	27-OCT-2000; 2000WO-US29789.	
XX		
PR	28-OCT-1999; 99US-0428692.	
PA	(NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.	
PI	Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;	
XX		
DR	WPI: 2001-397593/42.	
XX		
PT	New chimeric peptides used for treating pain comprise opioid receptor binding group and nociceptive receptor binding group	-
XX		
PS	Claim 10; Page 16; 34pp: English.	
XX		
CC	The present invention describes a number of chimeric peptides comprising an opioid receptor binding moiety and a nociceptive receptor binding moiety. These can be used as analgesics for the treatment of pain. Unlike opiolept, receptor based peptides alone, tolerance does not result from their long-term use. The present sequence is one of the peptides of the invention.	
CC		
CC		
SQ	Sequence 12 AA:	
	Query Match	78.7%; Score 48; DB 22; Length 12;
	Best Local Similarity	81.8%; Pred. No. 0.054;
	Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	1 RPKPOQFFGLM 11	
	:	
DB	1 rpkpqgfwlm 11	
RESULT 175		
AAB06260		
ID	AAB06260 standard; peptide; 11 AA.	
XX		
AC	AAB06260;	
XX		
DT	16-OCT-2000 (first entry)	
XX		
DE	Substance P.	
XX		
XX	Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; saporin; SAP; analgesic; anti-inflammatory; neuoprotective; anti-asthmatic;	
KW	anti-allergic; dermatological; anti-ulcer; tranquilliser;	
KW	immunosuppressive; anti-migraine; cyrostatic; substance P antagonist;	
KW	cyclooxic; ribosome inactivator; prostaglandin antagonist; cancer;	
KW	respiratory disease; asthma; allergic rhinitis; ophthalmic disease;	
KW	connectivitis; allergic dermatitis; psoriasis; ulcerative colitis;	
KW	Croh'n's disease; gastrointestinal disorder; anxiety; psychosis;	
KW	rheumatoid arthritis; carcinoma; lupus erythematosus connectivitis.	
XX		
OS	Unidentified.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	11
FT		/note= "C-terminal amide"
XX		
PN	US6063758-A.	
XX		
PD	16-MAY-2000.	
XX		

PF 09-JUL-1997; 97US-0890157.
XX
XX 09-JUL-1997; 97US-0890157.
PR (ADTA-) ADVANCED TARGETING SYSTEMS INC.
PA
XX
XX
PI Lappi DA, Wiley RG;
XX
DR WPI: 2000-430049/37.
XX
XX New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PR pain and treating disorders associated with neurokinin-1 receptor
XX
XX
PS Disclosure: Column 14; 21pp; English.
XX
XX The present sequence is substance P (SP), which binds to the neurokinin-1
CC receptor (NK-1R). SP is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce SP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.
XX
XX Sequence 11 AA:
SQ

Query Match 77.0%; Score 47; DB 21; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGSLM 11
DB 1 rpkpwffgflm 11

RESULT 176
AAW92711
ID AAW92711 standard; peptide; 8 AA.
XX
AC AAW92711;
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #57.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX
XX 29-JUL-1991; 91US-0737371.
PR
XX
XX 27-JUL-1990; 90US-0539173.
PR
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI

XX
DR WPI: 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX
PS Disclosure: Column 35-36; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 8 AA:
SQ

Query Match 75.4%; Score 46; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQPF 8
DB 1 rpkpqpf 8

RESULT 177
AAB91410
ID AAB91410 standard; peptide; 10 AA.
XX
XX AAB91410;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Tachykinins peptide SEQ ID NO:586.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR
XX
XX 10-SEP-1999; 99US-0153406.
PR
XX
XX 15-OCT-1999; 99US-0159783.
PR
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 391; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

SO Sequence 10 AA;

Query Match 75.4%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFF 8
|||||
Db 1 rpkpqgff 8

RESULT 178

AAB91422
ID AAB91422 standard; Peptide: 10 AA.

AC AAB91422;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:598.

KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

PT WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PS Disclosure: Page 395; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity.

CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

SO Sequence 10 AA;

Query Match 75.4%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFF 8
|||||
Db 1 rpkpqgff 8

RESULT 179

AAB91432
ID AAB91432 standard; Peptide: 10 AA.

AC AAB91432;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:608.

KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

PT WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PS Disclosure: Page 398; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

Query Match 75.4%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
| | | | | | | |
Db 1 rpkpqgff 8

RESULT 180

AAB06257

ID AAB06257 standard; peptide; 17 AA.

AC AAB06257;

DT 16-OCT-2000 (first entry)

DE Substance P analogue #1.

XX Substances P; SP; neurokinin-1 receptor; NK-1R; nociception; SSP-SAP;
KW Saporin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquilliser; immunosuppressive; anti-migraine; cyostatic;
KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 17 /note="linked to SarlMet(O2)-amide"

FT US6063758-A.

PN 16-MAY-2000.

PD 09-JUL-1997; 97US-0890157.

PR 09-JUL-1997; 97US-0890157.

PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.

XX Lappi DA, Wiley RG;

XX WPI; 2000-430049/37.

PT New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor
XX Claim 1; Column 2; 21pp; English.

XX The present sequence is an analogue of substance P (SP). SP, which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce SSP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these

CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.

XX Sequence 17 AA;

Query Match 75.4%; Score 46; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
| | | | | | | |
Db 10 rpkpqgff 17

RESULT 181

AAV06939

ID AAV06939 standard; peptide; 10 AA.

AC AAV06939;

DT 02-JUL-1999 (first entry)

DE Substance P from Bradykinin.

XX Peptide purification; hexylene glycol; biopharmaceutical; bradykinin;
KW protein separation; reversed-phase liquid chromatography.

XX Synthetic.

OS WO9921889-A1.

PN 06-MAY-1999.

PD 08-OCT-1998; 98WO-US21238.

PR 24-OCT-1997; 97US-0957760.

PA (GETH) GENENTECH INC.

XX Fahrner RL, Reifsnnyder D;

XX WPI; 1999-302984/25.

PT Purification of molecules, e.g. peptides

XX Example 2; Page 26; 47pp; English.

XX The invention relates to a process for purifying a molecule selected
CC from a peptide, a polypeptide, and a biologically active non-peptidyl
CC compound. The process comprises the elution of the molecule from the
CC column with a buffer containing hexylene glycol. The method is
CC specifically used for purifying biopharmaceuticals. While ethanol,
CC methanol, isopropanol, and, in particular, acetonitrile, used in prior
CC art purification, often provide good protein separations using reversed
CC phase liquid chromatography, they are flammable solvents, and using them
CC at large scale requires expensive non-flammable-capable equipment and
CC facilities. Further, acetonitrile is a denaturant and is toxic to the
CC environment. The new method purifies molecules by reversed-phase liquid
CC chromatography using the non-flammable eluent hexylene glycol rather
CC than a flammable eluent.

XX Sequence 10 AA;

Query Match 74.6%; Score 45.5; DB 20; Length 10;

Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 rpkp-qffglm 10

RESULT 182

AAG64746 standard; peptide: 10 AA.

AAG64746;

25-SEP-2001 (first entry)

Substance P amino acid sequence used in reversed-phase chromatography.

Protein purification; hexylene glycol; reversed-phase chromatography;

Insulin-like growth factor-I; IGF-I; thrombopoietin; hormone;

substance P.

Unidentified.

US6265542-B1.

24-JUL-2001.

08-OCT-1998; 98US-0168548.

24-OCT-1997; 97US-0063119.

(GENH) GENENTECH INC.

Fahrner RL, Relfnyder D;

WPI: 2001-463942/50.

Purifying polypeptides, e.g. insulin-like growth factor, by

reversed-phase liquid chromatography using hexylene glycol as eluate -

Example 2; Column 21-22; 27pp; English.

This invention relates to a process for purifying a polypeptide. The process comprises loading a mixture containing the polypeptide onto a reversed-phase liquid chromatography column and eluting the polypeptide from the column with a buffer containing hexylene glycol. The process is used for purifying a peptide from hydrophobic peptides, where the peptide to be purified is e.g. a growth factor (especially insulin-like growth factor-I IGF-I), thrombopoietin, a hormone, a chicken egg protein, a CC peptide of between 5 and 25 amino acids, an antibody and/or a hormone binding protein. The present sequence represents a peptide termed substance P which is used in an example illustrating the use of hexylene glycol as a reversed-phase eluent.

Sequence 10 AA:

Query Match 74.6%; Score 45.5; DB 22; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 rpkp-qffglm 10

RESULT 183

AAP40479 standard; peptide: 11 AA.

AAP40479;
XX

DT 27-NOV-1991 (first entry)

Substance P analogue.

Substance P; analogue; antiinflammatory agent; analgesic.

US4481139-A.

06-NOV-1984.

13-APR-1983; 83US-0484646.

13-APR-1983; 83US-0484646.

(UYTE-) UNIVERSITY OF TEXAS SYSTEM.

Folkers K, Ji-cheng X;

WPI: 1984-294258/47.

Peptide analogues of substance P - useful as antagonists, e.g. as

antiinflammatory agents and analgesics.

Claim 1; page 5; 5pp; English.

The peptide is a D-Arg1, D-Trp7, D-Trp9, Leu11 analogue of substance

P. The peptide is a substance P antagonist with higher activity than

known substance P analogues. It may be used as a biological

research tool, ophthalmological antiinflammatory agent and analgesic.

Sequence 11 AA:

OY 1 RPKPOQFFGLM 11
|||||
Db 1 rpkpqwfwll 11

RESULT 184

AAP80313 standard; protein: 11 AA.

AAP80313;

14-SEP-1990 (first entry)

Sequence of neuropeptide antagonist A which binds with polypeptide

receptor for bombesin type polypeptides.

Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;

cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;

antagonist A.

Swiss 3T3 cells.

Key Location/Qualifiers

Misc-difference 1 /label-OTHER

Misc-difference 2 /note="DArg"

Misc-difference 7 /label-OTHER

Misc-difference 9 /note="DTrp"

Misc-difference 11 /note="Dtrp"

```
FT FT /label=OTHER
FT FT /note="Leu-NH2"
PN W08807551-A.
XX
XX
XX 06-OCT-1988.
XX
XX 31-MAR-1988; 88WO-GB00255.
XX
XX 25-NOV-1987; 87GB-0027638.
XX
XX (IMCR ) IMPERIAL CANCER RES.
XX
XX Rosengurt E, Zachary I, Woll P;
XX WPI; 1988-292842/41.
XX
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
XX is isolated from surface of Swiss 3T3 cells, and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
XX cells which binds selectively with polypeptides of the bombesin type and
XX binds with antagonist A and antagonist D. Antagonist A is a
XX commercially available structural variant of substance P, known as
XX [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
XX [D-Pro2] spantide. Antagonist B is also commercially available structural
XX variant of substance P, known as [D-Phe5] spantide. Substance P is an
XX 11-mer neuropeptide, of interest in studies in pain transmission. Ten
XX substance P antagonists (see AAP80313-80322) were tested for their
XX ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
XX of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
XX potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
XX potent than either A or D. Spantide (B) had no antagonist activity even
XX at 100 uM. Polypeptide antagonists A and D and novel variants are useful
XX for diagnosis and therapy, esp. of cancers where uncontrolled cell
XX growth is associated with disorders of proteins of the bombesin family.
XX
XX Sequence 11 AA:
SQ
Query Match 73.8%; Score 45; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKQOQFGILM 11
DB 1 rpkpqgfwll 11
RESULT 185
AAP80314
ID AAP80314 standard; protein; 11 AA.
XX
XX AAP80314;
AC
XX
XX 14-SEP-1990 (first entry)
XX
XX Sequence of neuropeptide antagonist B which binds with polypeptide
XX receptor for bombesin type polypeptides.
DE
XX Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
XX cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX antagonist B.
XX
XX Swiss 3T3 cells.
XX
XX Key Location/Qualifiers
XX Misc-difference 1
XX FT /label=OTHER
XX FT /note="DArg"
```

```
FT FT Misc-difference 7
FT FT /label=OTHER
FT FT /note="DTrp"
FT FT Misc-difference 1
FT FT /label=OTHER
FT FT /note="DTrp"
FT FT Misc-difference 14
FT FT /label=OTHER
FT FT /note="Leu-NH2"
PN W08807551-A.
XX
XX
XX 06-OCT-1988.
XX
XX 31-MAR-1988; 88WO-GB00255.
XX
XX 25-NOV-1987; 87GB-0027638.
XX
XX (IMCR ) IMPERIAL CANCER RES.
XX
XX Rosengurt E, Zachary I, Woll P;
XX WPI; 1988-292842/41.
XX
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
XX is isolated from surface of Swiss 3T3 cells, and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
XX cells which binds selectively with polypeptides of the bombesin type and
XX binds with antagonist A and antagonist D. Antagonist A is a
XX commercially available structural variant of substance P, known as
XX [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
XX [D-Pro2] spantide. Antagonist B is also commercially available structural
XX variant of substance P, known as [D-Phe5] spantide. Substance P is an
XX 11-mer neuropeptide, of interest in studies in pain transmission. Ten
XX substance P antagonists (see AAP80313-80322) were tested for their
XX ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
XX of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
XX potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
XX potent than either A or D. Spantide (B) had no antagonist activity even
XX at 100 uM. Polypeptide antagonists A and D and novel variants are useful
XX for diagnosis and therapy, esp. of cancers where uncontrolled cell
XX growth is associated with disorders of proteins of the bombesin family.
XX
XX Sequence 11 AA:
SQ
Query Match 73.8%; Score 45; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKQOQFGILM 11
DB 1 rpkpqgfwll 11
RESULT 186
AAP805856
ID AAP805856 standard; protein; 11 AA.
XX
XX AAP805856;
AC
XX
XX 07-SEP-1990 (first entry)
XX
XX D-arginine 1, D-proline 2, D-tryptophan 7,9, Leucine 11,
XX -substance P angiotensin antagonist.
XX
XX Angiotensin; ectopic hormone; mas oncogene; cancer;
XX neuroblastoma; neuroendocrine.
XX
```

```

OS Synthetic.
XX
FH Key
FT Modified-site 1 Location/Qualifiers
FT Modified-site 2 /label=Dextrorotatory form.
FT Modified-site 7 /label=Dextrorotatory form.
FT Modified-site 7 /label=Dextrorotatory form.
FT Modified-site 9 /label=Dextrorotatory form.
FT Modified-site 9 /label=Dextrorotatory form.
FT
FT
XX WO9003181-A.
XX
XX
XX 05-APR-1990.
XX
XX 22-SEP-1989; 89WO-0001121.
XX
XX 24-SEP-1988; 88GB-0022483.
XX
XX (MEDI-) MED RES COUNCIL.
XX
XX Hanley MR, Goedert M;
XX
XX WPI; 1990-132106/17.
XX
XX Use of substances which block the activity of angiotensin -
PT for the treatment or prevention of tumour development or ectopic
PT hormone prodn.
XX
XX Claim 3; Page 19; 23pp; English.
XX
XX Peptida blocks biological activity of angiotensin and is active
CC against the mas oncogene, retarding tumour growth, esp
CC neuroendocrine and neuroblastoma tumours.
XX
XX Sequence 11 AA;
XX
Query Match 73.8%; Score 45; DB 11; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOQFGLM 11
DB 1 rpkpqgfwll 11

```

RESULT 187

AAR1144

ID AAR1144 standard; Protein; 11 AA.

XX

AC AAR1144;

XX

DT 21-MAY-1991 (first entry)

XX

DE Substance P analogue.

XX

KW Anti-proliferation agent; neurogenetic inflammation; fibroblasts;

KW agonist.

XX

OS Synthetic.

XX

FH Key

FT Modified-site 1 Location/Qualifiers

FT Modified-site 7 /label=D-Arg

FT Modified-site 7 /label=D-Trp

FT Modified-site 9 /label=D-Trp

FT Modified-site 9 /label=D-Trp

FT Modified-site 9.10 /label= non-peptide bond

FT /note= "Trp-L[CH2NH]-Trp"

```

FT Modified-site 11
FT /label= Nle
XX
XX WO9102745-A.
XX
XX 07-MAR-1991.
XX
XX 16-AUG-1990; 90WO-US04633.
XX
XX 16-AUG-1989; 89US-0394727.
XX
XX (TULA ) TULANE E FOUND ADMINISTRATOR.
XX
XX COY DH, Moreau JP;
XX
XX WPI; 1991-087240/12.
XX
XX Modified linear peptide analogue of natural substance P - acts as
PT competitive inhibitor of substance P and is used for treating
PT neuro genetic inflammation and as anti-proliferative agent.
XX
XX Claim 11; Page 34; 40pp; English.
XX
XX The peptide has a non-peptide bond introduced between Trp9 and
CC CC Leu10. This may alternatively be positioned between Leu10 and
CC CC Nle11. For prepn., a benzhydrylamine resin was coupled to Boc-Leu.
CC Boc-Leu aldehyde was dissolved in 5 ml DMF and added to the resin
CC Trp salt suspension followed by addn. of NaCNBH3 and stirring for
CC one hour. The remaining amino acids were then coupled successively.
CC In tests the peptide inhibited P-stimulated amylase release from
CC pancreatic acini.
CC See also AAR1143.
XX
XX Sequence 11 AA;
XX
Query Match 73.8%; Score 45; DB 12; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOQFGLM 11
DB 1 rpkpqgfwll 11

```

RESULT 188

AAR21968

ID AAR21968 standard; Peptide; 11 AA.

XX

AC AAR21968;

XX

DT 25-JUN-1992 (first entry)

XX

DE Cyclic substance P [D-Cys 5, Cys 8].

XX

KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

KW syndrome; hereditary cerebral haemorrhage.

XX

OS Synthetic.

XX

FH Key

FT Disulfide-bond 5.8 Location/Qualifiers

FT Modified-site 5 \note="D form"

XX

XX WO9202248-A.

XX

XX 20-FEB-1992.

XX

XX 29-JUL-1991; 91WO-US05323.

XX

XX 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D Cys
CC residue substituted at position 5 and a Cys at position 8, with
CC a disulphide bond formed between them, making the peptide cyclic.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
CC
SQ Sequence 11 AA;
XX
OY 1 RPKPOQFGIM 11
DB 1 rpkpcqcfglm 11
XX
OY 1 RPKPOQFGIM 11
DB 1 rpkpcqcfglm 11
XX
RESULT 189
AAR21969
ID AAR21969 standard; Peptide; 11 AA.
XX
AC AAR21969;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [D-Cys 5, Cys 7].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 5..7
FT Modified-site /note="D form"
XX
PN W09202248-A.
XX
PD 20-FEB-1992.
XX
PE 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D Cys
CC residue substituted at position 5 and a Cys at position 7, with
CC a disulphide bond formed between them, making the peptide cyclic.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
CC
SQ Sequence 11 AA;
XX
OY 1 RPKPOQFGIM 11
DB 1 rpkpcqcfglm 11
XX
OY 1 RPKPOQFGIM 11
DB 1 rpkpcqcfglm 11
XX
RESULT 190
AAR21970
ID AAR21970 standard; Peptide; 11 AA.
XX
AC AAR21970;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [D/L-Cys 3, Cys 6].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 3..6
FT Modified-site /note="D or L form"
XX
PN W09202248-A.
XX
PD 20-FEB-1992.
XX
PE 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D/L Cys
CC residue substituted at position 3 and a Cys at position 6, with
CC a disulphide bond formed between them, making the peptide cyclic.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-

CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA:

Query Match 73.8%; Score 45; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
1111111111
Db 1 rpkpqoffglm 11

RESULT 191

AAM50966
ID AAM50966 standard; peptide; 11 AA.

XX AAM50966;

DT 31-JUL-1998 (first entry)

DE Substance P analogue, spantide I.

XX Vasoactive intestinal peptide; VIP; antagonist: somatostatin; bombesin;

KW Substance P; cancer; inhibition; growth hormone releasing factor;

XX Spantide.

OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 1 /note= "D-form residue"

FT MISC-difference 7 /note= "D-form residue"

FT MISC-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

PN EP835662-A2.

PD 15-APR-1998.

PF 11-DEC-1996; 96EP-0309012.

PR 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

PA (NAIM-) NAT INST IMMUNOLOGY.

PI Jaggi M, Mukherjee R;

DR WPI; 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,

PT somatostatin - bombesin and substance P, for treatment of tumours

PT and for inhibiting over-expression of these peptide(s)

XX Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 ACCKNPFdWKTPSdc (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SPI). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or

CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue, spantide I.
XX
SQ Sequence 11 AA:

Query Match 73.8%; Score 45; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
1111111111
Db 1 rpkpqoffglm 11

RESULT 192

AAM50958
ID AAM50958 standard; peptide; 11 AA.

XX AAM50958;

DT 31-JUL-1998 (first entry)

DE Substance P analogue, [D-Arg1,D-Pro2,D-Trp7,9,Leu11]-Substance P.

XX Vasoactive intestinal peptide; VIP; antagonist: somatostatin; bombesin;

KW Substance P; cancer; inhibition; growth hormone releasing factor.

XX Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 1 /note= "D-form residue"

FT MISC-difference 2 /note= "D-form residue"

FT MISC-difference 7 /note= "D-form residue"

FT MISC-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

PN EP835662-A2.

PD 15-APR-1998.

PF 11-DEC-1996; 96EP-0309012.

PR 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

PA (NAIM-) NAT INST IMMUNOLOGY.

PI Jaggi M, Mukherjee R;

DR WPI; 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,

PT somatostatin - bombesin and substance P, for treatment of tumours

PT and for inhibiting over-expression of these peptide(s)

XX Disclosure; Page 12; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 ACCKNPFdWKTPSdc (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SPI). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or

CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 11 AA;

Query Match 73.8%; Score 45; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||||:| |
Db 1 rpkpgqgfwll 11

RESULT 193

AAW92687
ID AAW92687 standard; peptide; 11 AA.

AC AAW92687;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #33.

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 5 /note= "D-form residue"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their
effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 25-26; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 73.8%; Score 45; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||||:| |
Db 1 rpkpgqgfwll 11

RESULT 194

AAW92688
ID AAW92688 standard; peptide; 11 AA.

AC AAW92688;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #34.

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 5 /note= "D-form residue"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their
effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 25-26; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 73.8%; Score 45; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||||:| |
Db 1 rpkpgqgfwll 11

RESULT 195	
AAW92689	
ID	AAW92689 standard: peptide; 11 AA.
XX	
AC	AAW92689;
XX	
DT	30-APR-1999 (first entry)
XX	
DE	Human tachykinin agonist beta-amyloid peptide fragment #35.
XX	
KM	Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment;
KW	Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX	hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
OS	
XX	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 3
FT	/note= "D-form residue"
XX	
PM	US576948-A.
PD	
XX	02-MAR-1999.
PF	
XX	27-JUL-1991; 91US-0737371.
XX	
PR	29-JUL-1991; 91US-0737371.
PR	27-JUL-1990; 90US-0559173.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX	
PI	Yankner BA;
DR	
XX	WPI: 1999-189630/16.
XX	
PT	Screening for neurotoxin inhibitors - by testing compounds for their
PT	effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX	
PS	Disclosure: Column 25-26; 28pp; English.
XX	
CC	This invention describes a method for screening compounds for inhibiting
CC	a neurotoxin. The method involves incubating tachykinin agonists with
CC	neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC	used for identifying compounds for treating diseases characterised by an
CC	undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC	Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC	with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC	haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC	beta-amyloid peptide fragments.
XX	
XX	
SO	Sequence 11 AA;
Query Match	73.8%; Score 45; DB 20; Length 11;
Best Local Similarity	81.8%; Pred. No. 0.16;
Matches 9; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1 RPKPQGFGLM 11
Db	1 fpqpcqffglm 11
RESULT 196	
AAW92690	
ID	AAW92690 standard: peptide; 11 AA.
XX	
AC	AAW92690;
XX	
DT	30-APR-1999 (first entry)
XX	
DE	Human tachykinin agonist beta-amyloid peptide fragment #36.
XX	

KM	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM	Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM	hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX	
OS	Homo sapiens.
PN	US5876948-A.
XX	
PD	02-MAR-1999.
XX	
PF	27-JUL-1991; 91US-0737371.
XX	
PR	29-JUL-1991; 91US-0737371.
XX	
PR	27-JUL-1990; 90US-0559173.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX	
PI	Yankner BA;
XX	
DR	WPI: 1999-189630/16.
XX	
PT	Screening for neurotoxin inhibitors - by testing compounds for their
PT	effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX	
PS	Disclosure: Column 25-26; 28pp; English.
XX	
CC	This invention describes a method for screening compounds for inhibiting
CC	a neurotoxin. The method involves incubating tachykinin agonists with
CC	neuronal cells and a beta-amyloid peptide neurotoxin. The methods can
CC	be used for identifying compounds for treating diseases characterised by an
CC	undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC	Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC	with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC	haemorrhage. AAM92655-M92731 are tachykinin agonists derived from human
CC	beta-amyloid peptide fragments.
XX	
SO	Sequence 11 AA;
XX	
Query Match	73.8%; Score 45; DB 20; Length 11;
Best Local Similarity	81.8%; Pred. No. 0.16;
Matches 9; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1 RPKPOOFFGLM 11
Db	1 RPKPOOFFGLM 11
XX	
RESUIT 197	
AAM92657	
ID	AAM92657 standard; peptide; 11 AA.
XX	
AC	AAM92657;
XX	
DT	30-APR-1999 (first entry)
XX	
DE	Human tachykinin agonist beta-amyloid peptide fragment #3.
XX	
KM	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM	Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM	hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Misc-difference 1 Location/Qualifiers
FT	Misc-difference 7 /note= "D-form residue"
FT	Misc-difference 9 /note= "D-form residue"
FT	Misc-difference 9 /note= "D-form residue"
XX	
US5876948-A.	

XX 02-MAR-1999.
PD Best Local Similarity 72.7%; Score 45; DB 20; Length 11;
PT Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX 27-JUL-1991; 91US-0737371.
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Yankner BA;
XX WPI; 1999-189630/16.
DR Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX Disclosure; Column 11-12; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ

Query Match 73.8%; Score 45; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOOFFGLM 11
Db 1 rpkpqgfwl1 11

RESULT 198
AAB91434
ID AAB91434 standard; Peptide: 11 AA.
XX AAB91434;
AC 22-JUN-2001 (first entry)
XX DE Tachykinins peptide SEQ ID NO:610.
XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1, maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
PD 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Errin AM, Milner PG, Holmes DL, Thibaudau K;
PI WPI; 2001-112059/12.
XX

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT Disclosure; Page 398; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX Sequence 11 AA;
SQ

Query Match 73.8%; Score 45; DB 22; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOOFFGLM 11
Db 1 rpkpqgfwl1 11

RESULT 199
AAB50312
ID AAB50312 standard; peptide: 11 AA.
XX AAB50312;
AC 08-MAR-2001 (first entry)
XX DE Previn peptide #4.
XX KW Asian toad; antibacterial; Botulinum toxin inhibitor; BttxB;
KW previn; tetanus neurotoxin; butorfinin.
XX OS Bufo bufo gargarizans.
OS Synthetic.
XX WO200069891-A2.
XX 23-NOV-2000.
PD 15-MAY-2000; 2000WO-US13215.
XX 17-MAY-1999; 99US-0134446.
XX (USSA) US DEPT OF THE ARMY.
XX Gordon RK, Moorad DR, Doctor BP, Garcia GE;
PI WPI; 2001-025001/03.
XX Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins -
XX Claim 7; Page 29; 47pp; English.
XX The present sequence is a previn compound which inhibits the enzymatic

CC activity of BtxB and tetanus neurotoxins. Previns
 CC may be used to construct compounds such as butorinins.
 XX
 SO Sequence 11 AA:

Query Match 73.8%; Score 45; DB 22; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.16;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RPKPQDFEGLM 11
 1 1 1 1 1 1 1 1 1 1 1
 Db 1 rkpqdfeglm 11

RESULT 200

AAR28680
 ID AAR28680 standard; Protein; 24 AA.

XX
 AC AAR28680:

XX
 DF 22-MAR-1993 (first entry)

XX
 DE Galanin(1-12)-Pro-Spantide amide (C7).

XX
 KW Receptor; Substance P; insulin; growth hormone;

XX
 KW acetylcholine; dopamine; somatostatin; noradrenaline;

XX
 KW endocrinology; food intake; neurology; psychiatry;

XX
 KW Alzheimer-type senile dementia; schizophrenia;

XX
 OS Intestinal diseases.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

XX
 OS Synthetic.

CC to treat Alzheimer-type senile dementia, schizophrenia, intestinal
 CC diseases, and in analgesia. Dosage is 0.01-1000, pref. 0.1-1000
 CC microg/kg body wt.
 XX
 SO Sequence 24 AA:

Query Match 73.8%; Score 45; DB 13; Length 24;
 Best Local Similarity 72.7%; Pred. No. 0.34;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQDFEGLM 11
 1
 Db 14 rkpqdfeglm 11

Search completed: April 1, 2002, 16:18:20
 Job time: 51 sec

EP514361-A.
 19-NOV-1992.
 14-MAY-1992; 92EP-0850108.
 15-MAY-1991; 91SE-0001472.
 (ASTR) ASTRA AB.
 Ahren B, Bartfal T, Consolo S, Hoekfelt T, Land T;
 Langel U, Landskog S, Wiesenfeld-Hallin Z;
 WPI; 1992-384184/47.
 New galanin antagonist peptide(s) - used for treating
 Alzheimer's-type senile dementia, schizophrenia, analgesia and
 intestinal diseases
 PS Disclosure; Page 7; 21pp; English.
 CC The C-terminal of this peptide is amidated. MW= 2827; IC50= 0.2nM.
 CC The peptides given in AAR28679-90 are used to treat disorders in
 CC mammals caused by the function of galanin at its receptor. The
 CC peptides may be useful in the regulation of insulin release, growth
 CC hormone release, acetylcholine release, dopamine release, substance
 CC P release, somatostatin release and noradrenaline release. They are
 CC useful in endocrinology, food intake, neurology and psychiatry, and